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(71) Applicants (*for all designated States except US*): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US). MEDIMMUNE, INC. [US/US]; 35 West Watkins Mill Road, Gaithersburg, MD 20878 (US).

(72) Inventors; and
(75) Inventors/Applicants (*for US only*): CHOI, Gil, H. [KR/US]; 11429 Potomac Oaks Drive, Rockville, MD 20850 (US). ERWIN, Alice, L. [US/US]; 5101 Connecticut Avenue, N.W., Washington, DC 20008 (US). HANSON, Mark, S. [US/US]; 5962 Camelback Lane, Columbia, MD 21054 (US). LATHIGRA, Raju [IN/US]; 19051 Steeple Place, Germantown, MD 20874 (US).

(74) Agents: BROOKES, A., Anders et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 20850 (US).

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(54) Title: LYME DISEASE VACCINES

(57) Abstract

The present invention relates to novel vaccines for the prevention or attenuation of Lyme disease. The invention further relates to isolated nucleic acid molecules encoding antigenic polypeptides of *Borrelia burgdorferi*. Antigenic polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same. The invention additionally relates to diagnostic methods for detecting *Borrelia* gene expression.

Lyme Disease Vaccines

Field of the Invention

The present invention relates to novel vaccines for the prevention or attenuation of Lyme disease. The invention further relates to isolated nucleic acid molecules encoding antigenic polypeptides of *Borrelia burgdorferi*. Antigenic polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same. The invention additionally relates to diagnostic methods for detecting *Borrelia* gene expression.

Background of the Invention

Lyme disease (Steere, A.C., *Proc. Natl. Acad. Sci. USA 91*:2378-2383 (1991)), or Lyme borreliosis, is presently the most common human disease in the United States transmitted by an arthropod vector (Center for Disease Control, *Morbid. Mortal. Weekly Rep. 46(23)*:531-535 (1997)). Further, infection of house-hold pets, such as dogs, is a considerable problem.

While initial symptoms often include a rash at the infection point, Lyme disease is a multisystemic disorder that may include arthritic, carditic, and neurological manifestations. While antibiotics are currently used to treat active cases of Lyme disease, *B. burgdorferi* persists even after prolonged antibiotic treatment. Further, *B. burgdorferi* can persist for years in a mammalian host in the presence of an active immune response (Straubinger, R. *et al., J. Clin. Microbiol. 35*:111-116 (1997); Steere, A., *N. Engl. J. Med. 321*:586-596 (1989)).

Lyme disease is caused by the related tick-borne spirochetes classified as *Borrelia burgdorferi* sensu lato (including *B. burgdorferi* sensu stricto, *B. afzelii*, *B. garinii*). Although substantial progress has been made in the biochemical, ultrastructural, and genetic characterization of the organism, the spirochetal factors responsible for infectivity, immune evasion and disease pathogenesis remain largely obscure.

A number of antigenic *B. burgdorferi* cell surface proteins have been identified. These include the outer membrane surface proteins (Osp) OspA, OspB, OspC and OspD. OspA and OspB are encoded by tightly linked tandem genes which are transcribed as a single transcriptional unit (Brusca, J. *et al., J. Bacteriol. 173*:8004-8008 (1991)). The most-studied *B. burgdorferi* membrane protein is OspA, a lipoprotein antigen expressed by borreliae in resting ticks and the most abundant protein expressed *in vitro* by most borrelial isolates (Barbour, A.G., *et al., Infection & Immunity 41*:795-804 (1983); Howe, T.R., *et al., Science 227*:645 (1985)).

A number of different types of Lyme disease vaccines have been shown to induce immunological responses. Whole-cell *B. burgdorferi* vaccines, for example, have been shown to induce both immunological responses and protective immunity in several animal models (Reviewed in Wormser, G., *Clin. Infect. Dis. 21*:1267-1274 (1995)). Further, passive immunity has been demonstrated in both humans and other animals using *B. burgdorferi* specific antisera.

While whole-cell Lyme disease vaccines confer protective immunity in animal models, use of such vaccines presents the risk that responsive antibodies will produce an autoimmune response (Reviewed in Wormser, G., *supra*). This problem is at least partly the result of the production of *B. burgdorferi* specific antibodies which cross-react with hepatocytes and both muscle and nerve cells. *B. burgdorferi* heat shock proteins and the 41-kd flagellin subunit are believed to contain antigens which elicit production of these cross-reactive antibodies.

Single protein subunit vaccines for Lyme disease have also been tested. The cell surface proteins of *B. burgdorferi* are potential candidates for use in such vaccines and several have been shown to elicit protective immune responses in mammals (Probert, W. *et al., Vaccine 15*:15-19 (1997); Fikrig, E. *et al., Infect. Immun. 63*:1658-1662 (1995); Langerman S. *et al., Nature 372*:552-556 (1994); Fikrig, E. *et al., J. Immunol. 148*:2256-2260 (1992)). Experimental OspA vaccines, for example, have demonstrated efficacy in several animal models (Fikrig, E., *et al., Proc. Natl. Acad. Sci. USA 89*:5418-5421 (1992); Johnson, B.J., *et al., Vaccine 13*:1086-1094 (1996); Fikrig, E., *et al., Infect. Immun. 60*:657-661 (1992); Chang, Y.F., *et al., Infection & Immunity 63*:3543-3549 (1995)), and OspA vaccines for human use are under clinical evaluation (Keller, D., *et al., J. Am. Med. Assoc. 271*:1764-1768 (1994); Van Hoecke, C., *et al., Vaccine 14*:1620-1626 (1996)). Passive immunity is also conferred by antisera containing antibodies specific for the full-length OspA protein. Further, vaccination with plasmid DNA encoding OspA has been demonstrated to elicit protective immune responses in mice (Luke, C. *et al., J. Infect. Dis. 175*:91-97 (1997); Zhong, W. *et al., Eur. J. Immunol. 26*:2749-2757 (1996)).

Recent immunofluorescence assay observations indicate that during tick engorgement the expression of OspA by borreliae diminishes (deSilva, A.M., *et al., J. Exp. Med. 183*:271-275 (1996)) while expression of other proteins, exemplified by OspC, increases (Schwan, T.G., *et al., Proc. Natl. Acad. Sci. USA 92*:2909-2913 (1985)). By the time of transmission to hosts, spirochetes in the tick salivary glands express little or no OspA. This down-modulation of OspA appears to explain the difficulties in demonstrating immune responses to this antigen early in infection following tick bites (Kalish, R.A., *et al., Infect. Immun. 63*:2228-2235 (1995); Gern, L., *et al., J. Infect. Dis. 167*:971-975 (1993); Schiable, U.E., *et al., Immunol. Lett. 36*:219-226 (1993)) or following challenge with limiting doses of cultured borreliae (Schiable, U.E., *et al., Immunol. Lett. 36*:219-226 (1993); Barthold, S.W. and Bockenstedt, L.K., *Infect. Immun. 61*:4696-4702 (1993)).

Furthermore, OspA-specific antibodies are ineffective if administered after a borrelial challenge delivered by syringe (Schiable, U.E., *et al., Proc. Natl. Acad. Sci. USA 87*:3768-3772 (1990)) or tick bite (deSilva, A.M., *et al., J. Exp. Med. 183*:271-275 (1996)). To be efficacious,

OspA vaccines must elicit protective levels of antibody which are maintained throughout periods of tick exposure in order to block borrelia transmission from the arthropod vector.

Vaccines in current use against other pathogens include *in vivo*-expressed antigens which could boost anamnestic responses upon infection, potentiate the action of immune effector cells and complement, and inhibit key virulence mechanisms. OspC is both expressed during infection (Montgomery, R.R., *et al., J. Exp. Med. 183*:261-269 (1996)) and a target for protective immunity (Gilmore, R.D., *et al., Infect. Immun. 64*:2234-2239 (1996); Probert, W.S. and LeFebvre, R.B., *Infect. Immun. 62*:1920-1926 (1994); Preac-Mursic, V., *et al., Infection 20*:342-349 (1992)), but mice immunized with this protein were only protected against challenge with the homologous borrelial isolate (Probert, W.S., *et al., J. Infect. Dis. 175*:400-405 (1997)). Identification of *in vivo*-expressed, and broadly protective, antigens of *B. burgdorferi* has remained elusive.

Summary of the Invention

The present invention provides isolated nucleic acid molecules comprising polynucleotides encoding the *B. burgdorferi* peptides having the amino acid sequences shown in Table 1. Thus, one aspect of the invention provides isolated nucleic acid molecules comprising polynucleotides having a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding any of the amino acid sequences of the full-length polypeptides shown in Table 1; (b) a nucleotide sequence encoding any of the amino acid sequences of the full-length polypeptides shown in Table 1 but minus the N-terminal methionine residue, if present; (c) a nucleotide sequence encoding any of the amino acid sequences of the truncated polypeptides shown in Table 1; and (d) a nucleotide sequence complementary to any of the nucleotide sequences in (a), (b), or (c) above.

Further embodiments of the invention include isolated nucleic acid molecules that comprise a polynucleotide having a nucleotide sequence at least 90% identical, and more preferably at least 95%, 96%, 97%, 98% or 99% identical, to any of the nucleotide sequences in (a), (b), (c), or (d) above, or a polynucleotide which hybridizes under stringent hybridization conditions to a polynucleotide in (a), (b), (c), or (d) above. This polynucleotide which hybridizes does not hybridize under stringent hybridization conditions to a polynucleotide having a nucleotide sequence consisting of only A residues or of only T residues. Additional nucleic acid embodiments of the invention relate to isolated nucleic acid molecules comprising polynucleotides which encode the amino acid sequences of epitope-bearing portions of a *B. burgdorferi* polypeptide having an amino acid sequence in (a), (b), or (c) above.

The present invention also relates to recombinant vectors, which include the isolated nucleic acid molecules of the present invention, and to host cells containing the recombinant vectors, as well as to methods of making such vectors and host cells and for using these vectors for the production of *B. burgdorferi* polypeptides or peptides by recombinant techniques.

The invention further provides isolated *B. burgdorferi* polypeptides having an amino acid

sequence selected from the group consisting of: (a) an amino acid sequence of any of the full-length polypeptides shown in Table 1; (b) an amino acid sequence of any of the full-length polypeptides shown in Table 1 but minus the N-terminal methionine residue, if present; (c) an amino acid sequence of any of the truncated polypeptides shown in Table 1; and (d) an amino acid sequence of an epitope-bearing portion of any one of the polypeptides of (a), (b), or (c).

The polypeptides of the present invention also include polypeptides having an amino acid sequence with at least 70% similarity, and more preferably at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% similarity to those described in (a), (b), (c), or (d) above, as well as polypeptides having an amino acid sequence at least 70% identical, more preferably at least 75% identical, and still more preferably 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to those above; as well as isolated nucleic acid molecules encoding such polypeptides.

The present invention further provides a vaccine, preferably a multi-component vaccine comprising one or more of the *B. burgdorferi* polypeptides shown in Table 1, or fragments thereof, together with a pharmaceutically acceptable diluent, carrier, or excipient, wherein the *B. burgdorferi* polypeptide(s) are present in an amount effective to elicit an immune response to members of the *Borrelia* genus in an animal. The *B. burgdorferi* polypeptides of the present invention may further be combined with one or more immunogens of one or more other borrelial or non-borrelial organisms to produce a multi-component vaccine intended to elicit an immunological response against members of the *Borrelia* genus and, optionally, one or more non-borrelial organisms.

The vaccines of the present invention can be administered in a DNA form, *e.g.*, "naked" DNA, wherein the DNA encodes one or more borrelial polypeptides and, optionally, one or more polypeptides of a non-borrelial organism. The DNA encoding one or more polypeptides may be constructed such that these polypeptides are expressed fusion proteins.

The vaccines of the present invention may also be administered as a component of a genetically engineered organism. Thus, a genetically engineered organism which expresses one or more *B. burgdorferi* polypeptides may be administered to an animal. For example, such a genetically engineered organism may contain one or more *B. burgdorferi* polypeptides of the present invention intracellularly, on its cell surface, or in its periplasmic space. Further, such a genetically engineered organism may secrete one or more *B. burgdorferi* polypeptides.

The vaccines of the present invention may be co-administered to an animal with an immune system modulator (*e.g.*, CD86 and GM-CSF).

The invention also provides a method of inducing an immunological response in an animal to one or more members of the *Borrelia* genus, *e.g.*, *B. burgdorferi* sensu stricto, *B. afzelii*, and *B. garinii*, comprising administering to the animal a vaccine as described above.

The invention further provides a method of inducing a protective immune response in an animal, sufficient to prevent or attenuate an infection by members of the *Borrelia* genus, comprising administering to the animal a composition comprising one or more of the polypeptides shown in Table 1, or fragments thereof. Further, these polypeptides, or fragments thereof, may

be conjugated to another immunogen and/or administered in admixture with an adjuvant.

The invention further relates to antibodies elicited in an animal by the administration of one or more *B. burgdorferi* polypeptides of the present invention.

The invention also provides diagnostic methods for detecting the expression of genes of members of the *Borrelia* genus in an animal. One such method involves assaying for the expression of a gene encoding *Borrelia* peptides in a sample from an animal. This expression may be assayed either directly (*e.g.*, by assaying polypeptide levels using antibodies elicited in response to amino acid sequences shown in Table 1) or indirectly (*e.g.*, by assaying for antibodies having specificity for amino acid sequences shown in Table 1). An example of such a method involves the use of the polymerase chain reaction (PCR) to amplify and detect *Borrelia* nucleic acid sequences.

The present invention also relates to nucleic acid probes having all or part of a nucleotide sequence shown in Table 1 which are capable of hybridizing under stringent conditions to *Borrelia* nucleic acids. The invention further relates to a method of detecting one or more *Borrelia* nucleic acids in a biological sample obtained from an animal, said one or more nucleic acids encoding *Borrelia* polypeptides, comprising:

a) contacting the sample with one or more of the above-described nucleic acid probes, under conditions such that hybridization occurs, and

b) detecting hybridization of said one or more probes to the *Borrelia* nucleic acid present in the biological sample.

Detailed Description

The present invention relates to recombinant antigenic *B. burgdorferi* polypeptides and fragments thereof. The invention also relates to methods for using these polypeptides to produce immunological responses and to confer immunological protection to disease caused by members of the genus *Borrelia*. The invention further relates to nucleic acid sequences which encode antigenic *B. burgdorferi* polypeptides and to methods for detecting *Borrelia* nucleic acids and polypeptides in biological samples. The invention also relates to *Borrelia* specific antibodies and methods for detecting such antibodies produced in a host animal.

Definitions

The following definitions are provided to clarify the subject matter which the inventors consider to be the present invention.

As used herein, the phrase "pathogenic agent" means an agent which causes a disease state or affliction in an animal. Included within this definition, for examples, are bacteria, protozoans, fungi, viruses and metazoan parasites which either produce a disease state or render an animal infected with such an organism susceptible to a disease state (*e.g.*, a secondary infection). Further included are species and strains of the genus *Borrelia* which produce disease states in animals.

As used herein, the term "organism" means any living biological system, including viruses, regardless of whether it is a pathogenic agent.

As used herein, the term "*Borrelia*" means any species or strain of bacteria which is members of the genus *Borrelia*. Included within this definition are *Borrelia burgdorferi* sensu lato (including *B. burgdorferi* sensu stricto, *B. afzelii*, *B. garinii*), *B. andersonii*, *B. anserina*, *B. japonica*, *B. coriaceae*, and other members of the genus *Borrelia* regardless of whether they are known pathogenic agents.

As used herein, the phrase "one or more *B. burgdorferi* polypeptides of the present invention" means the amino acid sequence of one or more of the *B. burgdorferi* polypeptides disclosed in Table 1. These polypeptides may be expressed as fusion proteins wherein the *B. burgdorferi* polypeptides of the present invention are linked to additional amino acid sequences which may be of borrelial or non-borrelial origin. This phrase further includes fragments of the *B. burgdorferi* polypeptides of the present invention.

As used herein, the phrase "full-length amino acid sequence" and "full-length polypeptide" refer to an amino acid sequence or polypeptide encoded by a full-length open reading frame (ORF). An ORF may be defined as a nucleotide sequence bounded by stop codons which encodes a putative polypeptide. An ORF may also be defined as a nucleotide sequence within a stop codon bounded sequence which contains an initiation codon (*e.g.*, a methionine or valine codon) on the 5' end and a stop codon on the 3' end.

As used herein, the phrase "truncated amino acid sequence" and "truncated polypeptide" refer to a sub-sequence of a full-length amino acid sequence or polypeptide. Several criteria may also be used to define the truncated amino acid sequence or polypeptide. For example, a truncated polypeptide may be defined as a mature polypeptide (*e.g.*, a polypeptide which lacks a leader sequence). A truncated polypeptide may also be defined as an amino acid sequence which is a portion of a longer sequence that has been selected for ease of expression in a heterologous system but retains regions which render the polypeptide useful for use in vaccines (*e.g.*, antigenic regions which are expected to elicit a protective immune response).

Additional definitions are provided throughout the specification.

Explanation of Table 1

Table 1 lists *B. burgdorferi* nucleotide and amino acid sequences of the present invention. The nomenclature used therein is as follows:

"nt" refers to nucleotide sequences;

"aa" refers to amino acid sequences;

"f" refers to full-length nucleotide or amino acid sequences; and

"t" refers to truncated nucleotide or amino acid sequences.

Thus, for example, the designation "f101.aa" refers to the full-length amino acid sequence of *B. burgdorferi* polypeptide number 101. Further, "f101.nt" refers to the full-length nucleotide sequence encoding the full-length amino acid sequence of *B. burgdorferi* polypeptide number 101.

Explanation of Table 2

Table 2 lists accession numbers for the closest matching sequences between the polypeptides of the present invention and those available through GenBank and GeneSeq databases. These reference numbers are the database entry numbers commonly used by those of skill in the art, who will be familar with their denominations. The descriptions of the numenclature for GenBank are available from the National Center for Biotechnology Information. Column 1 lists the gene or ORF of the present invention. Column 2 lists the accession number of a "match" gene sequence in GenBank or GeneSeq databases. Column 3 lists the description of the "match" gene sequence. Columns 4 and 5 are the high score and smallest sum probability, respectively, calculated by BLAST. Polypeptides of the present invention that do not share significant identity/similarity with any polypeptide sequences of GenBank and GeneSeq are not represented in Table 2. Polypeptides of the present invention that share significant identity/similarity with more than one of the polypeptides of GenBank and GeneSeq are represented more than once.

Explanation of Table 3.

The *B. burgdorferi* polypeptides of the present invention may include one or more conservative amino acid substitutions from natural mutations or human manipulation as indicated in Table 3. Changes are preferably of a minor nature, such as conservative amino acid substitutions that do not significantly affect the folding or activity of the protein. Residues from the following groups, as indicated in Table 3, may be substituted for one another: Aromatic, Hydrophobic, Polar, Basic, Acidic, and Small,

Explanation of Table 4

Table 4 lists residues comprising antigenic epitopes of antigenic epitope-bearing fragments present in each of the full length *B. burgdorferi* polypeptides described in Table 1 as predicted by the inventors using the algorithm of Jameson and Wolf, (1988) Comp. Appl. Biosci. 4:181-186. The Jameson-Wolf antigenic analysis was performed using the computer program PROTEAN (Version 3.11 for the Power MacIntosh, DNASTAR, Inc., 1228 South Park Street Madison, WI). *B. burgdorferi* polypeptide shown in Table 1 may one or more antigenic epitopes comprising residues described in Table 4. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly. The residues and locations shown described in Table 4 correspond to the amino acid sequences for each full length gene sequence shown in Table 1 and in the Sequence Listing. Polypeptides of the present invention that do not have antigenic epitopes recognized by the Jameson-Wolf algorithm are not represented in Table 2.

Selection of Nucleic Acid Sequences Encoding Antigenic B. burgdorferi Polypeptides

The present invention provides a select number of ORFs from those presented in the fragments of the *Borrelia burgdorferi* genome which may prove useful for the generation of a protective immune response. The sequenced *B. burgdorferi* genomic DNA was obtained from a sub-cultured isolate of ATCC Deposit No. 35210. The sub-cultured isolate was deposited on August 8, 1997 at the American Type Culture Collection, 12301 Park Lawn Drive, Rockville, Maryland 20852, and given accession number 202012.

Some ORFs contained in the subset of fragments of the *B. burgdorferi* genome disclosed herein were derived through the use of a number of screening criteria detailed below. The ORFs are generally bounded at the amino terminus by a methionine residue and at the carboxy terminus by a stop codon.

Many of the selected sequences do not consist of complete ORFs. Although a polypeptide representing a complete ORF may be the closest approximation of a protein native to an organism, it is not always preferred to express a complete ORF in a heterologous system. It may be challenging to express and purify a highly hydrophobic protein by common laboratory methods. Some of the polypeptide vaccine candidates described herein have been modified slightly to simplify the production of recombinant protein. For example, nucleotide sequences which encode highly hydrophobic domains, such as those found at the amino terminal signal sequence, have been excluded from some constructs used for *in vitro* expression of the polypeptides. Furthermore, any highly hydrophobic amino acid sequences occurring at the carboxy terminus have also been excluded from the recombinant expression constructs. Thus, in one embodiment, a polypeptide which represents a truncated or modified ORF may be used as an antigen.

While numerous methods are known in the art for selecting potentially immunogenic polypeptides, many of the ORFs disclosed herein were selected on the basis of screening all theoretical *Borrelia burgdorferi* ORFs for several aspects of potential immunogenicity. One set of selection criteria are as follows:

1. *Type I signal sequence:* An amino terminal type I signal sequence generally directs a nascent protein across the plasma and outer membranes to the exterior of the bacterial cell. Experimental evidence obtained from studies with *Escherichia coli* suggests that the typical type I signal sequence consists of the following biochemical and physical attributes (Izard, J. W. and Kendall, D. A. *Mol. Microbiol. 13*:765-773 (1994)). The length of the type I signal sequence is approximately 15 to 25 primarily hydrophobic amino acid residues with a net positive charge in the extreme amino terminus. In addition, the central region of the signal sequence adopts an alpha-helical conformation in a hydrophobic environment. Finally, the region surrounding the actual site of cleavage is ideally six residues long, with small side-chain amino acids in the -1 and -3 positions.

2. *Type IV signal sequence:* The type IV signal sequence is an example of the several types of functional signal sequences which exist in addition to the type I signal sequence detailed

above. Although functionally related, the type IV signal sequence possesses a unique set of biochemical and physical attributes (Strom, M. S. and Lory, S., *J. Bacteriol. 174*:7345-7351 (1992)). These are typically six to eight amino acids with a net basic charge followed by an additional sixteen to thirty primarily hydrophobic residues. The cleavage site of a type IV signal sequence is typically after the initial six to eight amino acids at the extreme amino terminus. In addition, type IV signal sequences generally contain a phenylalanine residue at the +1 site relative to the cleavage site.

3. *Lipoprotein:* Studies of the cleavage sites of twenty-six bacterial lipoprotein precursors has allowed the definition of a consensus amino acid sequence for lipoprotein cleavage. Nearly three-fourths of the bacterial lipoprotein precursors examined contained the sequence L-(A,S)-(G,A)-C at positions -3 to +1, relative to the point of cleavage (Hayashi, S. and Wu, H. C., *J. Bioenerg. Biomembr. 22*:451-471 (1990)).

4. *LPXTG motif:* It has been experimentally determined that most anchored proteins found on the surface of gram-positive bacteria possess a highly conserved carboxy terminal sequence. More than fifty such proteins from organisms such as *S. pyogenes*, *S. mutans*, *B. burgdorferi*, *S. pneumoniae*, and others, have been identified based on their extracellular location and carboxy terminal amino acid sequence (Fischetti, V. A., *ASM News 62*:405-410 (1996)). The conserved region consists of six charged amino acids at the extreme carboxy terminus coupled to 15-20 hydrophobic amino acids presumed to function as a transmembrane domain. Immediately adjacent to the transmembrane domain is a six amino acid sequence conserved in nearly all proteins examined. The amino acid sequence of this region is L-P-X-T-G-X, where X is any amino acid.

An algorithm for selecting antigenic and immunogenic *Borrelia burgdorferi* polypeptides including the foregoing criteria was developed. The algorithm is similar to that described in U.S. patent application 08/781,986, filed January 3, 1997, which is fully incorporated by reference herein. Use of the algorithm by the inventors to select immunologically useful *Borrelia burgdorferi* polypeptides resulted in the selection of a number of the disclosed ORFs. Polypeptides comprising the polypeptides identified in this group may be produced by techniques standard in the art and as further described herein.

Nucleic Acid Molecules

The present invention provides isolated nucleic acid molecules comprising polynucleotides encoding the *B. burgdorferi* polypeptides having the amino acid sequences shown in Table 1, which were determined by sequencing the genome of *B. burgdorferi* deposited as ATCC deposit no. 202012 and selected as putative immunogens.

Unless otherwise indicated, all nucleotide sequences determined by sequencing a DNA molecule herein were determined using an automated DNA sequencer (such as the Model 373 from Applied Biosystems, Inc.), and all amino acid sequences of polypeptides encoded by DNA molecules determined herein were predicted by translation of DNA sequences determined as

above. Therefore, as is known in the art for any DNA sequence determined by this automated approach, any nucleotide sequence determined herein may contain some errors. Nucleotide sequences determined by automation are typically at least about 90% identical, more typically at least about 95% to at least about 99.9% identical to the actual nucleotide sequence of the sequenced DNA molecule. The actual sequence can be more precisely determined by other approaches including manual DNA sequencing methods well known in the art. As is also known in the art, a single insertion or deletion in a determined nucleotide sequence compared to the actual sequence will cause a frame shift in translation of the nucleotide sequence such that the predicted amino acid sequence encoded by a determined nucleotide sequence will be completely different from the amino acid sequence actually encoded by the sequenced DNA molecule, beginning at the point of such an insertion or deletion.

Unless otherwise indicated, each "nucleotide sequence" set forth herein is presented as a sequence of deoxyribonucleotides (abbreviated A, G , C and T). However, by "nucleotide sequence" of a nucleic acid molecule or polynucleotide is intended, for a DNA molecule or polynucleotide, a sequence of deoxyribonucleotides, and for an RNA molecule or polynucleotide, the corresponding sequence of ribonucleotides (A, G, C and U), where each thymidine deoxyribonucleotide (T) in the specified deoxyribonucleotide sequence is replaced by the ribonucleotide uridine (U). For instance, reference to an RNA molecule having a sequence of Table 1 set forth using deoxyribonucleotide abbreviations is intended to indicate an RNA molecule having a sequence in which each deoxyribonucleotide A, G or C of Table 1 has been replaced by the corresponding ribonucleotide A, G or C, and each deoxyribonucleotide T has been replaced by a ribonucleotide U.

Nucleic acid molecules of the present invention may be in the form of RNA, such as mRNA, or in the form of DNA, including, for instance, cDNA and genomic DNA obtained by cloning or produced synthetically. The DNA may be double-stranded or single-stranded. Single-stranded DNA or RNA may be the coding strand, also known as the sense strand, or it may be the non-coding strand, also referred to as the anti-sense strand.

By "isolated" nucleic acid molecule(s) is intended a nucleic acid molecule, DNA or RNA, which has been removed from its native environment. For example, recombinant DNA molecules contained in a vector are considered isolated for the purposes of the present invention. Further examples of isolated DNA molecules include recombinant DNA molecules maintained in heterologous host cells or purified (partially or substantially) DNA molecules in solution. Isolated RNA molecules include *in vivo* or *in vitro* RNA transcripts of the DNA molecules of the present invention. Isolated nucleic acid molecules according to the present invention further include such molecules produced synthetically.

In addition, isolated nucleic acid molecules of the invention include DNA molecules which comprise a sequence substantially different from those described above but which, due to the degeneracy of the genetic code, still encode a *B. burgdorferi* polypeptides and peptides of the present invention (e.g. polypeptides of Table 1). That is, all possible DNA sequences that encode

the *B. burgdorferi* polypeptides of the present invention. This includes the genetic code and species-specific codon preferences known in the art. Thus, it would be routine for one skilled in the art to generate the degenerate variants described above, for instance, to optimize codon expression for a particular host (e.g., change codons in the bacteria mRNA to those preferred by a mammalian or other bacterial host such as *E. coli*).

The invention further provides isolated nucleic acid molecules having the nucleotide sequence shown in Table 1 or a nucleic acid molecule having a sequence complementary to one of the above sequences. Such isolated molecules, particularly DNA molecules, are useful as probes for gene mapping and for identifying *B. burgdorferi* in a biological sample, for instance, by PCR, Southern blot, Northern blot, or other form of hybridization analysis.

The present invention is further directed to nucleic acid molecules encoding portions or fragments of the nucleotide sequences described herein. Fragments include portions of the nucleotide sequences of Table 1 at least 10 contiguous nucleotides in length selected from any two integers, one of which representing a 5' nucleotide position and a second of which representing a 3' nucleotide position, where the first nucleotide for each nucleotide sequence in Table 1 is position 1. That is, every combination of a 5' and 3' nucleotide position that a fragment at least 10 contiguous nucleotides in length could occupy is included in the invention. "At least" means a fragment may be 10 contiguous nucleotide bases in length or any integer between 10 and the length of an entire nucleotide sequence of Table 1 minus 1. Therefore, included in the invention are contiguous fragments specified by any 5' and 3' nucleotide base positions of a nucleotide sequences of Table 1 wherein the contiguous fragment is any integer between 10 and the length of an entire nucleotide sequence minus 1.

Further, the invention includes polynucleotides comprising fragments specified by size, in nucleotides, rather than by nucleotide positions. The invention includes any fragment size, in contiguous nucleotides, selected from integers between 10 and the length of an entire nucleotide sequence minus 1. Preferred sizes of contiguous nucleotide fragments include 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides. Other preferred sizes of contiguous nucleotide fragments, which may be useful as diagnostic probes and primers, include fragments 50-300 nucleotides in length which include, as discussed above, fragment sizes representing each integer between 50-300. Larger fragments are also useful according to the present invention corresponding to most, if not all, of the nucleotide sequences shown in Table 1or of the *B. burgdorferi* nucleotide sequences of the plasimd clones listed in Table 1. The preferred sizes are, of course, meant to exemplify not limit the present invention as all size fragments, representing any integer between 10 and the length of an entire nucleotide sequence minus 1, are included in the invention. Additional preferred nucleic acid fragments of the present invention include nucleic acid molecules encoding epitope-bearing portions of *B. burgdorferi* polypeptides identified in Table 4.

The present invention also provides for the exclusion of any fragment, specified by 5' and 3' base positions or by size in nucleotide bases as described above for any nucleotide sequence of

Table 1 or the plasimd clones listed in Table 1. Any number of fragments of nucleotide sequences in Table 1 or the plasimd clones listed in Table 1, specified by 5' and 3' base positions or by size in nucleotides, as described above, may be excluded from the present invention.

Preferred nucleic acid fragments of the present invention also include nucleic acid molecules encoding epitope-bearing portions of the *B. burgdorferi* polypeptides shown in Table 1. Such nucleic acid fragments of the present invention include, for example, nucleic acid molecules encoding polypeptide fragments comprising from about the amino terminal residue to about the carboxy terminal residue of each fragment shown in Table 4. The above referred to polypeptide fragments are antigenic regions of particular *B. burgdorferi* polypeptides shown in Table 1. Methods for determining other such epitope-bearing portions for the remaining polypeptides described in Table 1 are well known in the art and are described in detail below.

In another aspect, the invention provides isolated nucleic acid molecules comprising polynucleotides which hybridize under stringent hybridization conditions to a portion of a polynucleotide in a nucleic acid molecule of the invention described above, for instance, a nucleic acid sequence shown in Table 1. By "stringent hybridization conditions" is intended overnight incubation at 42 C in a solution comprising: 50% formamide, 5x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 g/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65 C.

By polynucleotides which hybridize to a "portion" of a polynucleotide is intended polynucleotides (either DNA or RNA) which hybridize to at least about 15 nucleotides (nt), and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably about 30-70 nt of the reference polynucleotide. These are useful as diagnostic probes and primers as discussed above and in more detail below.

Of course, polynucleotides hybridizing to a larger portion of the reference polynucleotide, for instance, a portion 50-100 nt in length, or even to the entire length of the reference polynucleotide, are also useful as probes according to the present invention, as are polynucleotides corresponding to most, if not all, of a nucleotide sequence as shown in Table 1. By a portion of a polynucleotide of "at least 20 nt in length," for example, is intended 20 or more contiguous nucleotides from the nucleotide sequence of the reference polynucleotide (*e.g.*, a nucleotide sequences as shown in Table 1). As noted above, such portions are useful diagnostically either as probes according to conventional DNA hybridization techniques or as primers for amplification of a target sequence by PCR, as described, for instance, in *Molecular Cloning, A Laboratory Manual*, 2nd. edition, Sambrook, J., Fritsch, E. F. and Maniatis, T., eds., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989), the entire disclosure of which is hereby incorporated herein by reference.

Since nucleic acid sequences encoding the *B. burgdorferi* polypeptides of the present invention are provided in Table 1, generating polynucleotides which hybridize to portions of these sequences would be routine to the skilled artisan. For example, the hybridizing polynucleotides

of the present invention could be generated synthetically according to known techniques.

As indicated, nucleic acid molecules of the present invention which encode *B. burgdorferi* polypeptides of the present invention may include, but are not limited to those encoding the amino acid sequences of the polypeptides by themselves; and additional coding sequences which code for additional amino acids, such as those which provide additional functionalities. Thus, the sequences encoding these polypeptides may be fused to a marker sequence, such as a sequence encoding a peptide which facilitates purification of the fused polypeptide. In certain preferred embodiments of this aspect of the invention, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (Qiagen, Inc.), among others, many of which are commercially available. As described in Gentz *et al., Proc. Natl. Acad. Sci. USA 86*:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the resulting fusion protein.

Thus, the present invention also includes genetic fusions wherein the *B. burgdorferi* nucleic acid sequences coding sequences provided in Table 1 are linked to additional nucleic acid sequences to produce fusion proteins. These fusion proteins may include epitopes of borrelial or non-borrelial origin designed to produce proteins having enhanced immunogenicity. Further, the fusion proteins of the present invention may contain antigenic determinants known to provide helper T-cell stimulation, peptides encoding sites for post-translational modifications which enhance immunogenicity (*e.g.*, acylation), peptides which facilitate purification (*e.g.*, histidine "tag"), or amino acid sequences which target the fusion protein to a desired location (*e.g.*, a heterologous leader sequence). For instance, hexa-histidine provides for convenient purification of the fusion protein. See Gentz et al. (1989) Proc. Natl. Acad. Sci. 86:821-24. The "HA" tag is another peptide useful for purification which corresponds to an epitope derived from the influenza hemagglutinin protein. See Wilson et al. (1984) Cell 37:767. As discussed below, other such fusion proteins include the *B. burgdorferi* polypeptides of the present invention fused to Fc at the N- or C-terminus.

Post-translational modification of the full-length *B. burgdorferi* OspA protein expressed in *E. coli* is believed to increase the immunogenicity of this protein. Erdile, L. *et al., Infect. Immun. 61*:81-90 (1993). *B. burgdorferi* OspA when expressed in *E. coli*, for example, is post-translationally modified in at least two ways. First, a signal peptide is cleaved; second, lipid moieties are attached. The presence of these lipid moieties is believed to confer enhanced immunogenicity and results in the elicitation of a strong protective immunological response.

Variant and Mutant Polynucleotides

The present invention thus includes nucleic acid molecules and sequences which encode fusion proteins comprising one or more *B. burgdorferi* polypeptides of the present invention fused to an amino acid sequence which allows for post-translational modification to enhance immunogenicity. This post-translational modification may occur either *in vitro* or when the fusion protein is expressed *in vivo* in a host cell. An example of such a modification is the introduction

of an amino acid sequence which results in the attachment of a lipid moiety. Such a lipid moiety attachment site of OspA, which is lipidated upon expression in *E. coli*, has been identified. Bouchon, B. *et al.*, *Anal. Biochem.* *246*:52-61 (1997).

Thus, as indicated above, the present invention includes genetic fusions wherein a *B. burgdorferi* nucleic acid sequence provided in Table 1 is linked to a nucleotide sequence encoding another amino acid sequence. These other amino acid sequences may be of borrelial origin (*e.g.*, another sequence selected from Table 1) or non-borrelial origin. An example of such a fusion protein is reported in Fikrig, E. *et al.*, *Science* *250*:553-556 (1990) where an OspA-glutathione-*S*-transferase fusion protein was produced and shown to elicit protective immunity against Lyme disease in immune competent mice.

The present invention further relates to variants of the nucleic acid molecules of the present invention, which encode portions, analogs or derivatives of the *B. burgdorferi* polypeptides shown in Table 1. Variants may occur naturally, such as a natural allelic variant. By an "allelic variant" is intended one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. *Genes II*, Lewin, B., ed., John Wiley & Sons, New York (1985). Non-naturally occurring variants may be produced using art-known mutagenesis techniques.

Such variants include those produced by nucleotide substitutions, deletions or additions. The substitutions, deletions or additions may involve one or more nucleotides. These variants may be altered in coding regions, non-coding regions, or both. Alterations in the coding regions may produce conservative or non-conservative amino acid substitutions, deletions or additions. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the *B. burgdorferi* polypeptides disclosed herein or portions thereof. Also especially preferred in this regard are conservative substitutions.

The present application is further directed to nucleic acid molecules at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleic acid sequence shown in Table 1. The above nucleic acid sequences are included irrespective of whether they encode a polypeptide having *B. burgdorferi* activity. This is because even where a particular nucleic acid molecule does not encode a polypeptide having *B. burgdorferi* activity, one of skill in the art would still know how to use the nucleic acid molecule, for instance, as a hybridization probe. Uses of the nucleic acid molecules of the present invention that do not encode a polypeptide having *B. burgdorferi* activity include, *inter alia*, isolating an *B. burgdorferi* gene or allelic variants thereof from a DNA library, and detecting *B. burgdorferi* mRNA expression samples, environmental samples, suspected of containing *B. burgdorferi* by Northern Blot analysis.

Embodiments of the invention include isolated nucleic acid molecules comprising a polynucleotide having a nucleotide sequence at least 90% identical, and more preferably at least 95%, 96%, 97%, 98% or 99% identical to (a) a nucleotide sequence encoding any of the amino acid sequences of the full-length polypeptides shown in Table 1; (b) a nucleotide sequence encoding any of the amino acid sequences of the full-length polypeptides shown in Table 1 but minus the N-terminal methionine residue, if present; (c) a nucleotide sequence encoding any of the

amino acid sequences of the truncated polypeptides shown in Table 1; and (d) a nucleotide sequence complementary to any of the nucleotide sequences in (a), (b), or (c) above.

Preferred, are nucleic acid molecules having sequences at least 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequence shown in Table 1, which do, in fact, encode a polypeptide having *B. burgdorferi* protein activity By "a polypeptide having *B. burgdorferi* activity" is intended polypeptides exhibiting activity similar, but not necessarily identical, to an activity of the *B. burgdorferi* protein of the invention, as measured in a particular biological assay suitable for measuring activity of the specified protein.

Due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 90%, 95%, 96%, 97%, 98%, or 99% identical to the nucleic acid sequences shown in Table 1 will encode a polypeptide having *B. burgdorferi* protein activity. In fact, since degenerate variants of these nucleotide sequences all encode the same polypeptide, this will be clear to the skilled artisan even without performing the above described comparison assay. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a polypeptide having *B. burgdorferi* protein activity. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not likely to significantly effect protein function (e.g., replacing one aliphatic amino acid with a second aliphatic amino acid), as further described below.

The biological activity or function of the polypeptides of the present invention are expected to be similar or identical to polypeptides from other bacteria that share a high degree of structural identity/similarity. Tables 2 lists accession numbers and descriptions for the closest matching sequences of polypeptides available through Genbank and Derwent databases. It is therefore expected that the biological activity or function of the polypeptides of the present invention will be similar or identical to those polypeptides from other bacterial genuses, species, or strains listed in Table 2.

By a polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the *B. burgdorferi* polypeptide. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% (5 of 100) of the nucleotides in the reference sequence may be deleted, inserted, or substituted with another nucleotide. The query sequence may be an entire sequence shown in Table 1, the ORF (open reading frame), or any fragment specified as described herein.

As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the presence invention can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention)

and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. *See* Brutlag et al. (1990) Comp. App. Biosci. 6:237-245. In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by first converting U's to T's. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the lenght of the subject nucleotide sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3' truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only nucleotides outside the 5' and 3' nucleotides of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

For example, a 90 nucleotide subject sequence is aligned to a 100 nucleotide query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 nucleotides at 5' end. The 10 unpaired nucleotides represent 10% of the sequence (number of nucleotides at the 5' and 3' ends not matched/total number of nucleotides in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 nucleotides were perfectly matched the final percent identity would be 90%. In another example, a 90 nucleotide subject sequence is compared with a 100 nucleotide query sequence. This time the deletions are internal deletions so that there are no nucleotides on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only nucleotides 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to made for the purposes of the present invention.

Vectors and Host Cells

The present invention also relates to vectors which include the isolated DNA molecules of

the present invention, host cells which are genetically engineered with the recombinant vectors, and the production of *B. burgdorferi* polypeptides or fragments thereof by recombinant techniques.

Recombinant constructs may be introduced into host cells using well known techniques such as infection, transduction, transfection, transvection, electroporation and transformation. The vector may be, for example, a phage, plasmid, viral or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged *in vitro* using an appropriate packaging cell line and then transduced into host cells.

Preferred are vectors comprising *cis*-acting control regions to the polynucleotide of interest. Appropriate *trans*-acting factors may be supplied by the host, supplied by a complementing vector or supplied by the vector itself upon introduction into the host.

In certain preferred embodiments in this regard, the vectors provide for specific expression, which may be inducible and/or cell type-specific. Particularly preferred among such vectors are those inducible by environmental factors that are easy to manipulate, such as temperature and nutrient additives.

Expression vectors useful in the present invention include chromosomal-, episomal- and virus-derived vectors, *e.g.*, vectors derived from bacterial plasmids, bacteriophage, yeast episomes, yeast chromosomal elements, viruses such as baculoviruses, papova viruses, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations thereof, such as cosmids and phagemids.

The DNA insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the *E. coli lac, trp* and *tac* promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination and, in the transcribed region, a ribosome binding site for translation. The coding portion of the mature transcripts expressed by the constructs will preferably include a translation initiating site at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase or neomycin resistance for eukaryotic cell culture and tetracycline or ampicillin resistance genes for culturing in *E. coli* and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as *E. coli*, *Streptomyces* and *Salmonella typhimurium* cells; fungal cells, such as yeast cells; insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells; animal cells such as CHO, COS and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the

above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from Qiagen; pBS vectors, Phagescript vectors, Bluescript vectors, pNH8A, pNH16a, pNH18A, pNH46A available from Stratagene; pET series of vectors available from Novagen; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

Among known bacterial promoters suitable for use in the present invention include the *E. coli lac*I and *lac*Z promoters, the T3 and T7 promoters, the *gpt* promoter, the lambda PR and PL promoters and the *trp* promoter. Suitable eukaryotic promoters include the CMV immediate early promoter, the HSV thymidine kinase promoter, the early and late SV40 promoters, the promoters of retroviral LTRs, such as those of the Rous sarcoma virus (RSV), and metallothionein promoters, such as the mouse metallothionein-I promoter.

Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection or other methods. Such methods are described in many standard laboratory manuals, such as Davis *et al., Basic Methods In Molecular Biology* (1986).

Transcription of DNA encoding the polypeptides of the present invention by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are *cis*-acting elements of DNA, usually about from 10 to 300 bp that act to increase transcriptional activity of a promoter in a given host cell-type. Examples of enhancers include the SV40 enhancer, which is located on the late side of the replication origin at bp 100 to 270, the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers.

For secretion of the translated polypeptide into the lumen of the endoplasmic reticulum, into the periplasmic space or into the extracellular environment, appropriate secretion signals may be incorporated into the expressed polypeptide. The signals may be endogenous to the polypeptide or they may be heterologous signals.

The polypeptide may be expressed in a modified form, such as a fusion protein, and may include not only secretion signals, but also additional heterologous functional regions. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence in the host cell, during purification, or during subsequent handling and storage. Also, peptide moieties may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to polypeptides to engender secretion or excretion, to improve stability and to facilitate purification, among others, are familiar and routine techniques in the art. A preferred fusion protein comprises a heterologous region from immunoglobulin that is useful to solubilize proteins. For example, EP-A-O 464 533 (Canadian

counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is thoroughly advantageous for use in therapy and diagnosis and thus results, for example, in improved pharmacokinetic properties (EP-A 0232 262). On the other hand, for some uses it would be desirable to be able to delete the Fc part after the fusion protein has been expressed, detected and purified in the advantageous manner described. This is the case when Fc portion proves to be a hindrance to use in therapy and diagnosis, for example when the fusion protein is to be used as antigen for immunizations. In drug discovery, for example, human proteins, such as, hIL5-receptor has been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. *See* Bennett, D. *et al.*, *J. Molec. Recogn. 8*:52-58 (1995) and Johanson, K. *et al.*, *J. Biol. Chem. 270 (16)*:9459-9471 (1995).

The *B. burgdorferi* polypeptides can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography, lectin chromatography and high performance liquid chromatography ("HPLC") is employed for purification. Polypeptides of the present invention include naturally purified products, products of chemical synthetic procedures, and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect and mammalian cells.

Polypeptides and Fragments

The invention further provides isolated polypeptides having the amino acid sequences in Table 1, and peptides or polypeptides comprising portions of the above polypeptides. The terms "peptide" and "oligopeptide" are considered synonymous (as is commonly recognized) and each term can be used interchangeably as the context requires to indicate a chain of at least to amino acids coupled by peptidyl linkages. The word "polypeptide" is used herein for chains containing more than ten amino acid residues. All oligopeptide and polypeptide formulas or sequences herein are written from left to right and in the direction from amino terminus to carboxy terminus.

As discussed in detail below, immunization using *B. burgdorferi* sensu stricto isolate B31 decorin-binding protein elicits the production of antiserum which confers passive immunity against *Borrelia* species and strains which express divergent forms of this protein. Cassatt, D. *et al.*, *Protection of Borrelia burgdorferi Infection by Antibodies to Decorin-binding Protein*, in VACCINES97, Cold Spring Harbor Press (1997), pages 191-195. Thus, some amino acid sequences of the *B. burgdorferi* polypeptides shown in Table 1 can be varied without significantly effecting the antigenicity of the polypeptides. If such differences in sequence are contemplated, it should be remembered that there will be critical areas on the polypeptide which determine antigenicity. In general, it is possible to replace residues which do not form part of an

antigenic epitope without significantly effecting the antigenicity of a polypeptide.

Variant and Mutant Polypeptides

To improve or alter the characteristics of *B. burgdorferi* polypeptides of the present invention, protein engineering may be employed. Recombinant DNA technology known to those skilled in the art can be used to create novel mutant proteins or muteins including single or multiple amino acid substitutions, deletions, additions, or fusion proteins. Such modified polypeptides can show, e.g., enhanced activity or increased stability. In addition, they may be purified in higher yields and show better solubility than the corresponding natural polypeptide, at least under certain purification and storage conditions.

N-Terminal and C-Terminal Deletion Mutants

It is known in the art that one or more amino acids may be deleted from the N-terminus or C-terminus without substantial loss of biological function. For instance, Ron et al. J. Biol. Chem., 268:2984-2988 (1993), reported modified KGF proteins that had heparin binding activity even if 3, 8, or 27 N-terminal amino acid residues were missing. Accordingly, the present invention provides polypeptides having one or more residues deleted from the amino terminus of the amino acid sequence of the *B. burgdorferi* polypeptides shown in Table 1, and polynucleotides encoding such polypeptides.

Similarly, many examples of biologically functional C-terminal deletion muteins are known. For instance, Interferon gamma shows up to ten times higher activities by deleting 8-10 amino acid residues from the carboxy terminus of the protein *See, e.g.*, Dobeli, et al. (1988) J. Biotechnology 7:199-216. Accordingly, the present invention provides polypeptides having one or more residues from the carboxy terminus of the amino acid sequence of the *B. burgdorferi* polypeptides shown in Table 1. The invention also provides polypeptides having one or more amino acids deleted from both the amino and the carboxyl termini as described below.

The present invention is further directed to polynucleotide encoding portions or fragments of the amino acid sequences described herein as well as to portions or fragments of the isolated amino acid sequences described herein. Fragments include portions of the amino acid sequences of Table 1, are at least 5 contiguous amino acid in length, are selected from any two integers, one of which representing a N-terminal position. The initiation codon of the polypeptides of the present inventions position 1. Every combination of a N-terminal and C-terminal position that a fragment at least 5 contiguous amino acid residues in length could occupy, on any given amino acid sequence of Table 1 is included in the invention. At least means a fragment may be 5 contiguous amino acid residues in length or any integer between 5 and the number of residues in a full length amino acid sequence minus 1. Therefore, included in the invention are contiguous fragments specified by any N-terminal and C-terminal positions of amino acid sequence set forth in Table 1 wherein the contiguous fragment is any integer between 5 and the number of residues in a full length sequence minus 1.

Further, the invention includes polypeptides comprising fragments specified by size, in

amino acid residues, rather than by N-terminal and C-terminal positions. The invention includes any fragment size, in contiguous amino acid residues, selected from integers between 5 and the number of residues in a full length sequence minus 1. Preferred sizes of contiguous polypeptide fragments include about 5 amino acid residues, about 10 amino acid residues, about 20 amino acid residues, about 30 amino acid residues, about 40 amino acid residues, about 50 amino acid residues, about 100 amino acid residues, about 200 amino acid residues, about 300 amino acid residues, and about 400 amino acid residues. The preferred sizes are, of course, meant to exemplify, not limit, the present invention as all size fragments representing any integer between 5 and the number of residues in a full length sequence minus 1 are included in the invention. The present invention also provides for the exclusion of any fragments specified by N-terminal and C-terminal positions or by size in amino acid residues as described above. Any number of fragments specified by N-terminal and C-terminal positions or by size in amino acid residues as described above may be excluded.

The above fragments need not be active since they would be useful, for example, in immunoassays, in epitope mapping, epitope tagging, to generate antibodies to a particular portion of the protein, as vaccines, and as molecular weight markers.

Other Mutants

In addition to N- and C-terminal deletion forms of the protein discussed above, it also will be recognized by one of ordinary skill in the art that some amino acid sequences of the *B. burgdorferi* polypeptide can be varied without significant effect of the structure or function of the protein. If such differences in sequence are contemplated, it should be remembered that there will be critical areas on the protein which determine activity.

Thus, the invention further includes variations of the *B. burgdorferi* polypeptides which show substantial *B. burgdorferi* polypeptide activity or which include regions of *B. burgdorferi* protein such as the protein portions discussed below. Such mutants include deletions, insertions, inversions, repeats, and type substitutions selected according to general rules known in the art so as to have little effect on activity. For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided. There are two main approaches for studying the tolerance of an amino acid sequence to change. *See*, Bowie, J. U. *et al.* (1990), Science 247:1306-1310. The first method relies on the process of evolution, in which mutations are either accepted or rejected by natural selection. The second approach uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene and selections or screens to identify sequences that maintain functionality.

These studies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The studies indicate which amino acid changes are likely to be permissive at a certain position of the protein. For example, most buried amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Other such phenotypically silent substitutions are described by Bowie et al. (*supra*) and the references cited

therein. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe, Tyr.

Thus, the fragment, derivative, analog, or homolog of the polypeptide of Table 1, or that encoded by the plaimds listed in Table 1, may be: (i) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code: or (ii) one in which one or more of the amino acid residues includes a substituent group: or (iii) one in which the *B. burgdorferi* polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol): or (iv) one in which the additional amino acids are fused to the above form of the polypeptide, such as an IgG Fc fusion region peptide or leader or secretory sequence or a sequence which is employed for purification of the above form of the polypeptide or a proprotein sequence. Such fragments, derivatives and analogs are deemed to be within the scope of those skilled in the art from the teachings herein.

Thus, the *B. burgdorferi* polypeptides of the present invention may include one or more amino acid substitutions, deletions, or additions, either from natural mutations or human manipulation. As indicated, changes are preferably of a minor nature, such as conservative amino acid substitutions that do not significantly affect the folding or activity of the protein (see Table 3).

Amino acids in the *B. burgdorferi* proteins of the present invention that are essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis. *See, e.g.*, Cunningham et al. (1989) Science 244:1081-1085. The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant molecules are then tested for biological activity using assays appropriate for measuring the function of the particular protein.

Of special interest are substitutions of charged amino acids with other charged or neutral amino acids which may produce proteins with highly desirable improved characteristics, such as less aggregation. Aggregation may not only reduce activity but also be problematic when preparing pharmaceutical formulations, because aggregates can be immunogenic. *See, e.g.*, Pinckard et al., (1967) Clin. Exp. Immunol. 2:331-340; Robbins, et al., (1987) Diabetes 36:838-845; Cleland, et al., (1993) Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377.

The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of the *B. burgdorferi* polypeptide can be substantially purified by the one-step method described by Smith et al. (1988) Gene 67:31-40. Polypeptides of the invention also can be purified from natural or recombinant sources using antibodies directed against the polypeptides of the invention in methods which are well known in the art of protein purification.

The invention further provides for isolated *B. burgdorferi* polypeptides comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of a full-length *B. burgdorferi* polypeptide having the complete amino acid sequence shown in Table 1; (b) the amino acid sequence of a full-length *B. burgdorferi* polypeptide having the complete amino acid sequence shown in Table 1 excepting the N-terminal methionine; (c) the complete amino acid sequence encoded by the plaimds listed in Table 1; and (d) the complete amino acid sequence excepting the N-terminal methionine encoded by the plaimds listed in Table 1. The polypeptides of the present invention also include polypeptides having an amino acid sequence at least 80% identical, more preferably at least 90% identical, and still more preferably 95%, 96%, 97%, 98% or 99% identical to those described in (a), (b), (c), and (d) above.

Further polypeptides of the present invention include polypeptides which have at least 90% similarity, more preferably at least 95% similarity, and still more preferably at least 96%, 97%, 98% or 99% similarity to those described above.

A further embodiment of the invention relates to a polypeptide which comprises the amino acid sequence of a *B. burgdorferi* polypeptide having an amino acid sequence which contains at least one conservative amino acid substitution, but not more than 50 conservative amino acid substitutions, not more than 40 conservative amino acid substitutions, not more than 30 conservative amino acid substitutions, and not more than 20 conservative amino acid substitutions. Also provided are polypeptides which comprise the amino acid sequence of a *B. burgdorferi* polypeptide, having at least one, but not more than 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 conservative amino acid substitutions.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequences shown in Table 1 or to the amino acid sequence encoded by the plaimds listed in Table 1 can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al., (1990) Comp. App. Biosci. 6:237-245. In a sequence alignment the

query and subject sequences are both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, the results, in percent identity, must be manually corrected. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity. For subject sequences truncated at the N- and C-termini, relative to the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are considered for the purposes of manually adjusting the percent identity score. That is, only query amino acid residues outside the farthest N- and C-terminal residues of the subject sequence.

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the FASTDB alignment does not match/align with the first 10 residues at the N-terminus. The 10 unpaired residues represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence. This time the deletions are internal so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query sequence are manually corrected. No other manual corrections are to made for the purposes of the present invention.

The above polypeptide sequences are included irrespective of whether they have their normal biological activity. This is because even where a particular polypeptide molecule does not have biological activity, one of skill in the art would still know how to use the polypeptide, for instance, as a vaccine or to generate antibodies. Other uses of the polypeptides of the present

invention that do not have *B. burgdorferi* activity include, *inter alia*, as epitope tags, in epitope mapping, and as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods known to those of skill in the art.

As described below, the polypeptides of the present invention can also be used to raise polyclonal and monoclonal antibodies, which are useful in assays for detecting *B. burgdorferi* protein expression or as agonists and antagonists capable of enhancing or inhibiting *B. burgdorferi* protein function. Further, such polypeptides can be used in the yeast two-hybrid system to "capture" *B. burgdorferi* protein binding proteins which are also candidate agonists and antagonists according to the present invention. *See, e.g.,* Fields et al. (1989) Nature 340:245-246.

Epitope-Bearing Portions

In another aspect, the invention provides peptides and polypeptides comprising epitope-bearing portions of the *B. burgdorferi* polypeptides of the present invention. These epitopes are immunogenic or antigenic epitopes of the polypeptides of the present invention. An "immunogenic epitope" is defined as a part of a protein that elicits an antibody response when the whole protein or polypeptide is the immunogen. These immunogenic epitopes are believed to be confined to a few loci on the molecule. On the other hand, a region of a protein molecule to which an antibody can bind is defined as an "antigenic determinant" or "antigenic epitope." The number of immunogenic epitopes of a protein generally is less than the number of antigenic epitopes. *See, e.g.,* Geysen, et al. (1983) Proc. Natl. Acad. Sci. USA 81:3998- 4002. Predicted antigenic epitopes are shown in Table 4, below. It is pointed out that Table 4 only lists amino acid residues comprising epitopes predicted to have the highest degree of antigenicity. The polypeptides not listed in Table 4 and portions of polypeptides not listed in Table 4 are not considered non-antigenic. This is because they may still be antigenic *in vivo* but merely not recognized as such by the particular algorithm used. Thus, Table 4 lists the amino acid residues comprising preferred antigenic epitopes but not a complete list. Amino acid residues comprising other anigenic epitopes may be determined by algorithms similar to the Jameson-Wolf analysis or by *in vivo* testing for an antigenic response using the methods described herein or those known in the art.

As to the selection of peptides or polypeptides bearing an antigenic epitope (*i.e.*, that contain a region of a protein molecule to which an antibody can bind), it is well known in that art that relatively short synthetic peptides that mimic part of a protein sequence are routinely capable of eliciting an antiserum that reacts with the partially mimicked protein. *See, e.g.,* Sutcliffe, et al., (1983) Science 219:660-666. Peptides capable of eliciting protein-reactive sera are frequently represented in the primary sequence of a protein, can be characterized by a set of simple chemical rules, and are confined neither to immunodominant regions of intact proteins (*i.e.*, immunogenic epitopes) nor to the amino or carboxyl terminals. Peptides that are extremely hydrophobic and those of six or fewer residues generally are ineffective at inducing antibodies that bind to the

mimicked protein; longer, peptides, especially those containing proline residues, usually are effective. *See,* Sutcliffe, et al., *supra*, p. 661. For instance, 18 of 20 peptides designed according to these guidelines, containing 8-39 residues covering 75% of the sequence of the influenza virus hemagglutinin HA1 polypeptide chain, induced antibodies that reacted with the HA1 protein or intact virus; and 12/12 peptides from the MuLV polymerase and 18/18 from the rabies glycoprotein induced antibodies that precipitated the respective proteins.

Antigenic epitope-bearing peptides and polypeptides of the invention are therefore useful to raise antibodies, including monoclonal antibodies, that bind specifically to a polypeptide of the invention. Thus, a high proportion of hybridomas obtained by fusion of spleen cells from donors immunized with an antigen epitope-bearing peptide generally secrete antibody reactive with the native protein. *See* Sutcliffe, et al., *supra*, p. 663. The antibodies raised by antigenic epitope-bearing peptides or polypeptides are useful to detect the mimicked protein, and antibodies to different peptides may be used for tracking the fate of various regions of a protein precursor which undergoes post-translational processing. The peptides and anti-peptide antibodies may be used in a variety of qualitative or quantitative assays for the mimicked protein, for instance in competition assays since it has been shown that even short peptides (*e.g.*, about 9 amino acids) can bind and displace the larger peptides in immunoprecipitation assays. *See, e.g.,* Wilson, et al., (1984) Cell 37:767-778. The anti-peptide antibodies of the invention also are useful for purification of the mimicked protein, for instance, by adsorption chromatography using methods known in the art.

Antigenic epitope-bearing peptides and polypeptides of the invention designed according to the above guidelines preferably contain a sequence of at least seven, more preferably at least nine and most preferably between about 10 to about 50 amino acids (i.e. any integer between 7 and 50) contained within the amino acid sequence of a polypeptide of the invention. However, peptides or polypeptides comprising a larger portion of an amino acid sequence of a polypeptide of the invention, containing about 50 to about 100 amino acids, or any length up to and including the entire amino acid sequence of a polypeptide of the invention, also are considered epitope-bearing peptides or polypeptides of the invention and also are useful for inducing antibodies that react with the mimicked protein. Preferably, the amino acid sequence of the epitope-bearing peptide is selected to provide substantial solubility in aqueous solvents (*i.e.*, the sequence includes relatively hydrophilic residues and highly hydrophobic sequences are preferably avoided); and sequences containing proline residues are particularly preferred.

Non-limiting examples of antigenic polypeptides or peptides that can be used to generate an Borrelia-specific immune response or antibodies include portions of the amino acid sequences identified in Table 1. More specifically, Table 4 discloses a list of non-limiting residues that are involved in the antigenicity of the epitope-bearing fragments of the present invention. Therefore, the present inventions provides for isolatd and purified antigenic epitope-bearing fragements of the polypeptides of the present invention comprising a peptide sequences of Table 4. The antigenic epitope-bearing fragments comprising a peptide sequence of Table 4 preferably contain a

sequence of at least seven, more preferably at least nine and most preferably between about 10 to about 50 amino acids (i.e. any integer between 7 and 50) of a polypeptide of the present invention. That is, included in the present invention are antigenic polypeptides between the integers of 7 and 50 amino acid in length comprising one or more of the sequences of Table 4. Therefore, in most cases, the polypeptides of Table 4 make up only a portion of the antigenic polypeptide. All combinations of sequences between the integers of 7 and 50 amino acid in length comprising one or more of the sequences of Table 4 are included. The antigenic epitope-bearing fragements may be specified by either the number of contiguous amino acid residues or by specific N-terminal and C-terminal positions as described above for the polypeptide fragements of the present invention, wherein the initiation codon is residue 1. Any number of the described antigenic epitope-bearing fragements of the present invention may also be excluded from the present invention in the same manner.

The epitope-bearing peptides and polypeptides of the invention may be produced by any conventional means for making peptides or polypeptides including recombinant means using nucleic acid molecules of the invention. For instance, an epitope-bearing amino acid sequence of the present invention may be fused to a larger polypeptide which acts as a carrier during recombinant production and purification, as well as during immunization to produce anti-peptide antibodies. Epitope-bearing peptides also may be synthesized using known methods of chemical synthesis. For instance, Houghten has described a simple method for synthesis of large numbers of peptides, such as 10-20 mg of 248 different 13 residue peptides representing single amino acid variants of a segment of the HA1 polypeptide which were prepared and characterized (by ELISA-type binding studies) in less than four weeks (Houghten, R. A. Proc. Natl. Acad. Sci. USA **82**:5131-5135 (1985)). This "Simultaneous Multiple Peptide Synthesis (SMPS)" process is further described in U.S. Patent No. 4,631,211 to Houghten and coworkers (1986). In this procedure the individual resins for the solid-phase synthesis of various peptides are contained in separate solvent-permeable packets, enabling the optimal use of the many identical repetitive steps involved in solid-phase methods. A completely manual procedure allows 500-1000 or more syntheses to be conducted simultaneously (Houghten et al. (1985) Proc. Natl. Acad. Sci. 82:5131-5135 at 5134.

Epitope-bearing peptides and polypeptides of the invention are used to induce antibodies according to methods well known in the art. *See, e.g.*, Sutcliffe, et al., *supra*;; Wilson, et al., *supra*;; and Bittle, et al. (1985) J. Gen. Virol. 66:2347-2354. Generally, animals may be immunized with free peptide; however, anti-peptide antibody titer may be boosted by coupling of the peptide to a macromolecular carrier, such as keyhole limpet hemacyanin (KLH) or tetanus toxoid. For instance, peptides containing cysteine may be coupled to carrier using a linker such as m-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS), while other peptides may be coupled to carrier using a more general linking agent such as glutaraldehyde. Animals such as rabbits, rats and mice are immunized with either free or carrier-coupled peptides, for instance, by intraperitoneal and/or intradermal injection of emulsions containing about 100 μg peptide or

carrier protein and Freund's adjuvant. Several booster injections may be needed, for instance, at intervals of about two weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid surface. The titer of anti-peptide antibodies in serum from an immunized animal may be increased by selection of anti-peptide antibodies, for instance, by adsorption to the peptide on a solid support and elution of the selected antibodies according to methods well known in the art.

Immunogenic epitope-bearing peptides of the invention, *i.e.*, those parts of a protein that elicit an antibody response when the whole protein is the immunogen, are identified according to methods known in the art. For instance, Geysen, *et al.*, *supra*, discloses a procedure for rapid concurrent synthesis on solid supports of hundreds of peptides of sufficient purity to react in an ELISA. Interaction of synthesized peptides with antibodies is then easily detected without removing them from the support. In this manner a peptide bearing an immunogenic epitope of a desired protein may be identified routinely by one of ordinary skill in the art. For instance, the immunologically important epitope in the coat protein of foot-and-mouth disease virus was located by Geysen *et al. supra* with a resolution of seven amino acids by synthesis of an overlapping set of all 208 possible hexapeptides covering the entire 213 amino acid sequence of the protein. Then, a complete replacement set of peptides in which all 20 amino acids were substituted in turn at every position within the epitope were synthesized, and the particular amino acids conferring specificity for the reaction with antibody were determined. Thus, peptide analogs of the epitope-bearing peptides of the invention can be made routinely by this method. U.S. Patent No. 4,708,781 to Geysen (1987) further describes this method of identifying a peptide bearing an immunogenic epitope of a desired protein.

Further still, U.S. Patent No. 5,194,392, to Geysen (1990), describes a general method of detecting or determining the sequence of monomers (amino acids or other compounds) which is a topological equivalent of the epitope (*i.e.*, a "mimotope") which is complementary to a particular paratope (antigen binding site) of an antibody of interest. More generally, U.S. Patent No. 4,433,092, also to Geysen (1989), describes a method of detecting or determining a sequence of monomers which is a topographical equivalent of a ligand which is complementary to the ligand binding site of a particular receptor of interest. Similarly, U.S. Patent No. 5,480,971 to Houghten, R. A. *et al.* (1996) discloses linear C_1-C_7-alkyl peralkylated oligopeptides and sets and libraries of such peptides, as well as methods for using such oligopeptide sets and libraries for determining the sequence of a peralkylated oligopeptide that preferentially binds to an acceptor molecule of interest. Thus, non-peptide analogs of the epitope-bearing peptides of the invention also can be made routinely by these methods. The entire disclosure of each document cited in this section on "Polypeptides and Fragments" is hereby incorporated herein by reference.

As one of skill in the art will appreciate, the polypeptides of the present invention and the epitope-bearing fragments thereof described above can be combined with parts of the constant domain of immunoglobulins (IgG), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life *in vivo*. This has been shown, *e.g.*, for

chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EPA 0,394,827; Traunecker et al. (1988) Nature 331:84-86. Fusion proteins that have a disulfide-linked dimeric structure due to the IgG part can also be more efficient in binding and neutralizing other molecules than a monomeric *B. burgdorferi* polypeptide or fragment thereof alone. *See* Fountoulakis et al. (1995) J. Biochem. 270:3958-3964. Nucleic acids encoding the above epitopes of *B. burgdorferi* polypeptides can also be recombined with a gene of interest as an epitope tag to aid in detection and purification of the expressed polypeptide.

Antibodies

B. burgdorferi protein-specific antibodies for use in the present invention can be raised against the intact *B. burgdorferi* protein or an antigenic polypeptide fragment thereof, which may be presented together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse) or, if it is long enough (at least about 25 amino acids), without a carrier.

As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is meant to include intact molecules, single chain whole antibodies, and antibody fragments. Antibody fragments of the present invention include Fab and F(ab')2 and other fragments including single-chain Fvs (scFv) and disulfide-linked Fvs (sdFv). Also included in the present invention are chimeric and humanized monoclonal antibodies and polyclonal antibodies specific for the polypeptides of the present invention. The antibodies of the present invention may be prepared by any of a variety of methods. For example, cells expressing a polypeptide of the present invention or an antigenic fragment thereof can be administered to an animal in order to induce the production of sera containing polyclonal antibodies. For example, a preparation of *B. burgdorferi* polypeptide or fragment thereof is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

In a preferred method, the antibodies of the present invention are monoclonal antibodies or binding fragments thereof. Such monoclonal antibodies can be prepared using hybridoma technology. *See, e.g.,* Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988); Hammerling, et al., in: MONOCLONAL ANTIBODIES AND T-CELL HYBRIDOMAS 563-681 (Elsevier, N.Y., 1981). Fab and F(ab')2 fragments may be produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')2 fragments). Alternatively, *B. burgdorferi* polypeptide-binding fragments, chimeric, and humanized antibodies can be produced through the application of recombinant DNA technology or through synthetic chemistry using methods known in the art.

Alternatively, additional antibodies capable of binding to the polypeptide antigen of the present invention may be produced in a two-step procedure through the use of anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and that,

therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, *B. burgdorferi* polypeptide-specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the *B. burgdorferi* polypeptide-specific antibody can be blocked by the *B. burgdorferi* polypeptide antigen. Such antibodies comprise anti-idiotypic antibodies to the *B. burgdorferi* polypeptide-specific antibody and can be used to immunize an animal to induce formation of further *B. burgdorferi* polypeptide-specific antibodies.

Antibodies and fragements thereof of the present invention may be described by the portion of a polypeptide of the present invention recognized or specifically bound by the antibody. Antibody binding fragements of a polypeptide of the present invention may be described or specified in the same manner as for polypeptide fragements discussed above., i.e, by N-terminal and C-terminal positions or by size in contiguous amino acid residues. Any number of antibody binding fragments, of a polypeptide of the present invention, specified by N-terminal and C-terminal positions or by size in amino acid residues, as described above, may also be excluded from the present invention. Therefore, the present invention includes antibodies the specifically bind a particuarlly discribed fragement of a polypeptide of the present invention and allows for the exclusion of the same.

Antibodies and fragements thereof of the present invention may also be described or specified in terms of their cross-reactivity. Antibodies and fragements that do not bind polypeptides of any other species of *Borrelia* other than *B. burgdorferi* are included in the present invention. Likewise, antibodies and fragements that bind only species of *Borrelia*, i.e. antibodies and fragements that do not bind bacteria from any genus other than *Borrelia*, are included in the present invention.

Diagnostic Assays

The present invention further relates to methods for assaying *staphylococcal* infection in an animal by detecting the expression of genes encoding *staphylococcal* polypeptides of the present invention. The methods comprise analyzing tissue or body fluid from the animal for *Borrelia*-specific antibodies, nucleic acids, or proteins. Analysis of nucleic acid specific to *Borrelia* is assayed by PCR or hybridization techniques using nucleic acid sequences of the present invention as either hybridization probes or primers. *See, e.g.,* Sambrook et al. Molecular cloning: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 2nd ed., 1989, page 54 reference); Eremeeva et al. (1994) J. Clin. Microbiol. 32:803-810 (describing differentiation among spotted fever group *Rickettsiae* species by analysis of restriction fragment length polymorphism of PCR-amplified DNA) and Chen et al. 1994 J. Clin. Microbiol. 32:589-595 (detecting *B. burgdorferi* nucleic acids *via* PCR).

Where diagnosis of a disease state related to infection with *Borrelia* has already been made, the present invention is useful for monitoring progression or regression of the disease state

whereby patients exhibiting enhanced *Borrelia* gene expression will experience a worse clinical outcome relative to patients expressing these gene(s) at a lower level.

By "biological sample" is intended any biological sample obtained from an animal, cell line, tissue culture, or other source which contains *Borrelia* polypeptide, mRNA, or DNA. Biological samples include body fluids (such as saliva, blood, plasma, urine, mucus, synovial fluid, etc.) tissues (such as muscle, skin, and cartilage) and any other biological source suspected of containing *Borrelia* polypeptides or nucleic acids. Methods for obtaining biological samples such as tissue are well known in the art.

The present invention is useful for detecting diseases related to *Borrelia* infections in animals. Preferred animals include monkeys, apes, cats, dogs, birds, cows, pigs, mice, horses, rabbits and humans. Particularly preferred are humans.

Total RNA can be isolated from a biological sample using any suitable technique such as the single-step guanidinium-thiocyanate-phenol-chloroform method described in Chomczynski et al. (1987) Anal. Biochem. 162:156-159. mRNA encoding *Borrelia* polypeptides having sufficient homology to the nucleic acid sequences identified in Table 1 to allow for hybridization between complementary sequences are then assayed using any appropriate method. These include Northern blot analysis, S1 nuclease mapping, the polymerase chain reaction (PCR), reverse transcription in combination with the polymerase chain reaction (RT-PCR), and reverse transcription in combination with the ligase chain reaction (RT-LCR).

Northern blot analysis can be performed as described in Harada et al. (1990) Cell 63:303-312. Briefly, total RNA is prepared from a biological sample as described above. For the Northern blot, the RNA is denatured in an appropriate buffer (such as glyoxal/dimethyl sulfoxide/sodium phosphate buffer), subjected to agarose gel electrophoresis, and transferred onto a nitrocellulose filter. After the RNAs have been linked to the filter by a UV linker, the filter is prehybridized in a solution containing formamide, SSC, Denhardt's solution, denatured salmon sperm, SDS, and sodium phosphate buffer. A *B. burgdorferi* polynucleotide sequence shown in Table 1 labeled according to any appropriate method (such as the ^{32}P-multiprimed DNA labeling system (Amersham)) is used as probe. After hybridization overnight, the filter is washed and exposed to x-ray film. DNA for use as probe according to the present invention is described in the sections above and will preferably at least 15 nucleotides in length.

S1 mapping can be performed as described in Fujita et al. (1987) Cell 49:357-367. To prepare probe DNA for use in S1 mapping, the sense strand of an above-described *B. burgdorferi* DNA sequence of the present invention is used as a template to synthesize labeled antisense DNA. The antisense DNA can then be digested using an appropriate restriction endonuclease to generate further DNA probes of a desired length. Such antisense probes are useful for visualizing protected bands corresponding to the target mRNA (*i.e.*, mRNA encoding *Borrelia* polypeptides).

Levels of mRNA encoding *Borrelia* polypeptides are assayed, for *e.g.*, using the RT-PCR method described in Makino et al. (1990) Technique 2:295-301. By this method, the radioactivities of the "amplicons" in the polyacrylamide gel bands are linearly related to the initial

concentration of the target mRNA. Briefly, this method involves adding total RNA isolated from a biological sample in a reaction mixture containing a RT primer and appropriate buffer. After incubating for primer annealing, the mixture can be supplemented with a RT buffer, dNTPs, DTT, RNase inhibitor and reverse transcriptase. After incubation to achieve reverse transcription of the RNA, the RT products are then subject to PCR using labeled primers. Alternatively, rather than labeling the primers, a labeled dNTP can be included in the PCR reaction mixture. PCR amplification can be performed in a DNA thermal cycler according to conventional techniques. After a suitable number of rounds to achieve amplification, the PCR reaction mixture is electrophoresed on a polyacrylamide gel. After drying the gel, the radioactivity of the appropriate bands (corresponding to the mRNA encoding the *Borrelia* polypeptides of the present invention) are quantified using an imaging analyzer. RT and PCR reaction ingredients and conditions, reagent and gel concentrations, and labeling methods are well known in the art. Variations on the RT-PCR method will be apparent to the skilled artisan. Other PCR methods that can detect the nucleic acid of the present invention can be found in PCR PRIMER: A LABORATORY MANUAL (C.W. Dieffenbach et al. eds., Cold Spring Harbor Lab Press, 1995).

The polynucleotides of the present invention, including both DNA and RNA, may be used to detect polynucleotides of the present invention or Borrelia species including *B. burgdorferi* using bio chip technology. The present invention includes both high density chip arrays (>1000 oligonucleotides per cm^2) and low density chip arrays (<1000 oligonucleotides per cm^2). Bio chips comprising arrays of polynucleotides of the present invention may be used to detect Borrelia species, including *B. burgdorferi*, in biological and environmental samples and to diagnose an animal, including humans, with an *B. burgdorferi* or other Borrelia infection. The bio chips of the present invention may comprise polynucleotide sequences of other pathogens including bacteria, viral, parasitic, and fungal polynucleotide sequences, in addition to the polynucleotide sequences of the present invention, for use in rapid diffenertial pathogenic detection and diagnosis. The bio chips can also be used to monitor an *B. burgdorferi* or other Borrelia infections and to monitor the genetic changes (deletions, insertions, mismatches, etc.) in response to drug therapy in the clinic and drug development in the laboratory. The bio chip technology comprising arrays of polynucleotides of the present invention may also be used to simultaneously monitor the expression of a multiplicity of genes, including those of the present invention. The polynucleotides used to comprise a selected array may be specified in the same manner as for the fragements, i.e, by their 5' and 3' positions or length in contigious base pairs and include from. Methods and particular uses of the polynucleotides of the present invention to detect Borrelia species, including *B. burgdorferi*, using bio chip technology include those known in the art and those of: U.S. Patent Nos. 5510270, 5545531, 5445934, 5677195, 5532128, 5556752, 5527681, 5451683, 5424186, 5607646, 5658732 and World Patent Nos. WO/9710365, WO/9511995, WO/9743447, WO/9535505, each incorporated herein in their entireties.

Biosensors using the polynucleotides of the present invention may also be used to detect, diagnose, and monitor *B. burgdorferi* or other Borrelia species and infections thereof.

Biosensors using the polynucleotides of the present invention may also be used to detect particular polynucleotides of the present invention. Biosensors using the polynucleotides of the present invention may also be used to monitor the genetic changes (deletions, insertions, mismatches, etc.) in response to drug therapy in the clinic and drug development in the laboratory. Methods and particular uses of the polynucleotides of the present invention to detect Borrelia species, including *B. burgdorferi*, using biosenors include those known in the art and those of: U.S. Patent Nos 5721102, 5658732, 5631170, and World Patent Nos. WO97/35011, WO/9720203, each incorporated herein in their entireties.

Thus, the present invention includes both bio chips and biosensors comprising polynucleotides of the present invention and methods of their use.

Assaying *Borrelia* polypeptide levels in a biological sample can occur using any art-known method, such as antibody-based techniques. For example, *Borrelia* polypeptide expression in tissues can be studied with classical immunohistological methods. In these, the specific recognition is provided by the primary antibody (polyclonal or monoclonal) but the secondary detection system can utilize fluorescent, enzyme, or other conjugated secondary antibodies. As a result, an immunohistological staining of tissue section for pathological examination is obtained. Tissues can also be extracted, *e.g.*, with urea and neutral detergent, for the liberation of *Borrelia* polypeptides for Western-blot or dot/slot assay. *See, e.g.,* Jalkanen, M. et al. (1985) J. Cell. Biol. 101:976-985; Jalkanen, M. et al. (1987) J. Cell . Biol. 105:3087-3096. In this technique, which is based on the use of cationic solid phases, quantitation of a *Borrelia* polypeptide can be accomplished using an isolated *Borrelia* polypeptide as a standard. This technique can also be applied to body fluids.

Other antibody-based methods useful for detecting *Borrelia* polypeptide gene expression include immunoassays, such as the ELISA and the radioimmunoassay (RIA). For example, a *Borrelia* polypeptide-specific monoclonal antibodies can be used both as an immunoabsorbent and as an enzyme-labeled probe to detect and quantify a *Borrelia* polypeptide. The amount of a *Borrelia* polypeptide present in the sample can be calculated by reference to the amount present in a standard preparation using a linear regression computer algorithm. Such an ELISA is described in Iacobelli et al. (1988) Breast Cancer Research and Treatment 11:19-30. In another ELISA assay, two distinct specific monoclonal antibodies can be used to detect *Borrelia* polypeptides in a body fluid. In this assay, one of the antibodies is used as the immunoabsorbent and the other as the enzyme-labeled probe.

The above techniques may be conducted essentially as a "one-step" or "two-step" assay. The "one-step" assay involves contacting the *Borrelia* polypeptide with immobilized antibody and, without washing, contacting the mixture with the labeled antibody. The "two-step" assay involves washing before contacting the mixture with the labeled antibody. Other conventional methods may also be employed as suitable. It is usually desirable to immobilize one component of the assay system on a support, thereby allowing other components of the system to be brought into contact with the component and readily removed from the sample. Variations of the above

and other immunological methods included in the present invention can also be found in Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988).

Suitable enzyme labels include, for example, those from the oxidase group, which catalyze the production of hydrogen peroxide by reacting with substrate. Glucose oxidase is particularly preferred as it has good stability and its substrate (glucose) is readily available. Activity of an oxidase label may be assayed by measuring the concentration of hydrogen peroxide formed by the enzyme-labeled antibody/substrate reaction. Besides enzymes, other suitable labels include radioisotopes, such as iodine (^{125}I, ^{121}I), carbon (^{14}C), sulphur (^{35}S), tritium (^{3}H), indium (^{112}In), and technetium (^{99m}Tc), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

Further suitable labels for the *Borrelia* polypeptide-specific antibodies of the present invention are provided below. Examples of suitable enzyme labels include malate dehydrogenase, Borrelia nuclease, delta-5-steroid isomerase, yeast-alcohol dehydrogenase, alpha-glycerol phosphate dehydrogenase, triose phosphate isomerase, peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, beta-galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase, and acetylcholine esterase.

Examples of suitable radioisotopic labels include ^{3}H, ^{111}In, ^{125}I, ^{131}I, ^{32}P, ^{35}S, ^{14}C, ^{51}Cr, ^{57}To, ^{58}Co, ^{59}Fe, ^{75}Se, ^{152}Eu, ^{90}Y, ^{67}Cu, ^{217}Ci, ^{211}At, ^{212}Pb, ^{47}Sc, ^{109}Pd, etc. ^{111}In is a preferred isotope where *in vivo* imaging is used since its avoids the problem of dehalogenation of the ^{125}I or ^{131}I-labeled monoclonal antibody by the liver. In addition, this radionucleotide has a more favorable gamma emission energy for imaging. *See, e.g.*, Perkins et al. (1985) Eur. J. Nucl. Med. 10:296-301; Carasquillo et al. (1987) J. Nucl. Med. 28:281-287. For example, ^{111}In coupled to monoclonal antibodies with 1-(P-isothiocyanatobenzyl)-DPTA has shown little uptake in non-tumors tissues, particularly the liver, and therefore enhances specificity of tumor localization. See, Esteban et al. (1987) J. Nucl. Med. 28:861-870.

Examples of suitable non-radioactive isotopic labels include ^{157}Gd, ^{55}Mn, ^{162}Dy, ^{52}Tr, and ^{56}Fe.

Examples of suitable fluorescent labels include an ^{152}Eu label, a fluorescein label, an isothiocyanate label, a rhodamine label, a phycoerythrin label, a phycocyanin label, an allophycocyanin label, an o-phthaldehyde label, and a fluorescamine label.

Examples of suitable toxin labels include, *Pseudomonas* toxin, diphtheria toxin, ricin, and cholera toxin.

Examples of chemiluminescent labels include a luminal label, an isoluminal label, an aromatic acridinium ester label, an imidazole label, an acridinium salt label, an oxalate ester label, a luciferin label, a luciferase label, and an aequorin label.

Examples of nuclear magnetic resonance contrasting agents include heavy metal nuclei such as Gd, Mn, and iron.

Typical techniques for binding the above-described labels to antibodies are provided by

Kennedy et al. (1976) Clin. Chim. Acta 70:1-31, and Schurs et al. (1977) Clin. Chim. Acta 81:1-40. Coupling techniques mentioned in the latter are the glutaraldehyde method, the periodate method, the dimaleimide method, the m-maleimidobenzyl-N-hydroxy-succinimide ester method, all of which methods are incorporated by reference herein.

In a related aspect, the invention includes a diagnostic kit for use in screening serum containing antibodies specific against *B. burgdorferi* infection. Such a kit may include an isolated *B. burgdorferi* antigen comprising an epitope which is specifically immunoreactive with at least one anti-*B. burgdorferi* antibody. Such a kit also includes means for detecting the binding of said antibody to the antigen. In specific embodiments, the kit may include a recombinantly produced or chemically synthesized peptide or polypeptide antigen. The peptide or polypeptide antigen may be attached to a solid support.

In a more specific embodiment, the detecting means of the above-described kit includes a solid support to which said peptide or polypeptide antigen is attached. Such a kit may also include a non-attached reporter-labeled anti-human antibody. In this embodiment, binding of the antibody to the *B. burgdorferi* antigen can be detected by binding of the reporter labeled antibody to the anti-*B. burgdorferi* polypeptide antibody.

In a related aspect, the invention includes a method of detecting *B. burgdorferi* infection in a subject. This detection method includes reacting a body fluid, preferably serum, from the subject with an isolated *B. burgdorferi* antigen, and examining the antigen for the presence of bound antibody. In a specific embodiment, the method includes a polypeptide antigen attached to a solid support, and serum is reacted with the support. Subsequently, the support is reacted with a reporter-labeled anti-human antibody. The support is then examined for the presence of reporter-labeled antibody.

The solid surface reagent employed in the above assays and kits is prepared by known techniques for attaching protein material to solid support material, such as polymeric beads, dip sticks, 96-well plates or filter material. These attachment methods generally include non-specific adsorption of the protein to the support or covalent attachment of the protein , typically through a free amine group, to a chemically reactive group on the solid support, such as an activated carboxyl, hydroxyl, or aldehyde group. Alternatively, streptavidin coated plates can be used in conjunction with biotinylated antigen(s).

The polypeptides and antibodies of the present invention, including fragments thereof, may be used to detect Borrelia species including *B. burgdorferi* using bio chip and biosensor technology. Bio chip and biosensors of the present invention may comprise the polypeptides of the present invention to detect antibodies, which specifically recognize Borrelia species, including *B. burgdorferi*. Bio chip and biosensors of the present invention may also comprise antibodies which specifically recognize the polypeptides of the present invention to detect Borrelia species, including *B. burgdorferi* or specific polypeptides of the present invention. Bio chips or biosensors comprising polypeptides or antibodies of the present invention may be used to detect Borrelia species, including *B. burgdorferi*, in biological and environmental samples and to

diagnose an animal, including humans, with an *B. burgdorferi* or other Borrelia infection. Thus, the present invention includes both bio chips and biosensors comprising polypeptides or antibodies of the present invention and methods of their use.

The bio chips of the present invention may further comprise polypeptide sequences of other pathogens including bacteria, viral, parasitic, and fungal polypeptide sequences, in addition to the polypeptide sequences of the present invention, for use in rapid diffenertial pathogenic detection and diagnosis. The bio chips of the present invention may further comprise antibodies or fragements thereof specific for other pathogens including bacteria, viral, parasitic, and fungal polypeptide sequences, in addition to the antibodies or fragements thereof of the present invention, for use in rapid diffenertial pathogenic detection and diagnosis. The bio chips and biosensors of the present invention may also be used to monitor an *B. burgdorferi* or other Borrelia infection and to monitor the genetic changes (amio acid deletions, insertions, substitutions, etc.) in response to drug therapy in the clinic and drug development in the laboratory. The bio chip and biosensors comprising polypeptides or antibodies of the present invention may also be used to simultaneously monitor the expression of a multiplicity of polypeptides, including those of the present invention. The polypeptides used to comprise a bio chip or biosensor of the present invention may be specified in the same manner as for the fragements, i.e, by their N-terminal and C-terminal positions or length in contigious amino acid residue. Methods and particular uses of the polypeptides and antibodies of the present invention to detect Borrelia species, including *B. burgdorferi*, or specific polypeptides using bio chip and biosensor technology include those known in the art, those of the U.S. Patent Nos. and World Patent Nos. listed above for bio chips and biosensors using polynucleotides of the present invention, and those of: U.S. Patent Nos. 5658732, 5135852, 5567301, 5677196, 5690894 and World Patent Nos. WO9729366, WO9612957, each incorporated herein in their entireties.

Treatment:

Agonists and Antagonists - Assays and Molecules

The invention also provides a method of screening compounds to identify those which enhance or block the biological activity of the *B. burgdorferi* polypeptides of the present invention. The present invention further provides where the compounds kill or slow the growth of *B. burgdorferi*. The ability of *B. burgdorferi* antagonists, including *B. burgdorferi* ligands, to prophylactically or therapeutically block antibiotic resistance may be easily tested by the skilled artisan. *See, e.g.,* Straden et al. (1997) J Bacteriol. 179(1):9-16.

An agonist is a compound which increases the natural biological function or which functions in a manner similar to the polypeptides of the present invention, while antagonists decrease or eliminate such functions. Potential antagonists include small organic molecules, peptides, polypeptides, and antibodies that bind to a polypeptide of the invention and thereby inhibit or extinguish its activity.

The antagonists may be employed for instance to inhibit peptidoglycan cross bridge

formation. Antibodies against *B. burgdorferi* may be employed to bind to and inhibit *B. burgdorferi* activity to treat antibiotic resistance. Any of the above antagonists may be employed in a composition with a pharmaceutically acceptable carrier.

Vaccines

The present invention also provides vaccines comprising one or more polypeptides of the present invention. Heterogeneity in the composition of a vaccine may be provided by combining *B. burgdorferi* polypeptides of the present invention. Multi-component vaccines of this type are desirable because they are likely to be more effective in eliciting protective immune responses against multiple species and strains of the *Borrelia* genus than single polypeptide vaccines. Thus, as discussed in detail below, a multi-component vaccine of the present invention may contain one or more, preferably 2 to about 20, more preferably 2 to about 15, and most preferably 3 to about 8, of the *B. burgdorferi* polypeptides shown in Table 1, or fragments thereof.

Multi-component vaccines are known in the art to elicit antibody production to numerous immunogenic components. Decker, M. and Edwards, K., *J. Infect. Dis. 174*:S270-275 (1996). In addition, a hepatitis B, diphtheria, tetanus, pertussis tetravalent vaccine has recently been demonstrated to elicit protective levels of antibodies in human infants against all four pathogenic agents. Aristegui, J. *et al., Vaccine 15*:7-9 (1997).

The present invention thus also includes multi-component vaccines. These vaccines comprise more than one polypeptide, immunogen or antigen. An example of such a multi-component vaccine would be a vaccine comprising more than one of the *B. burgdorferi* polypeptides shown in Table 1. A second example is a vaccine comprising one or more, for example 2 to 10, of the *B. burgdorferi* polypeptides shown in Table 1 and one or more, for example 2 to 10, additional polypeptides of either borrelial or non-borrelial origin. Thus, a multi-component vaccine which confers protective immunity to both a borrelial infection and infection by another pathogenic agent is also within the scope of the invention.

As indicated above, the vaccines of the present invention are expected to elicit a protective immune response against infections caused by species and strains of *Borrelia* other than *B. burgdorferi* sensu stricto isolate B31 (ATCC Accession No. 35210). Immunizations using decorin-binding protein and OspA derived from one strain of *B. burgdorferi* has been shown to elicit the production of antiserum which confers passive immunity against other strains of *B. burgdorferi*. Cassatt, D. *et al., Protection of Borrelia burgdorferi Infection by Antibodies to Decorin-binding Protein*, in VACCINES97, Cold Spring Harbor Press (1997), pages 191-195. Further, the inventors have found using an *in vitro* assay that antiserum produced in response to *B. burgdorferi* decorin-binding protein will kill several species of *Borrelia*. The amino acid sequences of decorin-binding protein expressed by different strains of *B. burgdorferi* are believed to diverge by as much as 25%. Thus, antisera elicited against decorin-binding proteins confers passive immunity against *Borrelia* expressing proteins having only 75% or less amino acid sequence similarity.

Further within the scope of the invention are whole cell and whole viral vaccines. Such vaccines may be produced recombinantly and involve the expression of one or more of the *B. burgdorferi* polypeptides shown in Table 1. For example, the *B. burgdorferi* polypeptides of the present invention may be either secreted or localized intracellular, on the cell surface, or in the periplasmic space. Further, when a recombinant virus is used, the *B. burgdorferi* polypeptides of the present invention may, for example, be localized in the viral envelope, on the surface of the capsid, or internally within the capsid. Whole cells vaccines which employ cells expressing heterologous proteins are known in the art. *See, e.g.*, Robinson, K. *et al., Nature Biotech. 15*:653-657 (1997); Sirard, J. *et al., Infect. Immun. 65*:2029-2033 (1997); Chabalgoity, J. *et al., Infect. Immun. 65*:2402-2412 (1997). These cells may be administered live or may be killed prior to administration. Chabalgoity, J. *et al.*, *supra*, for example, report the successful use in mice of a live attenuated *Salmonella* vaccine strain which expresses a portion of a platyhelminth fatty acid-binding protein as a fusion protein on its cells surface.

A multi-component vaccine can also be prepared using techniques known in the art by combining one or more *B. burgdorferi* polypeptides of the present invention, or fragments thereof, with additional non-borrelial components (*e.g.*, diphtheria toxin or tetanus toxin, and/or other compounds known to elicit an immune response). Such vaccines are useful for eliciting protective immune responses to both members of the *Borrelia* genus and non-borrelial pathogenic agents.

The vaccines of the present invention also include DNA vaccines. DNA vaccines are currently being developed for a number of infectious diseases. Boyer, J *et al., Nat. Med. 3*:526-532 (1997); reviewed in Spier, R., *Vaccine 14*:1285-1288 (1996). Such DNA vaccines contain a nucleotide sequence encoding one or more *B. burgdorferi* polypeptides of the present invention oriented in a manner that allows for expression of the subject polypeptide. The direct administration of plasmid DNA encoding OspA has been shown to elicit protective immunity in mice against borrelial challenge. Luke, C. *et al., J. Infect. Dis. 175*:91-97 (1997).

The present invention also relates to the administration of a vaccine which is co-administered with a molecule capable of modulating immune responses. Kim, J. *et al., Nature Biotech. 15*:641-646 (1997), for example, report the enhancement of immune responses produced by DNA immunizations when DNA sequences encoding molecules which stimulate the immune response are co-administered. In a similar fashion, the vaccines of the present invention may be co-administered with either nucleic acids encoding immune modulators or the immune modulators themselves. These immune modulators include granulocyte macrophage colony stimulating factor (GM-CSF) and CD86.

The vaccines of the present invention may be used to confer resistance to borrelial infection by either passive or active immunization. When the vaccines of the present invention are used to confer resistance to borrelial infection through active immunization, a vaccine of the present invention is administered to an animal to elicit a protective immune response which either prevents or attenuates a borrelial infection. When the vaccines of the present invention are used to

confer resistance to borrelial infection through passive immunization, the vaccine is provided to a host animal (*e.g.*, human, dog, or mouse), and the antisera elicited by this antisera is recovered and directly provided to a recipient suspected of having an infection caused by a member of the *Borrelia* genus.

The ability to label antibodies, or fragments of antibodies, with toxin molecules provides an additional method for treating borrelial infections when passive immunization is conducted. In this embodiment, antibodies, or fragments of antibodies, capable of recognizing the *B. burgdorferi* polypeptides disclosed herein, or fragments thereof, as well as other *Borrelia* proteins, are labeled with toxin molecules prior to their administration to the patient. When such toxin derivatized antibodies bind to *Borrelia* cells, toxin moieties will be localized to these cells and will cause their death.

The present invention thus concerns and provides a means for preventing or attenuating a borrelial infection resulting from organisms which have antigens that are recognized and bound by antisera produced in response to the polypeptides of the present invention. As used herein, a vaccine is said to prevent or attenuate a disease if its administration to an animal results either in the total or partial attenuation (*i.e.*, suppression) of a symptom or condition of the disease, or in the total or partial immunity of the animal to the disease.

The administration of the vaccine (or the antisera which it elicits) may be for either a "prophylactic" or "therapeutic" purpose. When provided prophylactically, the compound(s) are provided in advance of any symptoms of borrelial infection. The prophylactic administration of the compound(s) serves to prevent or attenuate any subsequent infection. When provided therapeutically, the compound(s) is provided upon or after the detection of symptoms which indicate that an animal may be infected with a member of the *Borrelia* genus. The therapeutic administration of the compound(s) serves to attenuate any actual infection. Thus, the *B. burgdorferi* polypeptides, and fragments thereof, of the present invention may be provided either prior to the onset of infection (so as to prevent or attenuate an anticipated infection) or after the initiation of an actual infection.

The polypeptides of the invention, whether encoding a portion of a native protein or a functional derivative thereof, may be administered in pure form or may be coupled to a macromolecular carrier. Example of such carriers are proteins and carbohydrates. Suitable proteins which may act as macromolecular carrier for enhancing the immunogenicity of the polypeptides of the present invention include keyhole limpet hemacyanin (KLH) tetanus toxoid, pertussis toxin, bovine serum albumin, and ovalbumin. Methods for coupling the polypeptides of the present invention to such macromolecular carriers are disclosed in Harlow *et al.*, *Antibodies: A Laboratory Manual, 2nd Ed.*; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1988), the entire disclosure of which is incorporated by reference herein.

A composition is said to be "pharmacologically acceptable" if its administration can be tolerated by a recipient animal and is otherwise suitable for administration to that animal. Such an agent is said to be administered in a "therapeutically effective amount" if the amount administered

is physiologically significant. An agent is physiologically significant if its presence results in a detectable change in the physiology of a recipient patient.

While in all instances the vaccine of the present invention is administered as a pharmacologically acceptable compound, one skilled in the art would recognize that the composition of a pharmacologically acceptable compound varies with the animal to which it is administered. For example, a vaccine intended for human use will generally not be co-administered with Freund's adjuvant. Further, the level of purity of the *B. burgdorferi* polypeptides of the present invention will normally be higher when administered to a human than when administered to a non-human animal.

As would be understood by one of ordinary skill in the art, when the vaccine of the present invention is provided to an animal, it may be in a composition which may contain salts, buffers, adjuvants, or other substances which are desirable for improving the efficacy of the composition. Adjuvants are substances that can be used to specifically augment a specific immune response. These substances generally perform two functions: (1) they protect the antigen(s) from being rapidly catabolized after administration and (2) they nonspecifically stimulate immune responses.

Normally, the adjuvant and the composition are mixed prior to presentation to the immune system, or presented separately, but into the same site of the animal being immunized. Adjuvants can be loosely divided into several groups based upon their composition. These groups include oil adjuvants (for example, Freund's complete and incomplete), mineral salts (for example, $AlK(SO_4)_2$, $AlNa(SO_4)_2$, $AlNH_4(SO_4)$, silica, kaolin, and carbon), polynucleotides (for example, poly IC and poly AU acids), and certain natural substances (for example, wax D from *Mycobacterium tuberculosis*, as well as substances found in *Corynebacterium parvum*, or *Bordetella pertussis*, and members of the genus *Brucella*. Other substances useful as adjuvants are the saponins such as, for example, Quil A. (Superfos A/S, Denmark). Preferred adjuvants for use in the present invention include aluminum salts, such as $AlK(SO_4)_2$, $AlNa(SO_4)_2$, and $AlNH_4(SO_4)$. Examples of materials suitable for use in vaccine compositions are provided in *Remington's Pharmaceutical Sciences* (Osol, A, Ed, Mack Publishing Co, Easton, PA, pp. 1324-1341 (1980), which reference is incorporated herein by reference).

The therapeutic compositions of the present invention can be administered parenterally by injection, rapid infusion, nasopharyngeal absorption (intranasopharangeally), dermoabsorption, or orally. The compositions may alternatively be administered intramuscularly, or intravenously. Compositions for parenteral administration include sterile aqueous or non-aqueous solutions, suspensions, and emulsions. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Carriers or occlusive dressings can be used to increase skin permeability and enhance antigen absorption. Liquid dosage forms for oral administration may generally comprise a liposome solution containing the liquid dosage form. Suitable forms for suspending liposomes include emulsions, suspensions, solutions, syrups, and elixirs containing inert diluents

commonly used in the art, such as purified water. Besides the inert diluents, such compositions can also include adjuvants, wetting agents, emulsifying and suspending agents, or sweetening, flavoring, or perfuming agents.

Therapeutic compositions of the present invention can also be administered in encapsulated form. For example, intranasal immunization of mice against *Bordetella pertussis* infection using vaccines encapsulated in biodegradable microsphere composed of poly(DL-lactide-co-glycolide) has been shown to stimulate protective immune responses. Shahin, R. *et al., Infect. Immun. 63*:1195-1200 (1995). Similarly, orally administered encapsulated *Salmonella typhimurium* antigens have also been shown to elicit protective immunity in mice. Allaoui-Attarki, K. *et al., Infect. Immun. 65*:853-857 (1997). Encapsulated vaccines of the present invention can be administered by a variety of routes including those involving contacting the vaccine with mucous membranes (*e.g.*, intranasally, intracolonicly, intraduodenally).

Many different techniques exist for the timing of the immunizations when a multiple administration regimen is utilized. It is possible to use the compositions of the invention more than once to increase the levels and diversities of expression of the immunoglobulin repertoire expressed by the immunized animal. Typically, if multiple immunizations are given, they will be given one to two months apart.

According to the present invention, an "effective amount" of a therapeutic composition is one which is sufficient to achieve a desired biological effect. Generally, the dosage needed to provide an effective amount of the composition will vary depending upon such factors as the animal's or human's age, condition, sex, and extent of disease, if any, and other variables which can be adjusted by one of ordinary skill in the art.

The antigenic preparations of the invention can be administered by either single or multiple dosages of an effective amount. Effective amounts of the compositions of the invention can vary from 0.01-1,000 μg/ml per dose, more preferably 0.1-500 μg/ml per dose, and most preferably 10-300 μg/ml per dose.

Having now generally described the invention, the same will be more readily understood through reference to the following example which is provided by way of illustration, and is not intended to be limiting of the present invention, unless specified.

Examples

1. Preparation of PCR Primers and Amplification of DNA

Various fragments of the *Borrelia burgdorferi* genome, such as those of Table 1, can be used, in accordance with the present invention, to prepare PCR primers for a variety of uses. The PCR primers are preferably at least 15 bases, and more preferably at least 18 bases in length. When selecting a primer sequence, it is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. The PCR primers and

amplified DNA of this Example find use in the Examples that follow.

2. *Isolation of a Selected DNA Clone From B. burgdorferi*

Three approaches are used to isolate a *B. burgdorferi* clone comprising a polynucleotide of the present invention from any *B. burgdorferi* genomic DNA library. The *B. burgdorferi* strain B31PU has been deposited as a convienent source for obtaining a *B. burgdorferi* strain although a wide varity of strains *B. burgdorferi* strains can be used which are known in the art.

B. burgdorferi genomic DNA is prepared using the following method. A 20ml overnight bacterial culture grown in a rich medium (e.g., Trypticase Soy Broth, Brain Heart Infusion broth or Super broth), pelleted, ished two times with TES (3OmM Tris-pH 8.0, 25mM EDTA, 50mM NaCl), and resuspended in 5ml high salt TES (2.5M NaCl). Lysostaphin is added to final concentration of approx 50ug/ml and the mixture is rotated slowly 1 hour at 37C to make protoplast cells. The solution is then placed in incubator (or place in a shaking water bath) and warmed to 55C. Five hundred micro liter of 20% sarcosyl in TES (final concentration 2%) is then added to lyse the cells. Next, guanidine HCl is added to a final concentration of 7M (3.69g in 5.5 ml). The mixture is swirled slowly at 55C for 60-90 min (solution should clear). A CsCl gradient is then set up in SW41 ultra clear tubes using 2.0ml 5.7M CsCl and overlaying with 2.85M CsCl. The gradient is carefully overlayed with the DNA-containing GuHCl solution. The gradient is spun at 30,000 rpm, 20C for 24 hr and the lower DNA band is collected. The volume is increased to 5 ml with TE buffer. The DNA is then treated with protease K (10 ug/ml) overnight at 37 C, and precipitated with ethanol. The precipitated DNA is resuspended in a desired buffer.

In the first method, a plasmid is directly isolated by screening a plasmid *B. burgdorferi* genomic DNA library using a polynucleotide probe corresponding to a polynucleotide of the present invention. Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported. The oligonucleotide is labeled, for instance, with ^{32}P-γ-ATP using T4 polynucleotide kinase and purified according to routine methods. (*See, e.g.*, Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982).) The library is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art. *See, e.g.*, Sambrook et al. MOLECULAR CLONING: A LABORATORY MANUAL (Cold Spring Harbor, N.Y. 2nd ed. 1989); Ausubel et al., CURRENT PROTOCALS IN MOLECULAR BIOLOGY (John Wiley and Sons, N.Y. 1989). The transformants are plated on 1.5% agar plates (containing the appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening. *See, e.g.*, Sambrook et al. MOLECULAR CLONING: A LABORATORY MANUAL (Cold Spring Harbor, N.Y. 2nd ed. 1989); Ausubel et al., CURRENT PROTOCALS IN

MOLECULAR BIOLOGY (John Wiley and Sons, N.Y. 1989) or other techniques known to those of skill in the art.

Alternatively, two primers of 15-25 nucleotides derived from the 5' and 3' ends of a polynucleotide of Table 1 are synthesized and used to amplify the desired DNA by PCR using a *B. burgdorferi* genomic DNA prep as a template. PCR is carried out under routine conditions, for instance, in 25 µl of reaction mixture with 0.5 ug of the above DNA template. A convenient reaction mixture is 1.5-5 mM $MgCl_2$, 0.01% (w/v) gelatin, 20 µM each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

Finally, overlapping oligos of the DNA sequences of Table 1 can be chemically synthesized and used to generate a nucleotide sequence of desired length using PCR methods known in the art.

3(a). Expression and Purification Borrelia polypeptides in E. coli

The bacterial expression vector pQE60 is used for bacterial expression of some of the polypeptide fragements of the present invention. (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311). pQE60 encodes ampicillin antibiotic resistance ("Ampr") and contains a bacterial origin of replication ("ori"), an IPTG inducible promoter, a ribosome binding site ("RBS"), six codons encoding histidine residues that allow affinity purification using nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin (QIAGEN, Inc., *supra*) and suitable single restriction enzyme cleavage sites. These elements are arranged such that an inserted DNA fragment encoding a polypeptide expresses that polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the carboxyl terminus of that polypeptide.

The DNA sequence encoding the desired portion of a *B. burgdorferi* protein of the present invention is amplified from *B. burgdorferi* genomic DNA using PCR oligonucleotide primers which anneal to the 5' and 3' sequences coding for the portions of the *B. burgdorferi* polynucleotide shown in Table 1. Additional nucleotides containing restriction sites to facilitate cloning in the pQE60 vector are added to the 5' and 3' sequences, respectively.

For cloning the mature protein, the 5' primer has a sequence containing an appropriate restriction site followed by nucleotides of the amino terminal coding sequence of the desired *B. burgdorferi* polynucleotide sequence in Table 1. One of ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begin may be varied to amplify a DNA segment encoding any desired portion of the complete protein shorter or longer than the mature form. The 3' primer has a sequence containing an appropriate restriction site

followed by nucleotides complementary to the 3' end of the polypeptide coding sequence of Table 1, excluding a stop codon, with the coding sequence aligned with the restriction site so as to maintain its reading frame with that of the six His codons in the pQE60 vector.

The amplified *B. burgdorferi* DNA fragment and the vector pQE60 are digested with restriction enzymes which recognize the sites in the primers and the digested DNAs are then ligated together. The *B. burgdorferi* DNA is inserted into the restricted pQE60 vector in a manner which places the *B. burgdorferi* protein coding region downstream from the IPTG-inducible promoter and in-frame with an initiating AUG and the six histidine codons.

The ligation mixture is transformed into competent *E. coli* cells using standard procedures such as those described by Sambrook et al., *supra*.. *E. coli* strain M15/rep4, containing multiple copies of the plasmid pREP4, which expresses the lac repressor and confers kanamycin resistance ("Kanr"), is used in carrying out the illustrative example described herein. This strain, which is only one of many that are suitable for expressing a *B. burgdorferi* polypeptide, is available commercially (QIAGEN, Inc., *supra*). Transformants are identified by their ability to grow on LB agar plates in the presence of ampicillin and kanamycin. Plasmid DNA is isolated from resistant colonies and the identity of the cloned DNA confirmed by restriction analysis, PCR and DNA sequencing.

Clones containing the desired constructs are grown overnight ("O/N") in liquid culture in LB media supplemented with both ampicillin (100 μg/ml) and kanamycin (25 μg/ml). The O/N culture is used to inoculate a large culture, at a dilution of approximately 1:25 to 1:250. The cells are grown to an optical density at 600 nm ("OD600") of between 0.4 and 0.6. Isopropyl-β-D-thiogalactopyranoside ("IPTG") is then added to a final concentration of 1 mM to induce transcription from the lac repressor sensitive promoter, by inactivating the lacI repressor. Cells subsequently are incubated further for 3 to 4 hours. Cells then are harvested by centrifugation.

The cells are then stirred for 3-4 hours at 4°C in 6M guanidine-HCl, pH 8. The cell debris is removed by centrifugation, and the supernatant containing the *B. burgdorferi* polypeptide is loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high affinity are purified in a simple one-step procedure (for details see: The QIAexpressionist, 1995, QIAGEN, Inc., *supra*). Briefly the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8, the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the *B. burgdorferi* polypeptide is eluted with 6 M guanidine-HCl, pH 5.

The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein could be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over

a period of 1.5 hours or more. After renaturation the proteins can be eluted by the addition of 250 mM immidazole. Immidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein is stored at 4° C or frozen at -80° C.

The polypeptide of the present invention are also prepared using a non-denaturing protein purification method. For these polypeptides, the cell pellet from each liter of culture is resuspended in 25 mls of Lysis Buffer A at 4°C (Lysis Buffer A = 50 mM Na-phosphate, 300 mM NaCl, 10 mM 2-mercaptoethanol, 10% Glycerol, pH 7.5 with 1 tablet of Complete EDTA-free protease inhibitor cocktail (Boehringer Mannheim #1873580) per 50 ml of buffer). Absorbance at 550 nm is approximately 10-20 O.D./ml. The suspension is then put through three freeze/thaw cycles from -70°C (using a ethanol-dry ice bath) up to room temperature. The cells are lysed via sonication in short 10 sec bursts over 3 minutes at approximately 80W while kept on ice. The sonicated sample is then centrifuged at 15,000 RPM for 30 minutes at 4°C. The supernatant is passed through a column containing 1.0 ml of CL-4B resin to pre-clear the sample of any proteins that may bind to agarose non-specifically, and the flow-through fraction is collected.

The pre-cleared flow-through is applied to a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (Quiagen, Inc., *supra*). Proteins with a 6 X His tag bind to the Ni-NTA resin with high affinity and can be purified in a simple one-step procedure. Briefly, the supernatant is loaded onto the column in Lysis Buffer A at 4°C, the column is first washed with 10 volumes of Lysis Buffer A until the A280 of the eluate returns to the baseline. Then, the column is washed with 5 volumes of 40 mM Imidazole (92% Lysis Buffer A / 8% Buffer B) (Buffer B = 50 mM Na-Phosphate, 300 mM NaCl, 10% Glycerol, 10 mM 2-mercaptoethanol, 500 mM Imidazole, pH of the final buffer should be 7.5). The protein is eluted off of the column with a series of increasing Imidazole solutions made by adjusting the ratios of Lysis Buffer A to Buffer B. Three different concentrations are used: 3 volumes of 75 mM Imidazole, 3 volumes of 150 mM Imidazole, 5 volumes of 500 mM Imidazole. The fractions containing the purified protein are analyzed using 8 %, 10 % or 14% SDS-PAGE depending on the protein size. The purified protein is then dialyzed 2X against phosphate-buffered saline (PBS) in order to place it into an easily workable buffer. The purified protein is stored at 4° C or frozen at -80°.

The following alternative method may be used to purify *B. burgdorferi* expressed in *E coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells are harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

The cells are then lysed by passing the solution through a microfluidizer (Microfuidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 x *g* for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 x *g* centrifugation for 15 min., the pellet is discarded and the *B. burgdorferi* polypeptide-containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

Following high speed centrifugation (30,000 x *g*) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

To clarify the refolded *B. burgdorferi* polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16 μm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 mm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the *B. burgdorferi* polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A_{280} monitoring of the effluent. Fractions containing the *B. burgdorferi* polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant *B. burgdorferi* polypeptide exhibits greater than 95% purity after the above refolding and purification steps. No major contaminant bands are observed from Commassie blue stained 16% SDS-PAGE gel when 5 μg of purified protein is loaded. The purified protein is also tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

3(b). Alternative Expression and Purification Borrelia polypeptides in E.

coli

Tthe vector pQE10 is alternatively used to clone and express some of the polypeptides of the present invention for use in the soft tissue and systemic infection models discussed below. The difference being such that an inserted DNA fragment encoding a polypeptide expresses that polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the amino terminus of that polypeptide. The bacterial expression vector pQE10 (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311) was used in this example . The components of the pQE10 plasmid are arranged such that the inserted DNA sequence encoding a polypeptide of the present invention expresses the polypeptide with the six His residues (*i.e.*, a "6 X His tag")) covalently linked to the amino terminus.

The DNA sequences encoding the desired portions of a polypeptide of Table 1 were amplified using PCR oligonucleotide primers from genomic *B. burgdorferi* DNA. The PCR primers anneal to the nucleotide sequences encoding the desired amino acid sequence of a polypeptide of the present invention. Additional nucleotides containing restriction sites to facilitate cloning in the pQE10 vector were added to the 5' and 3' primer sequences, respectively.

For cloning a polypeptide of the present invention, the 5' and 3' primers were selected to amplify their respective nucleotide coding sequences. One of ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begins may be varied to amplify a DNA segment encoding any desired portion of a polypeptide of the present invention. The 5' primer was designed so the coding sequence of the 6 X His tag is aligned with the restriction site so as to maintain its reading frame with that of *B. burgdorferi* polypeptide. The 3' was designed to include an stop codon. The amplified DNA fragment was then cloned, and the protein expressed, as described above for the pQE60 plasmid.

The DNA sequences of Table 1 encoding amino acid sequences may also be cloned and expressed as fusion proteins by a protocol similar to that described directly above, wherein the pET-32b(+) vector (Novagen, 601 Science Drive, Madison, WI 53711) is preferentially used in place of pQE10.

The above methods are not limited to the polypeptide fragements actually produced. The above method, like the methods below, can be used to produce either full length polypeptides or desired fragements therof.

3(c). Alternative Expression and Purification of Borrelia polypeptides in E. coli

The bacterial expression vector pQE60 is used for bacterial expression in this example (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311). However, in this example, the polypeptide coding sequence is inserted such that translation of the six His codons is prevented and, therefore, the polypeptide is produced with no 6 X His tag.

The DNA sequence encoding the desired portion of the *B. burgdorferi* amino acid sequence is amplified from an *B. burgdorferi* genomic DNA prep the deposited DNA clones

using PCR oligonucleotide primers which anneal to the 5' and 3' nucleotide sequences corresponding to the desired portion of the *B. burgdorferi* polypeptides. Additional nucleotides containing restriction sites to facilitate cloning in the pQE60 vector are added to the 5' and 3' primer sequences.

For cloning a *B. burgdorferi* polypeptides of the present invention, 5' and 3' primers are selected to amplify their respective nucleotide coding sequences. One of ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begin may be varied to amplify a DNA segment encoding any desired portion of a polypeptide of the present invention. The 3' and 5' primers contain appropriate restriction sites followed by nucleotides complementary to the 5' and 3' ends of the coding sequence respectively. The 3' primer is additionally designed to include an in-frame stop codon.

The amplified *B. burgdorferi* DNA fragments and the vector pQE60 are digested with restriction enzymes recognizing the sites in the primers and the digested DNAs are then ligated together. Insertion of the *B. burgdorferi* DNA into the restricted pQE60 vector places the *B. burgdorferi* protein coding region including its associated stop codon downstream from the IPTG-inducible promoter and in-frame with an initiating AUG. The associated stop codon prevents translation of the six histidine codons downstream of the insertion point.

The ligation mixture is transformed into competent *E. coli* cells using standard procedures such as those described by Sambrook et al. *E. coli* strain M15/rep4, containing multiple copies of the plasmid pREP4, which expresses the lac repressor and confers kanamycin resistance ("Kanr"), is used in carrying out the illustrative example described herein. This strain, which is only one of many that are suitable for expressing *B. burgdorferi* polypeptide, is available commercially (QIAGEN, Inc., *supra*). Transformants are identified by their ability to grow on LB plates in the presence of ampicillin and kanamycin. Plasmid DNA is isolated from resistant colonies and the identity of the cloned DNA confirmed by restriction analysis, PCR and DNA sequencing.

Clones containing the desired constructs are grown overnight ("O/N") in liquid culture in LB media supplemented with both ampicillin (100 μg/ml) and kanamycin (25 μg/ml). The O/N culture is used to inoculate a large culture, at a dilution of approximately 1:25 to 1:250. The cells are grown to an optical density at 600 nm ("OD600") of between 0.4 and 0.6. isopropyl-b-D-thiogalactopyranoside ("IPTG") is then added to a final concentration of 1 mM to induce transcription from the *lac* repressor sensitive promoter, by inactivating the lacI repressor. Cells subsequently are incubated further for 3 to 4 hours. Cells then are harvested by centrifugation.

To purify the *B. burgdorferi* polypeptide, the cells are then stirred for 3-4 hours at 4°C in 6M guanidine-HCl, pH 8. The cell debris is removed by centrifugation, and the supernatant containing the *B. burgdorferi* polypeptide is dialyzed against 50 mM Na-acetate buffer pH 6, supplemented with 200 mM NaCl. Alternatively, the protein can be successfully refolded by dialyzing it against 500 mM NaCl, 20% glycerol, 25 mM Tris/HCl pH 7.4, containing protease

inhibitors. After renaturation the protein can be purified by ion exchange, hydrophobic interaction and size exclusion chromatography. Alternatively, an affinity chromatography step such as an antibody column can be used to obtain pure *B. burgdorferi* polypeptide. The purified protein is stored at 4°C or frozen at -80°C.

The following alternative method may be used to purify *B. burgdorferi* polypeptides expressed in *E coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells are harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

The cells ware then lysed by passing the solution through a microfluidizer (Microfuidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 x *g* for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 x *g* centrifugation for 15 min., the pellet is discarded and the *B. burgdorferi* polypeptide-containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

Following high speed centrifugation (30,000 x *g*) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

To clarify the refolded *B. burgdorferi* polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16 μm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 mm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the *B. burgdorferi* polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20,

Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A_{280} monitoring of the effluent. Fractions containing the *B. burgdorferi* polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant *B. burgdorferi* polypeptide exhibits greater than 95% purity after the above refolding and purification steps. No major contaminant bands are observed from Commassie blue stained 16% SDS-PAGE gel when 5 μg of purified protein is loaded. The purified protein is also tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

3(d). Cloning and Expression of B. burgdorferi in Other Bacteria

B. burgdorferi polypeptides can also be produced in: *B. burgdorferi* using the methods of S. Skinner et al., (1988) Mol. Microbiol. 2:289-297 or J. I. Moreno (1996) Protein Expr. Purif. 8(3):332-340; *Lactobacillus* using the methods of C. Rush et al., 1997 Appl. Microbiol. Biotechnol. 47(5):537-542; or in *Bacillus subtilis* using the methods Chang et al., U.S. Patent No. 4,952,508.

4. Cloning and Expression in COS Cells

A *B. burgdorferi* expression plasmid is made by cloning a portion of the DNA encoding a *B. burgdorferi* polypeptide into the expression vector pDNAI/Amp or pDNAIII (which can be obtained from Invitrogen, Inc.). The expression vector pDNAI/amp contains: (1) an *E. coli* origin of replication effective for propagation in *E. coli* and other prokaryotic cells; (2) an ampicillin resistance gene for selection of plasmid-containing prokaryotic cells; (3) an SV40 origin of replication for propagation in eukaryotic cells; (4) a CMV promoter, a polylinker, an SV40 intron; (5) several codons encoding a hemagglutinin fragment (i.e., an "HA" tag to facilitate purification) followed by a termination codon and polyadenylation signal arranged so that a DNA can be conveniently placed under expression control of the CMV promoter and operably linked to the SV40 intron and the polyadenylation signal by means of restriction sites in the polylinker. The HA tag corresponds to an epitope derived from the influenza hemagglutinin protein described by Wilson et al. 1984 Cell 37:767. The fusion of the HA tag to the target protein allows easy detection and recovery of the recombinant protein with an antibody that recognizes the HA epitope. pDNAIII contains, in addition, the selectable neomycin marker.

A DNA fragment encoding a *B. burgdorferi* polypeptide is cloned into the polylinker region of the vector so that recombinant protein expression is directed by the CMV promoter. The plasmid construction strategy is as follows. The DNA from a *B. burgdorferi* genomic DNA prep is amplified using primers that contain convenient restriction sites, much as described above for

construction of vectors for expression of *B. burgdorferi* in *E. coli*. The 5' primer contains a Kozak sequence, an AUG start codon, and nucleotides of the 5' coding region of the *B. burgdorferi* polypeptide. The 3' primer, contains nucleotides complementary to the 3' coding sequence of the *B. burgdorferi* DNA, a stop codon, and a convenient restriction site.

The PCR amplified DNA fragment and the vector, pDNAI/Amp, are digested with appropriate restriction enzymes and then ligated. The ligation mixture is transformed into an appropriate *E. coli* strain such as SURE™ (Stratagene Cloning Systems, La Jolla, CA 92037), and the transformed culture is plated on ampicillin media plates which then are incubated to allow growth of ampicillin resistant colonies. Plasmid DNA is isolated from resistant colonies and examined by restriction analysis or other means for the presence of the fragment encoding the *B. burgdorferi* polypeptide

For expression of a recombinant *B. burgdorferi* polypeptide, COS cells are transfected with an expression vector, as described above, using DEAE-dextran, as described, for instance, by Sambrook et al. (*supra*). Cells are incubated under conditions for expression of *B. burgdorferi* by the vector.

Expression of the *B. burgdorferi*-HA fusion protein is detected by radiolabeling and immunoprecipitation, using methods described in, for example Harlow et al., *supra*.. To this end, two days after transfection, the cells are labeled by incubation in media containing ^{35}S-cysteine for 8 hours. The cells and the media are collected, and the cells are washed and the lysed with detergent-containing RIPA buffer: 150 mM NaCl, 1% NP-40, 0.1% SDS, 1% NP-40, 0.5% DOC, 50 mM TRIS, pH 7.5, as described by Wilson et al. (*supra*). Proteins are precipitated from the cell lysate and from the culture media using an HA-specific monoclonal antibody. The precipitated proteins then are analyzed by SDS-PAGE and autoradiography. An expression product of the expected size is seen in the cell lysate, which is not seen in negative controls.

5. Cloning and Expression in CHO Cells

The vector pC4 is used for the expression of *B. burgdorferi* polypeptide in this example. Plasmid pC4 is a derivative of the plasmid pSV2-dhfr (ATCC Accession No. 37146). The plasmid contains the mouse DHFR gene under control of the SV40 early promoter. Chinese hamster ovary cells or other cells lacking dihydrofolate activity that are transfected with these plasmids can be selected by growing the cells in a selective medium (alpha minus MEM, Life Technologies) supplemented with the chemotherapeutic agent methotrexate. The amplification of the DHFR genes in cells resistant to methotrexate (MTX) has been well documented. *See, e.g.*, Alt et al., 1978, J. Biol. Chem. 253:1357-1370; Hamlin et al., 1990, Biochem. et Biophys. Acta, 1097:107-143; Page et al., 1991, Biotechnology 9:64-68. Cells grown in increasing concentrations of MTX develop resistance to the drug by overproducing the target enzyme, DHFR, as a result of amplification of the DHFR gene. If a second gene is linked to the DHFR gene, it is usually co-amplified and over-expressed. It is known in the art that this approach may

be used to develop cell lines carrying more than 1,000 copies of the amplified gene(s). Subsequently, when the methotrexate is withdrawn, cell lines are obtained which contain the amplified gene integrated into one or more chromosome(s) of the host cell.

Plasmid pC4 contains the strong promoter of the long terminal repeat (LTR) of the Rouse Sarcoma Virus, for expressing a polypeptide of interest, Cullen, et al. (1985) Mol. Cell. Biol. 5:438-447; plus a fragment isolated from the enhancer of the immediate early gene of human cytomegalovirus (CMV), Boshart, et al., 1985, Cell 41:521-530. Downstream of the promoter are the following single restriction enzyme cleavage sites that allow the integration of the genes: *Bam* HI, *Xba* I, and *Asp* 718. Behind these cloning sites the plasmid contains the 3' intron and polyadenylation site of the rat preproinsulin gene. Other high efficiency promoters can also be used for the expression, e.g., the human ß-actin promoter, the SV40 early or late promoters or the long terminal repeats from other retroviruses, e.g., HIV and HTLVI. Clontech's Tet-Off and Tet-On gene expression systems and similar systems can be used to express the *B. burgdorferi* polypeptide in a regulated way in mammalian cells (Gossen et al., 1992, Proc. Natl. Acad. Sci. USA 89:5547-5551. For the polyadenylation of the mRNA other signals, e.g., from the human growth hormone or globin genes can be used as well. Stable cell lines carrying a gene of interest integrated into the chromosomes can also be selected upon co-transfection with a selectable marker such as gpt, G418 or hygromycin. It is advantageous to use more than one selectable marker in the beginning, e.g., G418 plus methotrexate.

The plasmid pC4 is digested with the restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel. The DNA sequence encoding the *B. burgdorferi* polypeptide is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' sequences of the desired portion of the gene. A 5' primer containing a restriction site, a Kozak sequence, an AUG start codon, and nucleotides of the 5' coding region of the *B. burgdorferi* polypeptide is synthesized and used. A 3' primer, containing a restriction site, stop codon, and nucleotides complementary to the 3' coding sequence of the *B. burgdorferi* polypeptides is synthesized and used. The amplified fragment is digested with the restriction endonucleases and then purified again on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC4 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene are used for transfection. Five μg of the expression plasmid pC4 is cotransfected with 0.5 μg of the plasmid pSVneo using a lipid-mediated transfection agent such as Lipofectin™ or LipofectAMINE.™ (LifeTechnologies Gaithersburg, MD). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus

MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 μM, 2 μM, 5 μM, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100-200 μM. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

6. Immunization and Detection of Immune Responses

6(a). B. burgdorferi propagation

B. burgdorferi sensu stricto isolate B31 is propagated in tightly-closed containers at 34°C in modified Barbour-Stoenner-Kelly (BSKII) medium (Barbour, A.G., *Yale J. Biol. Med.* 57:521-525 (1984)) overlaid with a 5%O_2/5%CO_2/90%N_2 gas mixture. Cell densities of these cultures are determined by darkfield microscopy at 400X.

Immunization of Mice and Challenge with B. burgdorferi. For active immunizations BALB/cByJ mice (BALB, Jackson Laboratories) are injected intraperitoneally (i.p.) at week 0 with 20 g of recombinant borrelial protein, or phosphate-buffered saline (PBS), emulsified with complete Freund's adjuvant (CFA), given a similar booster immunization in incomplete Freund's adjuvant (IFA) at week 4, and challenged at week 6. For challenge *B. burgdorferi* are diluted in BSKII from exponentially-growing cultures and mice are injected subcutaneously (s.c.) at the base of the tail with 0.1 ml of these dilutions (typically 10^3-10^4 borreliae; approximately 10-100 times the median infectious dose). Borreliae used for challenge are passaged fewer than six times *in vitro*. To assess infection, mice are sacrificed at 14-17 days post-challenge, and specimens derived from ear, bladder, and tibiotarsal joints are placed in BSKII plus 1.4% gelatin, 13 g/ml amphotericin B, 1.5 g/ml phosphomycin, and 15 g/ml rifampicin, and borrelia outgrowth at two or three weeks is quantified by darkfield microscopy. Batches of BSKII are qualified for infection testing by confirming that they supported the growth of 1-5 cells of isolate B31. In some instances seroconversion for protein P39 reactivity is also used to confirm infections (see below). Others have previously shown that mice elicited antibodies to P39 when inoculated with live borreliae by syringe or tick bite, but not with killed borreliae (Simpson, W.J., *et al., J. Clin. Microbiol.* 29:236-243 (1991)).

6(b). Immunoassays

Several immunoassay formats are used to quantify levels of borrelia-specific antibodies (ELISA and immunoblot), and to evaluate the functional properties of these antibodies (growth inhibition assay). The ELISA and immunoblot assays are also used to detect and quantify antibodies elicited in response to borrelial infection that react with specific borrelial antigens. Where antibodies to certain borrelial antigens are elicited by infection this is taken as evidence that

the borrelial proteins in question are expressed *in vivo*. Absence of infection-derived antibodies (seroconversion) following borrelial challenge is evidence that infection is prevented or suppressed. The immunoblot assay is also used to ascertain whether antibodies raised against recombinant borrelial antigens recognize a protein of similar size in extracts of whole borreliae. Where the natural protein is of similar, or identical, size in the immunoblot assay to the recombinant version of the same protein, this is taken as evidence that the recombinant protein is the product of a full-length clone of the respective gene.

Enzyme-Linked Immunosorbant Assay (ELISA). The ELISA is used to quantify levels of antibodies reactive with borrelial antigens elicited in response to immunization with these borrelial antigens. Wells of 96 well microtiter plates (Immunlon 4, Dynatech, Chantilly, Virginia, or equivalent) are coated with antigen by incubating 50 l of 1 g/ml protein antigen solution in a suitable buffer, typically 0.1 M sodium carbonate buffer at pH 9.6. After decanting unbound antigen, additional binding sites are blocked by incubating 100 l of 3% nonfat milk in wash buffer (PBS, 0.2% Tween 20, pH 7.4). After washing, duplicate serial two-fold dilutions of sera in PBS, Tween 20, 1% fetal bovine serum, are incubated for 1 hr, removed, wells are washed three times, and incubated with horseradish peroxidase-conjugated goat anti-mouse IgG. After three washes, bound antibodies are detected with H_2O_2 and 2,2'-azino-di-(3-ethylbenzthiazoline sulfonate) (Schwan, T.G., *et al., Proc. Natl. Acad. Sci. USA* 92:2909-2913 (1985)) (ABTS®, Kirkegaard & Perry Labs., Gaithersburg, MD) and A_{405} is quantified with a Molecular Devices, Corp. (Menlo Park, California) Vmax™ plate reader. IgG levels twice the background level in serum from naive mice are assigned the minimum titer of 1:100.

6(c). In Vitro Growth Inhibition Assay

Unlike other bacteria, borreliae can be killed by the binding of specific antibodies to their surface antigens. The mechanism for this *in vitro* killing or growth-inhibitory effect is not known, but can occur in the absence of serum complement, or other immune effector functions. Antibodies elicited in animals receiving immunizations with specific borrelial antigens that result in protection from borrelial challenge usually will directly kill borreliae *in vitro*. Thus, the *in vitro* growth inhibition assay also has a high predictive value for the protective potency of the borrelial antibodies, although exceptions, such as antibodies against OspC which are weak at *in vitro* growth inhibition, have been observed. Also, this assay can be used to evaluate the serologic conservation of epitope binding protective antibodies. A microwell antibody titration assay (Sadziene, A., *et al., J. Infect. Dis. 167*:165-172 (1993)) is used to evaluate the growth inhibition (GI) properties of antisera against recombinant borrelial antigens against the homologous B31 isolate, and against various strains of borrelia. Briefly, 10^5 borrelia in 100 l BSKII are added to serial two-fold dilutions of sera in 100 l BSKII in 96-well plates, and the plates are covered and incubated at 34°C in a 5%O_2/5%CO_2/90%N_2 gas mixture for 72 h prior to quantification of borrelia growth by darkfield microscopy.

6(d). Sodiumdodecylsulfate-Polyacrylamide Gel Electrophoresis (SDS-PAGE) and Immunoblotting

Using a single well format, total borrelial protein extracts, recombinant borrelial antigen, or recombinant P39 samples (2 g of purified protein, or more for total borrelial extracts) are boiled in SDS/2-ME sample buffer before electrophoresis through 3% acrylamide stacking gels, and resolving gels of higher acrylamide concentration, typically 10-15% acrylamide monomer. Gels are electro-blotted to nitrocellulose membranes and lanes are probed with dilutions of antibody to be tested for reactivity with specific borrelial antigens, followed by the appropriate secondary antibody-enzyme (horseradish peroxidase) conjugate. When it is desirable to confirm that the protein had transferred following electro-blotting, membranes are stained with Ponceau S. Immunoblot signals from bound antibodies are detected on x-ray film as chemiluminescence using ECL™ reagents (Amersham Corp., Arlington Heights, Illinois).

6(e). Detection of Borrelia mRNA expression

Northern blot analysis is carried out using methods described by, among others, Sambrook *et al., supra.* to detect the expression of the *B. burgdorferi* nucleotide sequences of the present invention in animal tissues. A cDNA probe containing an entire nucleotide sequence shown in Table 1 is labeled with ^{32}P using the *redi*prime™ DNA labeling system (Amersham Life Science), according to manufacturer's instructions. After labeling, the probe is purified using a CHROMA SPIN-100™ column (Clontech Laboratories, Inc.), according to manufacturer's protocol number PT1200-1. The purified labeled probe is then used to detect the expression of *Borrelia* mRNA in an animal tissue sample.

Animal tissues, such as blood or spinal fluid, are examined with the labeled probe using ExpressHyb™ hybridization solution (Clontech) according to manufacturer's protocol number PT1190-1. Following hybridization and washing, the blots are mounted and exposed to film at -70 C overnight, and films developed according to standard procedures.

The disclosure of all publications (including patents, patent applications, journal articles, laboratory manuals, books, or other documents) cited herein are hereby incorporated by reference in their entireties.

The present invention is not to be limited in scope by the specific embodiments described herein, which are intended as single illustrations of individual aspects of the invention. Functionally equivalent methods and components are within the scope of the invention, in addition to those shown and described herein and will become apparant to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

Provisional Application Serial No. 60/057,483 filed 3 September 1997 is incorporated by reference herein in its entirety.

TABLE 1. Nucleotide and Amino Acid Sequences

f101.aa

MSKIFLLFNAGFFFLKIIYVFSYPEIKNFSRQDPVFSDLKIKVLKYNKKQHIPLFFYSYKVKKGDTFFKIANKING
WQSGIATINLLDSPAVSVGQEILIPSKKGVFVFDSKDYRFNNLLLATRDLAKAEKVKIKRNDRVYEFYFFDFVKNP
DFGLFSGTELLFFLNANFIFPLKKFIVSSDFGFRNDPFTGNKSFHTGIDLAAPMNAEVYLLLLE

t101.aa

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LKKFIVSSDFGFRNDPFTGNKSFHTGIDLAAPMNAEVYLLLLE

f101.nt

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t101.nt

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f11.aa

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TINVLITRTTKINITNK

t11.aa

CCTTIKINHDYETDFKVLESPSKYINIDVIKATNEYIYIQITNNSLDVVKINWQNTSLNNDKIVLKKEDLTINNET
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f11.nt

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TABLE 1. Nucleotide and Amino Acid Sequences

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t11.nt

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TGA

f12.aa

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NRKTKK

t12.aa

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f12.nt

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TABLE 1. Nucleotide and Amino Acid Sequences

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t12.nt

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TABLE 1. Nucleotide and Amino Acid Sequences

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ACAAGAAAATGGTTTTATTTGGAGAGAATTTATGCTCCATATATTGATTTGAATTTTCAAAAAGATCTTTACAATA
ACCAATGGACATTTCCAGCTGATACTAAAGAAATGATAATGCGCCCAGAAATTAAAAATCTAGAAGATAAAGATAA
TGATAAAAAGAGTGTGAAGGAGAAAAATACTAAAAAAACAACAGAATTAACCAAAGATTTATATATTCCTCCAGAA
CCAATTACTTTAAAAAATATTGATCAATCCGATTCTTTTTTTATTAGGTTTGGCATTAATCCTTATTTAAGAAATA
ATGTTTTTTTTGATAATTATGGCATAACAAGTCCAAAGGACTTTAATTATGAAATAAAAAATTATTTATTTGATAT
AAAAAATAAAACGGATATAAAAATTCATGCTGATTTTTACAATCGTTTAATTACTTTTGAAAATTTATTATATCTT
AATACTATTGAGTATAGTCCTTTAAATAAAGATTTTAAAGTTGAAGATAAAGATAAAAAAAGTGAGCACTCTATTA
TTAACCAAATAAATTTAAACTTGCTTCCTTTTATTAGATATCCTTTATTTTCTAGAAGTACTTTAAAGTTTGAAAA
TAAGGCTACTTTATATTCATTTAATAAAAAATATGATTCTGATGTAAAATCTTTGGTTAATAAGAATAGTAGTATT
TTTTTATCTGATCCGGAAACTTTTTATCAAAGTTTAACAGCCTCTTTAATTTATGATTATGATTATTTTACTACTG
AGCTTTCAGGTGAATTAAAAAATAGTTTTGAAGATATTAAAGCTTCTTCTGAGCTTAAACTTTCTTTAGATTTTCC
TTATTTGCTACAAGAAGCTGGGATTGGAATTAAATATTATAAAAAGTTTAAAGAAGATGCTATGAAAAACTCTGGA
ATTTCTGCTGTTCAAAGTCCTTTGGAGCCTCAAAAACCATCATCGCCTTATAAAAATTTAGAAATGTCTCCTGCTT
TGTATTATAAAATTGAGCCGAGATATTTGGATTATTTTAAATTTAGTTTTTTAGTCGCCTATGATCCTTTGATAAA
TAGAGTTTCTGAACTTTCTTTTAAGCTTAATGTTTTTGATTTTCAATTTTTGTTTGCTATGAAAGACGACTTTGAA
TATAATTATGATCCTTTAAAAGGAGATTTTTCCAAGATTGGTACTACAACCAAACTTGTTCCATATTCTTTAGATT
CTAGTTACAAAAAGGAATTGTACGTTTTAACTTTTTTTGACAATAAGCTTTCTTTTACCTTGGGGGTAGATGTTGG
TTGGAAAATAAATTTGCAGAAATTTACGGATAATGAACTTCGATCTGCATTGACTTTGAAGTTTAAATATACAGAA
TTTTTAGAAATTTACTTTTCTACTTTATCTATTAATACTAAGACTTTTAAATATTTTAAAGGGTATATGGACCAAA
TTGGTCTAGAACCTGTTAATTTCTTTGTTGATTTATCAAAATCTTTCAATTTCTTTAATTCTCAAGACAGAAAAGA
TTCACTTTTTAAAATTAAAAAATTTTCATCAGGCTTTAAATTCAATTTTTATGATTGGAAATTTGTTGGAGAATAT
AATTTAGAACCAGATTTATTAAGGGGATCTGATGGGATTTATTCTCCTATTTGGAGAAATAATTTTACAATTTATA
TTTCTTGGAACTTTTTTGCTCCTATAAAAGCGTCATTTGAAAACAACAAAGATACAAACTACGAGTTTATTATTAA
TAGAAAAACAAAAAAATAA

f129.aa

MTKKLFVRVLIFLISNNYAFAKDTIKDLFFIQDILIKKKEKYSEVLNNASLEGIIEIEHNGPYIKDHDSEVKLILKE
NGYRRNFNFFNLLNTSNIIKSLSLFDSRPKNIKENEIILLETKMIKENPYKRYKDDDDFELKLSVTRKNNQIYLIL
DFNFLFDQRKTFPSIYIKEEDVSTIINSFMKLQDSSFLSPQAS

t129.aa

KDTIKDLFFIQDILIKKKEKYSEVLNNASLEGIIEIEHNGPYIKDHDSEVKLILKENGYRRNFNFFNLLNTSNIIKS
LSLFDSRPKNIKENEIILLETKMIKENPYKRYKDDDDFELKLSVTRKNNQIYLILDFNFLFDQRKTFPSIYIKEED
VSTIINSFMKLQDSSFLSPQAS

f129.nt

ATGACAAAAAAATTGTTTGTGAGGGTATTAATCTTTTTAATATCCAATAATTATGCTTTTGCAAAAGACACAATCA
AAGATTTGTTCTTTATACAAGATATACTAATAAAAAAAGAGAAATATTCCGAGGTTCTAAATAATGCAAGCCTTGA
AGGCATTATTGAAATTGAACATAACGGACCATACATTAAAGATCACGATTCAGAAGTTAAACTTATCCTAAAAGAA
AACGGATATAGAAGAAATTTCAACTTTTTTAATCTTTTAAATACTAGTAATATAATCAAAAGTCTAAGCTTATTTG
ACAGCAGACCAAAAAACATTAAAGAAAATGAAATCATATTATTAGAGACAAAAATGATTAAAGAAAATCCCTATAA
ACGATACAAAGACGATGATGATTTTGAATTAAAACTAAGTGTAACTCGAAAAAATAATCAAATTTATTTAATTCTT

TABLE 1. Nucleotide and Amino Acid Sequences

GATTTCAATTTCCTATTTGATCAAAGAAAAACGTTTCCATCAATTTACATCAAAGAAGAAGATGTATCAACAATAA
TAAACAGCTTCATGAAACTACAAGATTCAAGCTTTTTATCTCCTCAAGCTTCTTAA

t129.nt

AAAGACACAATCAAAGATTTGTTCTTTATACAAGATATACTAATAAAAAAAGAGAAATATTCCGAGGTTCTAAATA
ATGCAAGCCTTGAAGGCATTATTGAAATTGAACATAACGGACCATACATTAAAGATCACGATTCAGAAGTTAAACT
TATCCTAAAAGAAAACGGATATAGAAGAAATTTCAACTTTTTTAATCTTTTAAATACTAGTAATATAATCAAAAGT
CTAAGCTTATTTGACAGCAGACCAAAAAACATTAAAGAAAATGAAATCATATTATTAGAGACAAAAATGATTAAAG
AAAATCCCTATAAACGATACAAAGACGATGATGATTTTGAATTAAAACTAAGTGTAACTCGAAAAAATAATCAAAT
TTATTTAATTCTTGATTTCAATTTCCTATTTGATCAAAGAAAAACGTTTCCATCAATTTACATCAAAGAAGAAGAT
GTATCAACAATAATAAACAGCTTCATGAAACTACAAGATTCAAGCTTTTTATCTCCTCAAGCTTCTTAA

f142.aa

MDKISILYTLINIIIMLILISIVYLCKRKNVSFTKRVFIALAIGIVFGMTIQYFYGTNSEITNETINWISILGDGY
VRLLKMIIIPLIITSIISAIIKLTNSKDVGKMSLLVILTLVFTAGIAAIIGIFTALALGLTAEGLQAGTIEILQSE
KLQKGLEILNQTTITKKITDLIPQNIFEDFAGLRKNSTIGVVIFSAIIGIAALKTSIKKPESIEFFKKIILTLQDI
ILGVVTLILKLTPYAILALMTKITATSEIKSIIKLGEFVIASYIAIGLTFLMHMTLIAINKLNPITFIKKIFPALS
FAFISRSSAATIPINIEIQTKNLGVSEGIANLSSSFGTSIGQNGCAALHPAMLAIMIAPTQGINPTDISFILTLIG
LIIITSFGAAGAGGGATTASLMVLSAMNFPVGLVGLVISVEPIIDMGRTAVNVGGSMLAGVISAKQLKQFNHNIYN
QKELVNK

t142.aa

CKRKNVSFTKRVFIALAIGIVFGMTIQYFYGTNSEITNETINWISILGDGYVRLLKMIIIPLIITSIISAIIKLTN
SKDVGKMSLLVILTLVFTAGIAAIIGIFTALALGLTAEGLQAGTIEILQSEKLQKGLEILNQTTITKKITDLIPQN
IFEDFAGLRKNSTIGVVIFSAIIGIAALKTSIKKPESIEFFKKIILTLQDIILGVVTLILKLTPYAILALMTKITA
TSEIKSIIKLGEFVIASYIAIGLTFLMHMTLIAINKLNPITFIKKIFPALSFAFISRSSAATIPINIEIQTKNLGV
SEGIANLSSSFGTSIGQNGCAALHPAMLAIMIAPTQGINPTDISFILTLIGLIIITSFGAAGAGGGATTASLMVLS
AMNFPVGLVGLVISVEPIIDMGRTAVNVGGSMLAGVISAKQLKQFNHNIYNQKELVNK

f142.nt

TAAGAGGTAATAATGGATAAAATAAGTATATTATATACATTAATCAATATTATAATAATGCTTATTCTAATAAGCA
TAGTTTATCTTTGTAAAAGAAAAAATGTTTCTTTTACAAAAAGAGTGTTTATAGCGTTAGCAATCGGAATAGTATT
TGGAATGACCATTCAATATTTTTATGGAACAAATTCAGAAATAACAAACGAAACTATAAATTGGATAAGTATTTTG
GGCGATGGATACGTAAGGCTCCTTAAAATGATTATAATCCCCTTAATAATAACATCAATAATCTCTGCAATAATAA
AACTAACCAATAGTAAAGATGTTGGGAAAATGAGCCTACTTGTAATATTAACACTAGTATTTACAGCAGGTATTGC
TGCCATAATTGGCATTTTCACTGCTTTAGCATTGGGATTAACAGCCGAAGGACTACAAGCGGGAACCATCGAAATT
TTACAAAGTGAAAAATTGCAAAAAGGCCTTGAAATATTAAATCAAACAACAATCACAAAAAAAATCACAGATCTTA
TTCCACAAAATATATTTGAAGATTTTGCAGGGCTTAGAAAAAACTCAACCATCGGGGTCGTGATATTTTCAGCTAT
CATAGGAATAGCCGCCCTTAAAACATCTATCAAAAAGCCAGAATCAATAGAATTTTTTAAAAAAATAATATTAACA
CTCCAAGACATAATATTAGGTGTAGTAACTTTGATTTTAAAACTAACGCCTTATGCTATATTAGCTTTAATGACAA
AAATTACAGCAACCAGCGAAATCAAAAGCATAATAAAGCTTGGAGAATTTGTAATTGCTTCCTACATTGCCATAGG
TCTTACATTTCTTATGCATATGACATTAATTGCAATAAATAAATTAAACCCAATTACTTTTATAAAAAAAATATTC
CCAGCACTATCATTTGCATTCATATCTAGGTCGAGTGCTGCAACCATACCCATTAATATAGAAATTCAAACTAAAA
ATCTGGGAGTAAGCGAAGGAATAGCAAATTTATCAAGCTCCTTTGGAACATCAATTGGGCAAAATGGTTGTGCAGC
ACTACACCCCGCTATGCTTGCAATAATGATAGCACCAACTCAGGGAATAAACCCCACAGATATTTCATTTATACTC
ACACTTATTGGATTAATAATAATAACTTCATTTGGAGCTGCTGGCGCTGGTGGAGGCGCAACAACAGCCTCACTAA
TGGTGCTCTCAGCAATGAACTTTCCAGTGGGATTGGTAGGACTTGTAATATCTGTTGAGCCTATAATTGACATGGG
AAGAACAGCTGTTAATGTAGGCGGCTCAATGCTTGCAGGCGTTATATCTGCTAAACAGCTCAAACAATTCAACCAT
AATATATACAACCAAAAAGAGCTTGTAAACAAATAA

t142.nt

TABLE 1. Nucleotide and Amino Acid Sequences

TGTAAAAGAAAAAATGTTTCTTTTACAAAAAGAGTGTTTATAGCGTTAGCAATCGGAATAGTATTTGGAATGACCA
TTCAATATTTTTATGGAACAAATTCAGAAATAACAAACGAAACTATAAATTGGATAAGTATTTTGGGCGATGGATA
CGTAAGGCTCCTTAAAATGATTATAATCCCCTTAATAATAACATCAATAATCTCTGCAATAATAAAACTAACCAAT
AGTAAAGATGTTGGGAAAATGAGCCTACTTGTAATATTAACACTAGTATTTACAGCAGGTATTGCTGCCATAATTG
GCATTTTCACTGCTTTAGCATTGGGATTAACAGCCGAAGGACTACAAGCGGGAACCATCGAAATTTTACAAAGTGA
AAAATTGCAAAAAGGCCTTGAAATATTAAATCAAACAACAATCACAAAAAAAATCACAGATCTTATTCCACAAAAT
ATATTTGAAGATTTTGCAGGGCTTAGAAAAAACTCAACCATCGGGGTCGTGATATTTTCAGCTATCATAGGAATAG
CCGCCCTTAAAACATCTATCAAAAAGCCAGAATCAATAGAATTTTTTAAAAAAATAATATTAACACTCCAAGACAT
AATATTAGGTGTAGTAACTTTGATTTTAAAACTAACGCCTTATGCTATATTAGCTTTAATGACAAAAATTACAGCA
ACCAGCGAAATCAAAAGCATAATAAAGCTTGGAGAATTTGTAATTGCTTCCTACATTGCCATAGGTCTTACATTTC
TTATGCATATGACATTAATTGCAATAAATAAATTAAACCCAATTACTTTTATAAAAAAAATATTCCCAGCACTATC
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AGCGAAGGAATAGCAAATTTATCAAGCTCCTTTGGAACATCAATTGGGCAAAATGGTTGTGCAGCACTACACCCCG
CTATGCTTGCAATAATGATAGCACCAACTCAGGGAATAAACCCCACAGATATTTCATTTATACTCACACTTATTGG
ATTAATAATAATAACTTCATTTGGAGCTGCTGGCGCTGGTGGAGGCGCAACAACAGCCTCACTAATGGTGCTCTCA
GCAATGAACTTTCCAGTGGGATTGGTAGGACTTGTAATATCTGTTGAGCCTATAATTGACATGGGAAGAACAGCTG
TTAATGTAGGCGGCTCAATGCTTGCAGGCGTTATATCTGCTAAACAGCTCAAACAATTCAACCATAATATATACAA
CCAAAAAGAGCTTGTAAACAAATAA

f147.aa

MKIIIIGGTSAGTSAAAKANRLNKKLDITIYEKTNIVSFGTCGLPYFVGGFFDNPNTMISRTQEEFEKTGISVKTN
HEVIKVDAKNNTIVIKNQKTGTIFNNTYDQLMIATGAKPIIPPINNINLENFHTLKNLEDGQKIKKLMDREEIKNI
VIIGGGYIGIEMVEAAKNKRKNVRLIQLDKHILIDSFDEEIVTIMEEELTKKGVNLHTNEFVKSLIGEKKAEGVVT
NKNTYQADAVILATGIKPDTEFLENQLKTTKNGAIIVNEYGETSIKNIFSAGDCATIYNIVSKKNEYIPLATTANK
LGRIVGENLAGNHTAFKGTLGSASIKILSLEAARTGLTEKDAKKLQIKYKTIFVKDKNHTNYYPGQEDLYIKLIYE
ENTKIILGAQAIGKNGAVIRIHALSIAIYSKLTTKELGMMDFSYSPPFSRTWDILNIAGNAAK

t147.aa

AAAKANRLNKKLDITIYEKTNIVSFGTCGLPYFVGGFFDNPNTMISRTQEEFEKTGISVKTNHEVIKVDAKNNTIV
IKNQKTGTIFNNTYDQLMIATGAKPIIPPINNINLENFHTLKNLEDGQKIKKLMDREEIKNIVIIGGGYIGIEMVE
AAKNKRKNVRLIQLDKHILIDSFDEEIVTIMEEELTKKGVNLHTNEFVKSLIGEKKAEGVVTNKNTYQADAVILAT
GIKPDTEFLENQLKTTKNGAIIVNEYGETSIKNIFSAGDCATIYNIVSKKNEYIPLATTANKLGRIVGENLAGNHT
AFKGTLGSASIKILSLEAARTGLTEKDAKKLQIKYKTIFVKDKNHTNYYPGQEDLYIKLIYEENTKIILGAQAIGK
NGAVIRIHALSIAIYSKLTTKELGMMDFSYSPPFSRTWDILNIAGNAAK

f147.nt

ATGAAAATAATAATTATTGGGGGCACATCAGCAGGAACTAGTGCCGCAGCTAAAGCAAACCGCTTAAACAAAAAGC
TAGACATTACTATCTATGAAAAAACAAATATTGTATCTTTTGGAACCTGTGGCCTGCCTTACTTTGTGGGGGGATT
CTTTGACAACCCCAATACAATGATCTCAAGAACACAAGAAGAATTCGAAAAAACTGGAATCTCTGTTAAAACTAAC
CACGAAGTTATCAAAGTAGATGCAAAAAACAATACAATTGTAATAAAAAATCAAAAAACAGGAACCATTTTTAACA
ATACTTACGATCAACTTATGATAGCAACTGGTGCAAAACCTATTATTCCACCAATCAATAATATCAATCTAGAAAA
TTTTCATACTCTGAAAAATTTAGAAGACGGTCAAAAAATAAAAAAATTAATGGATAGAGAAGAGATTAAAAATATA
GTGATAATTGGTGGTGGATACATTGGAATTGAAATGGTAGAAGCAGCAAAAAATAAAAGAAAAAATGTAAGATTAA
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AACAAAAATACTTATCAAGCTGACGCTGTTATACTTGCTACCGGAATAAAACCTGACACTGAATTTTTAGAAAACC
AGCTTAAAACTACTAAAAATGGAGCAATAATTGTAAATGAGTATGGCGAAACTAGCATAAAAAATATTTTTTCTGC
AGGAGATTGTGCAACTATTTATAATATAGTAAGTAAAAAAAATGAATACATACCCTTGGCAACAACAGCCAACAAA
CTTGGAAGAATAGTTGGTGAAAATTTAGCTGGGAATCATACAGCATTTAAAGGCACATTGGGCTCAGCTTCAATTA
AAATACTATCTTTAGAAGCTGCAAGAACAGGACTTACAGAAAAAGATGCAAAAAAGCTCCAAATAAAATATAAAAC
GATTTTTGTAAAGGACAAAAATCATACAAATTATTATCCAGGCCAAGAAGATCTTTATATTAAATTAATTTATGAG
GAAAATACCAAAATAATCCTTGGGGCACAAGCAATAGGAAAAAATGGAGCCGTAATAAGAATTCATGCTTTATCAA

TABLE 1. Nucleotide and Amino Acid Sequences

TTGCAATCTATTCAAAACTTACAACAAAAGAGCTAGGGATGATGGATTTCTCATATTCCCCACCCTTCTCAAGAAC
TTGGGATATATTAAATATTGCTGGCAATGCTGCCAAATAG

t147.nt

GCCGCAGCTAAAGCAAACCGCTTAAACAAAAAGCTAGACATTACTATCTATGAAAAAACAAATATTGTATCTTTTG
GAACCTGTGGCCTGCCTTACTTTGTGGGGGATTCTTTGACAACCCCAATACAATGATCTCAAGAACACAAGAAGA
ATTCGAAAAAACTGGAATCTCTGTTAAAACTAACCACGAAGTTATCAAAGTAGATGCAAAAAACAATACAATTGTA
ATAAAAAATCAAAAAACAGGAACCATTTTTAACAATACTTACGATCAACTTATGATAGCAACTGGTGCAAAACCTA
TTATTCCACCAATCAATAATATCAATCTAGAAAATTTTCATACTCTGAAAAATTTAGAAGACGGTCAAAAAATAAA
AAAATTAATGGATAGAGAAGAGATTAAAAATATAGTGATAATTGGTGGTGGATACATTGGAATTGAAATGGTAGAA
GCAGCAAAAAATAAAAGAAAAAATGTAAGATTAATTCAACTAGATAAGCACATACTCATAGATTCCTTTGACGAAG
AAATAGTCACAATAATGGAAGAAGAACTAACAAAAAAGGGGGTTAATCTTCATACAAATGAGTTTGTAAAAAGTTT
AATAGGAGAAAAAAAGGCAGAAGGAGTAGTAACAAACAAAAATACTTATCAAGCTGACGCTGTTATACTTGCTACC
GGAATAAAACCTGACACTGAATTTTTAGAAAACCAGCTTAAAACTACTAAAAATGGAGCAATAATTGTAAATGAGT
ATGGCGAAACTAGCATAAAAAATATTTTTTCTGCAGGAGATTGTGCAACTATTTATAATATAGTAAGTAAAAAAAA
TGAATACATACCCTTGGCAACAACAGCCAACAAACTTGGAAGAATAGTTGGTGAAAATTTAGCTGGGAATCATACA
GCATTTAAAGGCACATTGGGCTCAGCTTCAATTAAAATACTATCTTTAGAAGCTGCAAGAACAGGACTTACAGAAA
AAGATGCAAAAAAGCTCCAAATAAAATATAAAACGATTTTTGTAAAGGACAAAAATCATACAAATTATTATCCAGG
CCAAGAAGATCTTTATATTAAATTAATTTATGAGGAAAATACCAAAATAATCCTTGGGGCACAAGCAATAGGAAAA
AATGGAGCCGTAATAAGAATTCATGCTTTATCAATTGCAATCTATTCAAAACTTACAACAAAAGAGCTAGGGATGA
TGGATTTCTCATATTCCCCACCCTTCTCAAGAACTTGGGATATATTAAATATTGCTGGCAATGCTGCCAAATAG

f152.aa

MLKFEFSDRFLLFSYFVLIMFIGSLLLMLPISWEGDGKLAYIDALFTAVSAVSITGLTTVKMEGFSTFGFILIMLL
IQLGGLGFISITTFYLLIPKKKMNLTDARIIKQYSLSNIEYNPIRILKSILFITFSIEMIGLILILICFKLRGVNI
SFLEALFTTISAFCNAGFSMHSESIYAWRDVPEAIVVVSILIICGGLGFMVYRDVNNTIKNKKKLSLHAKIVFSLS
FFLIIIGAILFFFTEMHKLKAGYSMSTLIFNSIFYSISTRTAGFNYLDNSLISGRTQIISLPFMFIGGAPGSTAGG
IKITTFFLIVLAVVKNQNGNGYIIGSYKVSIDSIRFALLFFARAIFILSFSFFMLLFFEGGSGNWKVIDLGYEVFS
AFGTVGLSVGVTQDLSFWGKVIIIFTMFAGRIGLFSMAVFVSRKSRFEEFTRPRQDILVG

t152.aa

WEGDGKLAYIDALFTAVSAVSITGLTTVKMEGFSTFGFILIMLLIQLGGLGFISITTFYLLIPKKKMNLTDARIIK
QYSLSNIEYNPIRILKSILFITFSIEMIGLILILICFKLRGVNISFLEALFTTISAFCNAGFSMHSESIYAWRDVP
EAIVVVSILIICGGLGFMVYRDVNNTIKNKKKLSLHAKIVFSLSFFLIIIGAILFFFTEMHKLKAGYSMSTLIFNS
IFYSISTRTAGFNYLDNSLISGRTQIISLPFMFIGGAPGSTAGGIKITTFFLIVLAVVKNQNGNGYIIGSYKVSID
SIRFALLFFARAIFILSFSFFMLLFFEGGSGNWKVIDLGYEVFSAFGTVGLSVGVTQDLSFWGKVIIIFTMFAGRI
GLFSMAVFVSRKSRFEEFTRPRQDILVG

f152.nt

ATGTTGAAATTTGAATTTAGCGACAGGTTTTTACTTTTTAGTTATTTTGTTTTAATTATGTTTATAGGCTCTCTTT
TGTTGATGTTGCCTATTTCCTGGGAAGGTGATGGCAAATTAGCATACATTGATGCTCTTTTTACTGCTGTTTCTGC
TGTAAGTATTACGGGCCTTACAACGGTTAAAATGGAAGGCTTTTCTACTTTTGGATTTATTTTGATAATGTTGCTA
ATCCAGCTTGGGGGACTTGGATTTATAAGTATTACTACTTTTTATTTGCTTATACCTAAAAAGAAAATGAATTTAA
CAGATGCAAGAATAATAAAGCAGTATTCCCTTTCAAATATAGAATATAATCCTATTAGAATTTTAAAAAGCATATT
GTTTATAACTTTTTCAATTGAAATGATAGGTTTAATATTAATACTTATTTGTTTTAAACTTAGGGGAGTGAATATT
TCATTCTTAGAGGCTTTGTTTACGACAATTTCTGCTTTTTGCAATGCAGGTTTTTCCATGCATTCTGAGAGTATTT
ATGCATGGCGAGATGTTCCTGAAGCTATAGTTGTGGTCTCTATTTTAATAATTTGTGGTGGGCTTGGGTTTATGGT
CTATAGAGATGTAAATAACACTATTAAAAACAAAAAAAAACTATCGCTTCATGCCAAGATAGTTTTTTCTTTAAGC
TTCTTTTTAATTATAATTGGTGCAATTTTATTTTTTTTACAGAGATGCATAAATTAAAAGCTGGTTATTCAATGA
GCACTTTAATATTTAATTCAATTTTTTATTCGATTAGTACCAGAACAGCTGGTTTTAATTATCTTGATAATTCTTT
AATAAGCGGAAGAACTCAAATAATTTCTCTACCATTCATGTTTATTGGTGGTGCACCCGGATCAACTGCAGGAGGG
ATTAAGATTACAACATTTTTTTTAATTGTATTGGCTGTTGTTAAAAATCAAAACGGCAATGGATATATTATTGGTT

TABLE 1. Nucleotide and Amino Acid Sequences

CTTACAAGGTTTCAATAGATAGTATAAGATTTGCACTTTTATTTTTTGCAAGAGCTATTTTTATTTTAAGTTTTTC
TTTTTTCATGCTTCTTTTTTTTGAGGGAGGATCTGGCAATTGGAAGGTTATTGATTTAGGTTATGAAGTATTTTCT
GCTTTTGGAACGGTTGGTCTTTCAGTTGGAGTAACTCAGGATTTGTCATTTTGGGGGAAAGTCATTATAATTTTTA
CTATGTTTGCAGGACGAATAGGGCTTTTTTCAATGGCTGTTTTTGTTTCAAGAAAGTCGCGTTTTGAAGAATTTAC
AAGGCCAAGGCAAGATATTTTGGTTGGTTGA

t152.nt

TGGGAAGGTGATGGCAAATTAGCATACATTGATGCTCTTTTTACTGCTGTTTCTGCTGTAAGTATTACGGGCCTTA
CAACGGTTAAAATGGAAGGCTTTTCTACTTTTGGATTTATTTTGATAATGTTGCTAATCCAGCTTGGGGGACTTGG
ATTTATAAGTATTACTACTTTTTATTTGCTTATACCTAAAAAGAAAATGAATTTAACAGATGCAAGAATAATAAAG
CAGTATTCCCTTTCAAATATAGAATATAATCCTATTAGAATTTTAAAAAGCATATTGTTTATAACTTTTTCAATTG
AAATGATAGGTTTAATATTAATACTTATTTGTTTTAAACTTAGGGGAGTGAATATTTCATTCTTAGAGGCTTTGTT
TACGACAATTTCTGCTTTTTGCAATGCAGGTTTTTCCATGCATTCTGAGAGTATTTATGCATGGCGAGATGTTCCT
GAAGCTATAGTTGTGGTCTCTATTTTAATAATTTGTGGTGGGCTTGGGTTTATGGTCTATAGAGATGTAAATAACA
CTATTAAAAACAAAAAAAAACTATCGCTTCATGCCAAGATAGTTTTTTCTTTAAGCTTCTTTTTAATTATAATTGG
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ATTTTTATTCGATTAGTACCAGAACAGCTGGTTTTAATTATCTTGATAATTCTTTAATAAGCGGAAGAACTCAAA
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TTTAATTGTATTGGCTGTTGTTAAAAATCAAAACGGCAATGGATATATTATTGGTTCTTACAAGGTTTCAATAGAT
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GGGCTTTTTTCAATGGCTGTTTTTGTTTCAAGAAAGTCGCGTTTTGAAGAATTTACAAGGCCAAGGCAAGATATTT
TGGTTGGTTGA

f154.aa

MKINKTFILLFLFTKFSFVQAQANQILTEISPLSILSKNGKGSVYLKVSKSSDYILTLDKSSNSDFVFKIYDISNK
KYITDKVKRRDFKIRLDKNSLYAIIYVGTKNENIKFSLTDLDFSILSSDSLKAKTSKIEKEDLFFTLKDLPVLNLT
AKLKKYVLRIYKSNIYIAYQLENSDDIKVAEFIEDVGWFNLDSSVNRNITNIVNFDFSINSKGNLYIAFVTKSGAD
FASELIVKKFNSRKWIDISPGHIENFGSLLNISIDLKDRLYLAYLREIRGEYKINLISNMGYGSIWTDVIHAYLSK
GDSNVNSSNIGLISEPFLGIFYNYKSNNEIKSEFIVNNENAWVNANIPSVYMANFIKGFFDSNFNQIIMSFVSENR
PIVNICPLKSSRWINISPNVEMEGLSADIGLYKNNLFLAFEDNNNVRLIYFKNKNWYFLNKLENFKSNVKSPQIGI
YGNQGLVISTLSSNSNELFFTLICQ

t154.aa

NQILTEISPLSILSKNGKGSVYLKVSKSSDYILTLDKSSNSDFVFKIYDISNKKYITDKVKRRDFKIRLDKNSLYA
IIYVGTKNENIKFSLTDLDFSILSSDSLKAKTSKIEKEDLFFTLKDLPVLNLTAKLKKYVLRIYKSNIYIAYQLEN
SDDIKVAEFIEDVGWFNLDSSVNRNITNIVNFDFSINSKGNLYIAFVTKSGADFASELIVKKFNSRKWIDISPGHI
ENFGSLLNISIDLKDRLYLAYLREIRGEYKINLISNMGYGSIWTDVIHAYLSKGDSNVNSSNIGLISEPFLGIFYN
YKSNNEIKSEFIVNNENAWVNANIPSVYMANFIKGFFDSNFNQIIMSFVSENRPIVNICPLKSSRWINISPNVEME
GLSADIGLYKNNLFLAFEDNNNVRLIYFKNKNWYFLNKLENFKSNVKSPQIGIYGNQGLVISTLSSNSNELFFTLI
CQ

f154.nt

ATGAAAATAAATAAGACATTCATTTTGCTATTTTTATTTACAAAATTTTCTTTTGTTCAAGCTCAAGCAAATCAAA
TATTAACAGAAATTAGTCCTTTAAGTATTTTAAGCAAAAATGGGAAAGGAAGTGTTTACTTAAAAGTTAGCAAATC
TTCCGATTATATTTTAACCCTAGATAAGAGTTCAAATTCCGATTTTGTTTTTAAAATTTATGACATTTCTAATAAA
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ATGTTGGTACTAAAAATGAAAACATAAAGTTTTCGCTTACAGATTTAGATTTTTCAATTTTAAGTAGCGATTCCCT
GAAAGCTAAAACATCTAAGATTGAAAAAGAAGATTTATTTTTTACTTTAAAAGATTTGCCTGTTTTAAATTTAACT

TABLE 1. Nucleotide and Amino Acid Sequences

GCCAAGCTTAAAAAATATGTATTAAGGATTTATAAAAGCAATATTTATATTGCTTATCAGCTAGAAAATAGCGATG
ATATTAAAGTTGCTGAATTTATTGAGGATGTTGGTTGGTTTAATCTTGATTCATCTGTTAATAGAAATATTACTAA
TATAGTTAATTTTGATTTTTCAATTAATTCTAAAGGAAATTTATATATTGCTTTTGTTACGAAATCAGGGGCTGAT
TTTGCCAGCGAGCTTATAGTTAAAAAATTTAATAGTAGAAAATGGATTGATATTAGTCCTGGTCACATAGAAAATT
TTGGATCTTTATTAAATATTAGCATTGATTTAAAAGATAGGTTGTATTTAGCATATTTAAGGGAAATTAGGGGTGA
ATATAAAATTAATTTAATCTCGAATATGGGTTACGGAAGTATTTGGACCGATGTAATACATGCTTATTTAAGTAAA
GGTGATTCTAATGTTAATTCATCAAACATTGGTTTAATATCTGAACCTTTTTTGGGCATTTTTTATAATTATAAGT
CAAATAATGAGATTAAATCTGAATTTATTGTAAACAATGAAAATGCTTGGGTAAATGCAAATATTCCTTCTGTTTA
TATGGCCAATTTTATTAAAGGCTTTTTTGATTCTAATTTTAATCAAATAATTATGAGTTTTGTTTCTGAAAATAGA
CCTATTGTAAACATTTGTCCTTTGAAAAGTAGTAGATGGATTAATATAAGTCCTAATGTTGAAATGGAAGGTTTAA
GTGCTGACATTGGGCTTTATAAAAATAATTTGTTTTTAGCTTTTGAGGACAATAATAATGTGAGATTAATTTATTT
TAAGAATAAAAATTGGTATTTTTTAAATAAGCTTGAGAATTTTAAGAGTAATGTTAAAAGCCCTCAGATTGGAATT
TATGGCAATCAAGGGCTTGTAATCTCTACTTTAAGCTCTAATTCCAATGAATTATTTTTTACTTTGATTTGCCAAT
GA

t154.nt

AATCAAATATTAACAGAAATTAGTCCTTTAAGTATTTTAAGCAAAAATGGGAAAGGAAGTGTTTACTTAAAAGTTA
GCAAATCTTCCGATTATATTTTAACCCTAGATAAGAGTTCAAATTCCGATTTTGTTTTTAAAATTTATGACATTTC
TAATAAAAAATATATAACCGATAAAGTAAAAAGAAGAGATTTTAAAATAAGATTAGATAAAAATTCTCTTTATGCA
ATAATATATGTTGGTACTAAAAATGAAAACATAAAGTTTTCGCTTACAGATTTAGATTTTTCAATTTTAAGTAGCG
ATTCCCTGAAAGCTAAAACATCTAAGATTGAAAAAGAAGATTTATTTTTTACTTTAAAAGATTTGCCTGTTTTAAA
TTTAACTGCCAAGCTTAAAAAATATGTATTAAGGATTTATAAAAGCAATATTTATATTGCTTATCAGCTAGAAAAT
AGCGATGATATTAAAGTTGCTGAATTTATTGAGGATGTTGGTTGGTTTAATCTTGATTCATCTGTTAATAGAAATA
TTACTAATATAGTTAATTTTGATTTTTCAATTAATTCTAAAGGAAATTTATATATTGCTTTTGTTACGAAATCAGG
GGCTGATTTTGCCAGCGAGCTTATAGTTAAAAAATTTAATAGTAGAAAATGGATTGATATTAGTCCTGGTCACATA
GAAAATTTTGGATCTTTATTAAATATTAGCATTGATTTAAAAGATAGGTTGTATTTAGCATATTTAAGGGAAATTA
GGGGTGAATATAAAATTAATTTAATCTCGAATATGGGTTACGGAAGTATTTGGACCGATGTAATACATGCTTATTT
AAGTAAAGGTGATTCTAATGTTAATTCATCAAACATTGGTTTAATATCTGAACCTTTTTTGGGCATTTTTTATAAT
TATAAGTCAAATAATGAGATTAAATCTGAATTTATTGTAAACAATGAAAATGCTTGGGTAAATGCAAATATTCCTT
CTGTTTATATGGCCAATTTTATTAAAGGCTTTTTTGATTCTAATTTTAATCAAATAATTATGAGTTTTGTTTCTGA
AAATAGACCTATTGTAAACATTTGTCCTTTGAAAAGTAGTAGATGGATTAATATAAGTCCTAATGTTGAAATGGAA
GGTTTAAGTGCTGACATTGGGCTTTATAAAAATAATTTGTTTTTAGCTTTTGAGGACAATAATAATGTGAGATTAA
TTTATTTTAAGAATAAAAATTGGTATTTTTTAAATAAGCTTGAGAATTTTAAGAGTAATGTTAAAAGCCCTCAGAT
TGGAATTTATGGCAATCAAGGGCTTGTAATCTCTACTTTAAGCTCTAATTCCAATGAATTATTTTTTACTTTGATT
TGCCAATGA

f157.aa

MKIFLKVIGRGILGRLMVFRKNYDYLALISLLIVSFVGILLIYSSDYNISGSLTKNEYIKQTFWVIIGFFLIFIVG
KYDLKFVYSMVYPLYFLLILALIFTAFFGMTVNGARSWIGIWKLGGQPSEFGKVVIILTLSKFYTEKKGYNEFFTF
ITAFLLIFPSVILILLQPDFGTAIVYLTIFIFISFFAGIDLHYVLAFALIGFFSFVFAILPVWYEYKVNMGNVFYL
IFSNPFYFRVIMGVLLLILLISVLGFFISKYGLSIKIIYFYVFFASSILLVSIVFSKVLSKLMKTYQIKRFLVFLD
PAIDAKGAGWNLNQVKIAIGSGGLLGKGFLKGPYTHANYVPSQSTDFIFSILAEEFGFLGVSTILILFFFLFFKFL
IIMNKSQDRYMALVISGILGLLFFHTSFNVGMSLGVLPITGIPFPFLSYGGSSTITFFLAMSFYFNIESIVAMD

t157.aa

RKNYDYLALISLLIVSFVGILLIYSSDYNISGSLTKNEYIKQTFWVIIGFFLIFIVGKYDLKFVYSMVYPLYFLLI
LALIFTAFFGMTVNGARSWIGIWKLGGQPSEFGKVVIILTLSKFYTEKKGYNEFFTFITAFLLIFPSVILILLQPD
FGTAIVYLTIFIFISFFAGIDLHYVLAFALIGFFSFVFAILPVWYEYKVNMGNVFYLIFSNPFYFRVIMGVLLLIL

TABLE 1. Nucleotide and Amino Acid Sequences

LISVLGFFISKYGLSIKIIYFYVFFASSILLVSIVFSKVLSKLMKTYQIKRFLVFLDPAIDAKGAGWNLNQVKIAI
GSGGLLGKGFLKGPYTHANYVPSQSTDFIFSILAEEFGFLGVSTILILFFFLFFKFLIIMNKSQDRYMALVISGIL
GLLFFHTSFNVGMSLGVLPITGIPFPFLSYGGSSTITFFLAMSFYFNIESIVAMD

f157.nt

ATGAAGATATTCTTAAAGGTTATAGGCCGTGGTATATTAGGTAGATTAATGGTTTTTAGAAAAAATTATGATTATT
TGGCTTTGATAAGCTTACTTATAGTTTCTTTTGTTGGTATATTGTTGATTTATTCTAGCGATTATAATATTAGTGG
ATCTTTAACCAAGAATGAATATATAAAACAAACCTTTTGGGTAATTATTGGATTTTTTCTAATTTTTATAGTGGGC
AAATATGATTTAAAATTTGTTTATAGCATGGTATATCCTTTATATTTTTTATTAATATTGGCTTTAATTTTTACTG
CATTTTTTGGAATGACAGTAAATGGAGCAAGATCTTGGATTGGCATATGGAAACTTGGAGGACAGCCTTCTGAATT
TGGTAAAGTTGTTATTATTTTAACCCTTTCAAAATTTTACACTGAAAAAAAGGGTTATAATGAATTTTTTACCTTT
ATTACTGCATTTTTATTAATTTTTCCATCGGTAATTCTTATATTATTGCAACCTGATTTTGGTACAGCAATAGTAT
ATTTAACCATTTTTATATTTATTTCTTTTTTTGCAGGAATAGATTTGCACTATGTTTTAGCATTTGCGTTGATAGG
GTTTTTTTCTTTTGTTTTTGCAATTTTACCGGTTTGGTATGAATATAAGGTGAATATGGGTAATGTATTTTATCTT
ATTTTCTCAAATCCTTTTTATTTTAGAGTAATAATGGGAGTGCTGCTTTTAATTCTTTTGATTTCTGTTTTAGGAT
TTTTCATTTCTAAATATGGTTTGAGTATTAAAATAATTTATTTTTATGTATTTTTTGCAAGTTCTATTTTATTAGT
TTCAATAGTGTTTTCAAAGGTTCTTTCAAAGTTAATGAAGACTTATCAGATTAAACGGTTTTTGGTATTCTTAGAT
CCGGCTATTGATGCTAAGGGTGCTGGTTGGAATTTAAATCAGGTTAAAATAGCAATTGGTTCTGGCGGTCTTTTGG
GCAAAGGATTTTTAAAGGGACCTTATACCCACGCTAATTATGTGCCATCTCAAAGCACAGATTTTATTTTTTCTAT
TCTTGCCGAAGAGTTTGGGTTTTTGGGTGTTAGCACTATTTTAATATTATTTTTTTTCCTTTTTTTTAAATTTTTG
ATAATAATGAATAAAAGTCAAGATAGATATATGGCCTTAGTAATATCTGGAATTTTGGGACTTTTATTTTTTCATA
CTTCTTTTAATGTTGGAATGTCTTTAGGAGTTCTTCCTATTACCGGGATTCCCTTTCCTTTTCTCTCTTATGGAGG
TTCTTCTACTATTACATTTTTTTTAGCAATGTCTTTTTATTTTAATATTGAATCAATAGTTGCTATGGATTGA

t157.nt

AGAAAAAATTATGATTATTTGGCTTTGATAAGCTTACTTATAGTTTCTTTTGTTGGTATATTGTTGATTTATTCTA
GCGATTATAATATTAGTGGATCTTTAACCAAGAATGAATATATAAAACAAACCTTTTGGGTAATTATTGGATTTTT
TCTAATTTTTATAGTGGGCAAATATGATTTAAAATTTGTTTATAGCATGGTATATCCTTTATATTTTTTATTAATA
TTGGCTTTAATTTTTACTGCATTTTTTGGAATGACAGTAAATGGAGCAAGATCTTGGATTGGCATATGGAAACTTG
GAGGACAGCCTTCTGAATTTGGTAAAGTTGTTATTATTTTAACCCTTTCAAAATTTTACACTGAAAAAAAGGGTTA
TAATGAATTTTTTACCTTTATTACTGCATTTTTATTAATTTTTCCATCGGTAATTCTTATATTATTGCAACCTGAT
TTTGGTACAGCAATAGTATATTTAACCATTTTTATATTTATTTCTTTTTTTGCAGGAATAGATTTGCACTATGTTT
TAGCATTTGCGTTGATAGGGTTTTTTTCTTTTGTTTTTGCAATTTTACCGGTTTGGTATGAATATAAGGTGAATAT
GGGTAATGTATTTTATCTTATTTTCTCAAATCCTTTTTATTTTAGAGTAATAATGGGAGTGCTGCTTTTAATTCTT
TTGATTTCTGTTTTAGGATTTTTCATTTCTAAATATGGTTTGAGTATTAAAATAATTTATTTTTATGTATTTTTTG
CAAGTTCTATTTTATTAGTTTCAATAGTGTTTTCAAAGGTTCTTTCAAAGTTAATGAAGACTTATCAGATTAAACG
GTTTTTGGTATTCTTAGATCCGGCTATTGATGCTAAGGGTGCTGGTTGGAATTTAAATCAGGTTAAAATAGCAATT
GGTTCTGGCGGTCTTTTGGGCAAAGGATTTTTAAAGGGACCTTATACCCACGCTAATTATGTGCCATCTCAAAGCA
CAGATTTTATTTTTTCTATTCTTGCCGAAGAGTTTGGGTTTTTGGGTGTTAGCACTATTTTAATATTATTTTTTTT
CCTTTTTTTTAAATTTTTGATAATAATGAATAAAAGTCAAGATAGATATATGGCCTTAGTAATATCTGGAATTTTG
GGACTTTTATTTTTTCATACTTCTTTTAATGTTGGAATGTCTTTAGGAGTTCTTCCTATTACCGGGATTCCCTTTC
CTTTTCTCTCTTATGGAGGTTCTTCTACTATTACATTTTTTTTAGCAATGTCTTTTTATTTTAATATTGAATCAAT
AGTTGCTATGGATTGA

f17.aa

MIVFLFFSIYLIILFKRSSNSPLYFVPDTKFETLSIRIVLSCSLLLIPFCTMLDARPSTIAVFPTPGSPISIALFL
FLLKSIFVRVLISASLPTKGSNFLAFASAVKFLTYFPISKCSFSSRISSSNSL

TABLE 1. Nucleotide and Amino Acid Sequences

t17.aa

PLYFVPDTKFETLSIRIVLSCSLLLIFFCTMLDARPSTIAVFPTPGSPISIALFLFLLKSIFVRVLISASLPTKGS
NFLAFASAVKFLTYFPISKCSFSSRISSSNSL

f17.nt

ATGATTGTGTTTTTGTTTTTTTCAATATACTTAATTATATTATTTAAACGATCTTCAAACTCGCCTCTATATTTTG
TTCCCGATACCAAGTTTGAAACCTTAAGCATTAGAATTGTTTTGTCTTGTAGTTTGCTACTTATTTTTTTTTGCAC
TATGCTTGATGCAAGGCCTTCAACTATTGCTGTTTTTCCCACACCAGGTTCGCCTATTAGCATTGCACTATTTTTA
TTTCTTCTCAAGAGTATATTTGTAAGAGTTTTAATCTCTGCTTCTCTTCCAACCAAGGGGTCTAATTTTTTGGCTT
TTGCAAGTGCTGTTAAATTTTTGACATACTTTCCAATTTCAAAGTGCTCATTTTCAAGTCGTATTTCTTCATCAAA
TTCTTTGTAG

t17.nt

CCTCTATATTTTGTTCCCGATACCAAGTTTGAAACCTTAAGCATTAGAATTGTTTTGTCTTGTAGTTTGCTACTTA
TTTTTTTTTGCACTATGCTTGATGCAAGGCCTTCAACTATTGCTGTTTTTCCCACACCAGGTTCGCCTATTAGCAT
TGCACTATTTTTATTTCTTCTCAAGAGTATATTTGTAAGAGTTTTAATCTCTGCTTCTCTTCCAACCAAGGGGTCT
AATTTTTTGGCTTTTGCAAGTGCTGTTAAATTTTTGACATACTTTCCAATTTCAAAGTGCTCATTTTCAAGTCGTA
TTTCTTCATCAAATTCTTTGTAG

f170.aa

MKAFKVKNLRRFSNFIRILVIVLFLNSLLSLFVFLAGSYNIFVYNFQKFYLDLAIILSSVSFGLESTRLIFFYFLK
NKKIKYYLILIFSFIIFFIALVFKIFLSGNK

t170.aa

YNIFVYNFQKFYLDLAIILSSVSFGLESTRLIFFYFLKNKKIKYYLILIFSFIIFFIALVFKIFLSGNK

f170.nt

ATGAAAGCTTTTAAAGTAAAAAATCTAAGACGTTTTTCAAATTTTATTAGAATTTTGGTTATTGTATTGTTTTTAA
ATTCTTTGTTAAGTTTGTTCGTGTTTTTGGCTGGTTCTTACAATATTTTTGTTTACAATTTTCAGAAATTTTATCT
TGATCTTGCTATTATTTTAAGCTCTGTTTCTTTTGGACTTGAATCTACTAGACTGATATTTTTTTATTTTTTGAAA
AATAAAAAAATTAAGTATTATTTAATTTTAATTTTTAGTTTTATAATTTTTTTTATTGCTCTTGTTTTTAAAATTT
TTCTTTCTGGTAATAA
ATAG

t170.nt

TABLE 1. Nucleotide and Amino Acid Sequences

TACAATATTTTTGTTTACAATTTTCAGAAATTTTATCTTGATCTTGCTATTATTTTAAGCTCTGTTTCTTTTGGAC
TTGAATCTACTAGACTGATATTTTTTTATTTTTTGAAAAATAAAAAAATTAAGTATTATTTAATTTTAATTTTTAG
TTTTATAATTTTTTTTATTGCTCTTGTTTTTAAAATTTTTCTTTCTGGTAATAAATAG

f186.aa

MKKLIIIFTLFLSQACNLSTMHKIDTKEDMKILYSEIAELRKKLNLNHLEIDDTLEKVAKEYAIKLGENRTITHTL
FGTTPMQRIHKYDQSFNLTREILASGIELNRVVNAWLNSPSHKEALINTDTDKIGGYRLKTTDNIDIFVVLFGKRK
YKN

t186.aa

TMHKIDTKEDMKILYSEIAELRKKLNLNHLEIDDTLEKVAKEYAIKLGENRTITHTLFGTTPMQRIHKYDQSFNLT
REILASGIELNRVVNAWLNSPSHKEALINTDTDKIGGYRLKTTDNIDIFVVLFGKRKYKN

f186.nt

ATGAAAAAATTGATTATAATTTTTACACTGTTTTTATCTCAAGCATGCAATTTAAGTACAATGCATAAAATAGATA
CAAAAGAAGATATGAAAATTCTATATTCAGAAATTGCTGAATTGAGAAAAAAATTAAATCTAAACCATCTAGAAAT
AGATGATACCCTTGAAAAAGTTGCAAAAGAATATGCCATTAAACTGGGAGAAAATAGAACAATAACTCACACCCTT
TTTGGCACAACCCCAATGCAAAGAATACATAAATACGATCAATCCTTTAATTTAACAAGAGAAATACTGGCATCAG
GAATTGAACTTAACAGAGTAGTTAATGCATGGCTTAATAGTCCAAGCCACAAAGAAGCTCTTATTAATACAGATAC
CGATAAAATAGGTGGCTATAGATTAAAAACGACTGACAATATAGATATATTTGTAGTTCTTTTTGGAAAAAGAAAA
TATAAGAATTGA

t186.nt

ACAATGCATAAAATAGATACAAAAGAAGATATGAAAATTCTATATTCAGAAATTGCTGAATTGAGAAAAAAATTAA
ATCTAAACCATCTAGAAATAGATGATACCCTTGAAAAAGTTGCAAAAGAATATGCCATTAAACTGGGAGAAAATAG
AACAATAACTCACACCCTTTTTGGCACAACCCCAATGCAAAGAATACATAAATACGATCAATCCTTTAATTTAACA
AGAGAAATACTGGCATCAGGAATTGAACTTAACAGAGTAGTTAATGCATGGCTTAATAGTCCAAGCCACAAAGAAG
CTCTTATTAATACAGATACCGATAAAATAGGTGGCTATAGATTAAAAACGACTGACAATATAGATATATTTGTAGT
TCTTTTTGGAAAAAGAAAATATAAGAATTGA

f196.aa

MKLKARMLLLVLILIAFFISILFFAFGMLINSKLVDQQFNLMINLIESIKSSFNLYISSMEEKVRVSSMYFNSAEK
FNEASKIKSKRLSFISDQSEILIQTGSNMMVTDKEGKIVFTTAVKDNSDFGKSIGDREYFTKLKESNSIVYNSFVM
LADPGSIEESLLKDISKIKNKKGQIPYILIGMPLRDFETDNIFGYFMFLYSMDYIYRSFRGINFGILSSGRALAYD
TTGRLLVHHVVLPGDILTDISASYSNIIKKTSEDLLQKNKEISTVYYYDPKSNKKYVGISQKVLLNLSNNKFILLM
RTSEDDFYYMSRATTIILAISFVFTLLMLAIATLYLVKKLSSSLNKILEYSERLASGNFTADINFGKWDTVELYSL
YEGLEQLRTNFSSVAKGVIENLDYLYENAIQIANASQNLSSGAVEQASTLEQMTANIEQISQGVSENTENAATTEK
IAVNTNERTKEGHKSVVKAIEAMTVITEKIGIIDEITRQTNLLALNASIEAARVGEKGKGFEVVAAEVRKLADQSK
ESAREIIDIANRSLTVASRAGENFEQIVPGMEQTARLVKNISNESYKQSVQIEQFKNAIEQVSQLVQTTASSSEEL
SAMSEKMLESVKDLKESVDYFKIEK

TABLE 1. Nucleotide and Amino Acid Sequences

t196.aa

MLINSKLVDQQFNLMINLIESIKSSFNLYISSMEEKVRVSSMYFNSAEKFNEASKIKSKRLSFISDQSEILIQTGS
NMMVTDKEGKIVFTTAVKDNSDFGKSIGDREYFTKLKESNSIVYNSFVMLADPGSIEESLLKDISKIKNKKGQIPY
ILIGMPLRDFETDNIFGYFMFLYSMDYIYRSFRGINFGILSSGRALAYDTTGRLLVHHVVLPGDILTDISASYSNI
IKKTSEDLLQKNKEISTVYYYDPKSNKKYVGISQKVLLNLSNNKFILLMRTSEDDFYYMSRATTIILAISFVFTLL
MLAIATLYLVKKLSSSLNKILEYSERLASGNFTADINFGKWDTVELYSLYEGLEQLRTNFSSVAKGVIENLDYLYE
NAIQIANASQNLSSGAVEQASTLEQMTANIEQISQGVSENTENAATTEKIAVNTNERTKEGHKSVVKAIEAMTVIT
EKIGIIDEITRQTNLLALNASIEAARVGEKGKGFEVVAAEVRKLADQSKESAREIIDIANRSLTVASRAGENFEQI
VPGMEQTARLVKNISNESYKQSVQIEQFKNAIEQVSQLVQTTASSSEELSAMSEKMLESVKDLKESVDYFKIEK

f196.nt

ATGAAGCTTAAAGCTAGGATGTTGCTACTTGTTCTTATTCTGATAGCATTCTTTATATCAATTTTGTTTTTTGCTT
TTGGAATGCTTATTAATAGTAAATTGGTGGATCAACAGTTTAATCTTATGATAAATCTTATTGAAAGCATTAAAAG
TTCTTTTAATCTTTACATCTCTTCAATGGAAGAGAAAGTTAGGGTTAGTTCCATGTATTTCAACTCTGCTGAAAAA
TTTAATGAGGCTAGTAAAATTAAATCCAAAAGGTTGAGCTTTATTTCAGATCAATCTGAAATTCTTATTCAAACCG
GTAGTAATATGATGGTTACAGACAAAGAAGGTAAAATAGTGTTTACTACGGCGGTTAAGGATAATAGTGATTTTGG
CAAATCTATTGGGGATAGAGAATATTTTACAAAACTTAAGGAGTCTAATAGTATTGTTTACAATTCCTTTGTCATG
TTGGCAGATCCCGGGTCTATTGAGGAGTCTTTACTTAAAGATATTTCCAAGATAAAAAATAAAAAAGGTCAGATTC
CTTACATATTAATAGGTATGCCATTAAGAGATTTTGAAACAGATAACATTTTTGGTTATTTTATGTTTCTTTATTC
AATGGATTATATATATAGGTCTTTTAGAGGGATTAATTTTGGAATACTCTCTAGCGGTCGTGCGCTAGCTTATGAT
ACTACGGGTAGATTGTTGGTTCATCATGTAGTATTGCCAGGTGATATTTTGACTGATATTAGTGCTTCTTATTCCA
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TACTTATGCTTGCTATTGCAACTCTTTATCTTGTGAAAAAGTTAAGCTCTTCTTTGAATAAGATACTGGAATATTC
TGAGAGACTTGCTTCTGGTAATTTTACTGCTGATATTAATTTTGGCAAATGGGATACTGTAGAGCTTTACAGTTTG
TACGAAGGGCTTGAGCAGTTGAGAACCAATTTTTCTTCAGTTGCAAAAGGAGTTATTGAAAATCTAGATTATCTTT
ATGAAAATGCAATTCAAATAGCAAATGCAAGCCAGAATTTAAGTTCTGGCGCTGTTGAGCAGGCTTCTACTTTAGA
GCAAATGACAGCAAATATTGAGCAAATTTCACAAGGTGTTTCTGAGAATACTGAAAATGCAGCTACTACTGAAAAA
ATTGCTGTTAATACTAATGAAAGGACTAAAGAGGGGCATAAATCTGTTGTTAAGGCTATTGAGGCAATGACTGTAA
TTACTGAAAAAATTGGAATTATTGATGAGATAACAAGGCAAACCAATTTGCTTGCTTTAAATGCCTCGATTGAAGC
TGCACGAGTGGGAGAAAAGGGCAAGGGATTTGAAGTGGTAGCTGCTGAGGTTAGAAAGCTTGCAGATCAAAGCAAA
GAATCAGCAAGAGAGATTATTGATATTGCAAACAGAAGTTTAACTGTTGCAAGTCGTGCTGGGGAAAATTTTGAAC
AAATAGTTCCTGGTATGGAACAAACAGCCAGACTTGTAAAAAATATTTCTAATGAAAGTTATAAGCAAAGTGTTCA
AATAGAGCAATTTAAAAATGCAATAGAGCAGGTTAGTCAGTTAGTCCAAACTACAGCCTCAAGCAGTGAAGAGCTT
TCTGCAATGTCTGAAAAGATGTTAGAGAGTGTAAAAGATTTAAAAGAATCTGTTGATTATTTTAAGATCGAAAAGT
AA

t196.nt

ATGCTTATTAATAGTAAATTGGTGGATCAACAGTTTAATCTTATGATAAATCTTATTGAAAGCATTAAAAGTTCTT
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TGAGGCTAGTAAAATTAAATCCAAAAGGTTGAGCTTTATTTCAGATCAATCTGAAATTCTTATTCAAACCGGTAGT
AATATGATGGTTACAGACAAAGAAGGTAAAATAGTGTTTACTACGGCGGTTAAGGATAATAGTGATTTTGGCAAAT
CTATTGGGGATAGAGAATATTTTACAAAACTTAAGGAGTCTAATAGTATTGTTTACAATTCCTTTGTCATGTTGGC
AGATCCCGGGTCTATTGAGGAGTCTTTACTTAAAGATATTTCCAAGATAAAAAATAAAAAAGGTCAGATTCCTTAC
ATATTAATAGGTATGCCATTAAGAGATTTTGAAACAGATAACATTTTTGGTTATTTTATGTTTCTTTATTCAATGG
ATTATATATATAGGTCTTTTAGAGGGATTAATTTTGGAATACTCTCTAGCGGTCGTGCGCTAGCTTATGATACTAC
GGGTAGATTGTTGGTTCATCATGTAGTATTGCCAGGTGATATTTTGACTGATATTAGTGCTTCTTATTCCAATATT

TABLE 1. Nucleotide and Amino Acid Sequences

ATTAAGAAAACATCTGAAGATTTGTTGCAAAAGAATAAAGAAATTTCAACTGTTTATTATTATGATCCTAAAAGCA
ATAAGAAATATGTGGGAATTAGTCAAAAGGTGTTATTAAACTTGTCTAATAATAAATTTATTCTTTTAATGAGAAC
TTCAGAGGACGATTTTTATTACATGTCACGAGCTACAACTATAATCTTAGCAATTAGTTTTGTATTTACATTACTT
ATGCTTGCTATTGCAACTCTTTATCTTGTGAAAAAGTTAAGCTCTTCTTTGAATAAGATACTGGAATATTCTGAGA
GACTTGCTTCTGGTAATTTTACTGCTGATATTAATTTTGGCAAATGGGATACTGTAGAGCTTTACAGTTTGTACGA
AGGGCTTGAGCAGTTGAGAACCAATTTTTCTTCAGTTGCAAAAGGAGTTATTGAAAATCTAGATTATCTTTATGAA
AATGCAATTCAAATAGCAAATGCAAGCCAGAATTTAAGTTCTGGCGCTGTTGAGCAGGCTTCTACTTTAGAGCAAA
TGACAGCAAATATTGAGCAAATTTCACAAGGTGTTTCTGAGAATACTGAAAATGCAGCTACTACTGAAAAAATTGC
TGTTAATACTAATGAAAGGACTAAAGAGGGGCATAAATCTGTTGTTAAGGCTATTGAGGCAATGACTGTAATTACT
GAAAAAATTGGAATTATTGATGAGATAACAAGGCAAACCAATTTGCTTGCTTTAAATGCCTCGATTGAAGCTGCAC
GAGTGGGAGAAAAGGGCAAGGGATTTGAAGTGGTAGCTGCTGAGGTTAGAAAGCTTGCAGATCAAAGCAAAGAATC
AGCAAGAGAGATTATTGATATTGCAAACAGAAGTTTAACTGTTGCAAGTCGTGCTGGGAAAATTTTGAACAAATA
GTTCCTGGTATGGAACAAACAGCCAGACTTGTAAAAAATATTTCTAATGAAAGTTATAAGCAAAGTGTTCAAATAG
AGCAATTTAAAAATGCAATAGAGCAGGTTAGTCAGTTAGTCCAAACTACAGCCTCAAGCAGTGAAGAGCTTTCTGC
AATGTCTGAAAAGATGTTAGAGAGTGTAAAAGATTTAAAAGAATCTGTTGATTATTTTAAGATCGAAAAGTAA

f899.aa

MRFIIAFLMILNQGFSNLFSLPPEDIIFESSYEVAIKKAQKLNKNVLILVGRDIKENLIKDFLNSFTNGEIIHKVS
RKSVFLVIDKDNEIFNKINLQKSPTIFFVDSKNEQIKAAYVGAVLSSVQFDKDFLNYVMGAIKSTSVLKKQKDYEI
NTADERTFFYKTLKGDWRLKFNGKDRKLVLFDTDLKEFLVFKDINENKLYAIPKSRIGNIYFSLLGNEEWKLFGKI
K

t899.aa

f899.nt

ATGAGATTTATAATTGCATTTTTAATGATTTTAAATCAAGGATTTTCAAATTTGTTTTCTTTGCCTCCGGAAGATA
TTATTTTTGAGAGTTCTTATGAGGTTGCAATTAAAAAAGCTCAAAAATTGAATAAAAATGTTTTAATTTTGGTTGG
TAGAGATATTAAAGAAAATTTAATAAAAGATTTTTTAAACTCTTTTACAAATGGTGAAATTATTCACAAAGTATCT
AGAAAAAGTGTTTTTTTAGTTATTGATAAGGATAATGAAATTTTTAATAAAATTAATCTACAAAAAAGTCCGACTA
TTTTTTTTGTTGATTCTAAGAATGAGCAAATAAAGGCAGCTTATGTGGGAGCTGTTTTGAGCAGTGTTCAATTTGA
TAAGGATTTTTTAAACTATGTTATGGGAGCTATAAAATCAACAAGTGTTTTAAAAAAGCAAAAAGATTATGAAATT
AATACTGCTGATGAGAGAACCTTTTTTTACAAAACATTAAAAGGTGATTGGCGATTAAAGTTTAATGGTAAAGACA
GAAAGCTTGTTCTTTTTGATACAGATCTTAAAGAATTTTTAGTTTTTAAAGATATTAATGAAAACAAGCTTTATGC
TATTCCTAAGTCTAGGATTGGTAATATTTATTTTTCATTATTGGGAAATGAAGAATGGAAGCTTTTTGGAAAAATA
AAATAA

t899.nt

TTGCCTCCGGAAGATATTATTTTTGAGAGTTCTTATGAGGTTGCAATTAAAAAAGCTCAAAAATTGAATAAAAATG
TTTTAATTTTGGTTGGTAGAGATATTAAAGAAAATTTAATAAAAGATTTTTTAAACTCTTTTACAAATGGTGAAAT
TATTCACAAAGTATCTAGAAAAAGTGTTTTTTTAGTTATTGATAAGGATAATGAAATTTTTAATAAAATTAATCTA
CAAAAAAGTCCGACTATTTTTTTTGTTGATTCTAAGAATGAGCAAATAAAGGCAGCTTATGTGGGAGCTGTTTTGA
GCAGTGTTCAATTTGATAAGGATTTTTTAAACTATGTTATGGGAGCTATAAAATCAACAAGTGTTTTAAAAAAGCA
AAAAGATTATGAAATTAATACTGCTGATGAGAGAACCTTTTTTTACAAAACATTAAAAGGTGATTGGCGATTAAAG
TTTAATGGTAAAGACAGAAAGCTTGTTCTTTTTGATACAGATCTTAAAGAATTTTTAGTTTTTAAAGATATTAATG
AAAACAAGCTTTATGCTATTCCTAAGTCTAGGATTGGTAATATTTATTTTTCATTATTGGGAAATGAAGAATGGAA
GCTTTTTGGAAAAATAAAATAA

TABLE 1. Nucleotide and Amino Acid Sequences

f924.aa

MQDRKFSFRKYFLISVFLIFIVSGITYFYSTQMLEKSQKCVEDNLDAKVKLVDMEDFYFDLNECLNMDDFFIPRPD
FLNENLNKNLVVDGLIKNKFLDENFFKDLWIKKENLFNVDIEKENEKLIDKILEISK

t924.aa

TQMLEKSQKCVEDNLDAKVKLVDMEDFYFDLNECLNMDDFFIPRPDFLNENLNKNLVVDGLIKNKFLDENFFKDLW
IKKENLFNVDIEKENEKLIDKILEISK

f924.nt

ATGCAAGATAGAAAGTTTAGTTTTAGAAAATATTTTTTAATTTCAGTATTTTTGATTTTTATTGTTTCTGGTATTA
CTTATTTCTATTCAACACAAATGTTGGAAAAATCTCAAAAGTGTGTTGAAGACAATTTAGACGCTAAGGTTAAATT
AGTTGATATGGAAGATTTTTATTTTGATTTAAATGAATGTCTAAATATGGATGATTTTTTTATTCCAAGACCTGAT
TTTTTAAATGAAAATTTAAATAAGAATTTAGTTGTTGATGGATTGATTAAAAATAAATTTCTTGATGAGAATTTTT
TCAAGGATCTTTGGATTAAAAAGGAAAATTTATTTAACGTTGATATTGAGAAGGAGAATGAAAAATTAATAGATAA
GATTTTAGAAATTTCCAAATGA

t924.nt

ACACAAATGTTGGAAAAATCTCAAAAGTGTGTTGAAGACAATTTAGACGCTAAGGTTAAATTAGTTGATATGGAAG
ATTTTTATTTTGATTTAAATGAATGTCTAAATATGGATGATTTTTTTATTCCAAGACCTGATTTTTTAAATGAAAA
TTTAAATAAGAATTTAGTTGTTGATGGATTGATTAAAAATAAATTTCTTGATGAGAATTTTTTCAAGGATCTTTGG
ATTAAAAAGGAAAATTTATTTAACGTTGATATTGAGAAGGAGAATGAAAAATTAATAGATAAGATTTTAGAAATTT
CCAAATGA

f925.aa

MIRKYLIYISLLFIVFEVYSKPAFISQDDSYELDFSSGEVDISVNTNSKFNLSFKDESWIYIKSIENEAFIKLIGE
SYDNGAVFTFQTFKKEGKIKLVFTYQNVKDSSEFNKIIILKITKNFEVAIPQGVGGGSSRDNNIETGNNLELGGGS
ISGATSKEIIVRALNLSYINDYKGAIDLLNKYNFNDDKYILLKAEIHYKNGDYLKSYENYLKLKSKYFQSIVFDLI
RLAIELNIKEEVLENARYLVEKNVDFSESIYLEIFEFLVTRGEHEFALNFSSLYFPKYINSSFSDKYSYLLGKLYE
SESKHKDFLKALHYYKLVIDNYPFSYYYERAKIRYLFLKRFF

t925.aa

KPAFISQDDSYELDFSSGEVDISVNTNSKFNLSFKDESWIYIKSIENEAFIKLIGESYDNGAVFTFQTFKKEGKIK
LVFTYQNVKDSSEFNKIIILKITKNFEVAIPQGVGGGSSRDNNIETGNNLELGGGSISGATSKEIIVRALNLSYIN
DYKGAIDLLNKYNFNDDKYILLKAEIHYKNGDYLKSYENYLKLKSKYFQSIVFDLIRLAIELNIKEEVLENARYLV
EKNVDFSESIYLEIFEFLVTRGEHEFALNFSSLYFPKYINSSFSDKYSYLLGKLYESESKHKDFLKALHYYKLVID
NYPFSYYYERAKIRYLFLKRFF

f925.nt

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GTCAAGACGATTCGTATGAGCTTGATTTTAGTAGTGGAGAGGTAGATATTAGTGTAAATACCAATTCAAAATTTAA
TCTTTCTTTTAAAGATGAGTCTTGGATTTATATCAAAAGCATTGAAAATGAAGCTTTTATTAAGTTAATTGGAGAA

TABLE 1. Nucleotide and Amino Acid Sequences

TCTTATGATAACGGTGCTGTTTTTACTTTTCAGACTTTTAAAAAAGAAGGCAAAATTAAATTGGTTTTCACTTATC
AAAATGTTAAAGATTCAAGTGAATTTAATAAAATAATTATCTTGAAAATTACAAAGAATTTTGAAGTTGCAATTCC
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AGGCTTGCTATAGAATTAAATATTAAAGAAGAGGTTTTAGAGAACGCTAGATATTTAGTTGAAAAGAATGTTGATT
TTTCTGAGAGCATTTATCTTGAGATCTTTGAATTCTTAGTAACAAGGGGAGAGCATGAGTTTGCTTTAAATTTTAG
CTCTCTTTACTTTCCTAAGTATATTAATTCAAGCTTTTCAGACAAATATAGTTATTTGTTGGGAAAACTTTATGAG
TCTGAGAGCAAGCATAAAGATTTTTTAAAGGCTTTGCATTACTATAAATTGGTTATTGATAATTACCCTTTTAGTT
ATTATTATGAGAGAGCCAAGATAAGATATTTATTTTTAAAGCGGTTTTTTTAG

t925.nt

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CCAATTCAAAATTTAATCTTTCTTTTAAAGATGAGTCTTGGATTTATATCAAAAGCATTGAAAATGAAGCTTTTAT
TAAGTTAATTGGAGAATCTTATGATAACGGTGCTGTTTTTACTTTTCAGACTTTTAAAAAAGAAGGCAAAATTAAA
TTGGTTTTCACTTATCAAAATGTTAAAGATTCAAGTGAATTTAATAAAATAATTATCTTGAAAATTACAAAGAATT
TTGAAGTTGCAATTCCACAAGGCGTTGGTGGTGGCTCTAGCAGGGACAATAACATTGAAACTGGTAATAATCTTGA
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GATTACAAAGGAGCAATAGATTTGCTTAATAAGTATAATTTCAATGACGATAAATATATTTTATTGAAGGCGGAAA
TTCATTATAAAAATGGTGATTATTTAAAATCTTATGAAAATTATTTGAAATTGAAGAGTAAATATTTTCAAAGCAT
TGTTTTTGATCTAATTAGGCTTGCTATAGAATTAAATATTAAAGAAGAGGTTTTAGAGAACGCTAGATATTTAGTT
GAAAAGAATGTTGATTTTTCTGAGAGCATTTATCTTGAGATCTTTGAATTCTTAGTAACAAGGGGAGAGCATGAGT
TTGCTTTAAATTTTAGCTCTCTTTACTTTCCTAAGTATATTAATTCAAGCTTTTCAGACAAATATAGTTATTTGTT
GGGAAAACTTTATGAGTCTGAGAGCAAGCATAAAGATTTTTTAAAGGCTTTGCATTACTATAAATTGGTTATTGAT
AATTACCCTTTTAGTTATTATTATGAGAGAGCCAAGATAAGATATTTATTTTTAAAGCGGTTTTTTTAG

f929.aa

MTKVLVVSAIALLSKDKELIPFYKFLFLFFFFTLLACSKVSKDFIVFNKDVKTSSRIDNPNSNVLEVNKMEDFFGD
IIDLKGYKILSVQQENLNLDVYFEQVVLAQNFSNLNAYLFIIGFDPKIKAGTILFKTQIDIDPKNSYNMYLEDITG
DYDFNIVIQGFLKDKSVLYVFQKSVLNDVSSYRPIFFDKVNGTVLINKYARSSAYEENRSRESYPISLEKYEKVGE
DLIISKIEKYEYSNVQGRYCLSSVSEKVGKIDNNIYKTLKNLSKDEVYKFLHGVWYDVHDYNKMHVKDIDEVLFLS
FERQSSEINLFRKNSQEVAKIEYISKPAYNTLNVSAKSLFSDLIVYNFWIKIVDKENIEIKIDTSTNSYDNSGFSG
TFKRFDENVLNVKKGSSDIYFIPSGNYVYKDKIYDFSYPHLTYIDENKIYYGIFNIFPLKNNFVLEYEIDMGSYKL
VESFFLEHSERIVQKQKFSTIILNPIKILKDDVSLVKGQKLKLERIEKI

t929.aa

KDKELIPFYKFLFLFFFFTLLACSKVSKDFIVFNKDVKTSSRIDNPNSNVLEVNKMEDFFGDIIDLKGYKILSVQQ
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KSVLYVFQKSVLNDVSSYRPIFFDKVNGTVLINKYARSSAYEENRSRESYPISLEKYEKVGEDLIISKIEKYEYSN
VQGRYCLSSVSEKVGKIDNNIYKTLKNLSKDEVYKFLHGVWYDVHDYNKMHVKDIDEVLFLSFERQSSEINLFRKN
SQEVAKIEYISKPAYNTLNVSAKSLFSDLIVYNFWIKIVDKENIEIKIDTSTNSYDNSGFSGTFKRFDENVLNVKK
GSSDIYFIPSGNYVYKDKIYDFSYPHLTYIDENKIYYGIFNIFPLKNNFVLEYEIDMGSYKLVESFFLEHSERIVQ
KQKFSTIILNPIKILKDDVSLVKGQKLKLERIEKI

f929.nt

TABLE 1. Nucleotide and Amino Acid Sequences

ATGACAAAGGTTTTGGTTGTTAGTGCGATTGCTCTTCTGAGTAAGGATAAAGAATTAATCCCATTTTATAAATTTT
TGTTTTTATTCTTTTTTTTTACATTACTTGCTTGTTCCAAGGTAAGCAAAGATTTTATTGTTTTTAACAAAGATGT
AAAGACTTCTTCCAGGATCGATAATCCAAATTCCAATGTTTTAGAAGTTAATAAAATGGAAGATTTTTTTGGAGAT
ATTATAGATTTAAAAGGTTATAAAATTCTTTCAGTTCAGCAGGAAAATTTAAATTTAGATGTGTATTTTGAGCAGG
TGGTTTTAGCTCAAAATTTTTCAAATCTTAATGCATATTTGTTTATTATTGGTTTTGATCCTAAAATTAAAGCTGG
AACGATTCTTTTTAAAACTCAAATAGATATTGATCCAAAAAATTCTTATAACATGTATCTTGAAGATATTACAGGT
GATTATGATTTTAATATAGTTATTCAAGGATTTTTAAAAGATAAATCTGTTTTGTATGTTTTTCAAAAATCTGTTT
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ATCTTCAGCTTATGAAGAAAACAGATCAAGAGAAAGCTATCCTATTTCTTTAGAAAAATATGAAAAAGTGGGGGAA
GATTTAATAATTAGCAAGATTGAAAAATATGAATATTCTAATGTTCAGGGTAGATATTGTCTTTCTTCTGTGAGCG
AAAAAGTTGGTAAAATTGATAATAATATTTATAAAACTTTAAAGAATTTAAGCAAAGATGAAGTTTATAAATTTTT
GCATGGAGTTTGGTATGATGTTCATGACTATAATAAAATGCATGTCAAAGATATTGATGAAGTTTTATTCTTGTCT
TTTGAAAGGCAATCAAGCGAGATTAATCTTTTCAGGAAAAATTCTCAAGAAGTTGCAAAGATTGAATATATTTCAA
AACCTGCTTACAATACTCTTAATGTTAGTGCAAAGTCTCTTTTTTCAGATTTGATAGTTTATAACTTTTGGATCAA
AATTGTAGATAAAGAAAACATTGAAATCAAAATTGACACTAGCACAAATTCTTATGATAATAGTGGATTTTCGGGT
ACATTTAAGAGGTTTGATGAGAATGTCTTAAATGTTAAAAAAGGGAGTAGTGATATTTATTTTATTCCTAGTGGAA
ATTACGTGTATAAGGATAAAATTTATGATTTTTCTTACCCCCATTTAACTTATATTGATGAGAATAAAATTTATTA
TGGCATTTTTAATATTTTTCCTTTAAAAAATAATTTTGTTCTTGAATATGAGATTGACATGGGTAGTTACAAGCTT
GTTGAATCTTTTTTCCTTGAGCATAGCGAAAGAATTGTTCAAAAGCAAAAATTTTCTACAATCATTTTAAATCCTA
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TAAGCAAAGATTTTATTGTTTTTAACAAAGATGTAAAGACTTCTTCCAGGATCGATAATCCAAATTCCAATGTTTT
AGAAGTTAATAAAATGGAAGATTTTTTTGGAGATATTATAGATTTAAAAGGTTATAAAATTCTTTCAGTTCAGCAG
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TTAATGGAACTGTTCTTATTAATAAGTATGCAAGATCTTCAGCTTATGAAGAAAACAGATCAAGAGAAAGCTATCC
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TGTCAAAGATATTGATGAAGTTTTATTCTTGTCTTTTGAAAGGCAATCAAGCGAGATTAATCTTTTCAGGAAAAAT
TCTCAAGAAGTTGCAAAGATTGAATATATTTCAAAACCTGCTTACAATACTCTTAATGTTAGTGCAAAGTCTCTTT
TTTCAGATTTGATAGTTTATAACTTTTGGATCAAAATTGTAGATAAAGAAAACATTGAAATCAAAATTGACACTAG
CACAAATTCTTATGATAATAGTGGATTTTCGGGTACATTTAAGAGGTTTGATGAGAATGTCTTAAATGTTAAAAAA
GGGAGTAGTGATATTTATTTTATTCCTAGTGGAAATTACGTGTATAAGGATAAAATTTATGATTTTTCTTACCCCC
ATTTAACTTATATTGATGAGAATAAAATTTATTATGGCATTTTTAATATTTTTCCTTTAAAAAATAATTTTGTTCT
TGAATATGAGATTGACATGGGTAGTTACAAGCTTGTTGAATCTTTTTTCCTTGAGCATAGCGAAAGAATTGTTCAA
AAGCAAAAATTTTCTACAATCATTTTAAATCCTATTAAAATTTTAAAAGATGATGTAAGCTTAGTTAAAGGGCAAA
AATTAAAGCTTGAGCGAATAGAAAAAAATATGA

f933.aa

MNKLLIFVLATFCVFSSFAQANDSKNGAFGMSAGEKLLVYETSKQDPIVPFLLNLFLGFGIGSFAQGDILGGSLIL
GFDAVGIGLILAGAYLDIKALDGITKKAAFQWTWGKGVMLAGVVTMAVTRLTEIILPFTFANSYNRKLKNSLNVAL
GGFEPSFDVAMGQSSALGFELSFKKSY

t933.aa

TABLE 1. Nucleotide and Amino Acid Sequences

NDSKNGAFGMSAGEKLLVYETSKQDPIVPFLLNLFLGFGIGSFAQGDILGGSLILGFDAVGIGLILAGAYLDIKAL
DGITKKAAFQWTWGKGVMLAGVVTMAVTRLTEIILPFTFANSYNRKLKNSLNVALGGFEPSFDVAMGQSSALGFEL
SFKKSY

f933.nt

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ATGGTGCGTTTGGGATGAGTGCTGGAGAAAAACTTTTGGTTTATGAAACTAGCAAGCAAGATCCTATTGTACCATT
TTTATTGAACCTTTTTTTAGGGTTTGGAATAGGCTCCTTTGCTCAAGGAGATATTCTTGGAGGTTCTCTTATTCTT
GGATTTGATGCGGTTGGTATAGGGCTTATACTTGCGGGGGCTTATTTGGATATCAAAGCGCTTGATGGTATTACTA
AAAAAGCTGCTTTTCAATGGACTTGGGGTAAGGGAGTTATGTTAGCAGGTGTGGTTACTATGGCTGTGACAAGATT
AACAGAAATTATTCTTCCATTTACATTTGCTAATAGTTATAATAGGAAGCTAAAAAATAGCCTTAATGTAGCTTTA
GGAGGATTTGAACCTAGTTTTGATGTTGCAATGGGCCAATCCAGTGCTCTTGGGTTTGAACTGTCTTTCAAAAAAA
GCTATTAA

t933.nt

AATGATTCTAAAAATGGTGCGTTTGGGATGAGTGCTGGAGAAAAACTTTTGGTTTATGAAACTAGCAAGCAAGATC
CTATTGTACCATTTTTATTGAACCTTTTTTTAGGGTTTGGAATAGGCTCCTTTGCTCAAGGAGATATTCTTGGAGG
TTCTCTTATTCTTGGATTTGATGCGGTTGGTATAGGGCTTATACTTGCGGGGGCTTATTTGGATATCAAAGCGCTT
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CTGTGACAAGATTAACAGAAATTATTCTTCCATTTACATTTGCTAATAGTTATAATAGGAAGCTAAAAAATAGCCT
TAATGTAGCTTTAGGAGGATTTGAACCTAGTTTTGATGTTGCAATGGGCCAATCCAGTGCTCTTGGGTTTGAACTG
TCTTTCAAAAAAAGCTATTAA

f940.aa

MRKYIFIILIAVLLIGVNIKKIAAAANIDRHTNSTLGIDLSVGIPIFYNDLSKAYPTNLYPGGIGAIKYQYHILNN
LAIGLELRYMFNFDINHSFNILNPDSSVGKIFYSVPITFSINYIFDIGELFQIPVFTNIGFSLNTYGDRNNNITNL
RTFDALPTISFGSGILWNFNYKWAFGATASWWMMFEFGNSAKMAHFALVSLSVTVNVNKL

t940.aa

ANIDRHTNSTLGIDLSVGIPIFYNDLSKAYPTNLYPGGIGAIKYQYHILNNLAIGLELRYMFNFDINHSFNILNPD
SSVGKIFYSVPITFSINYIFDIGELFQIPVFTNIGFSLNTYGDRNNNITNLRTFDALPTISFGSGILWNFNYKWAF
GATASWWMMFEFGNSAKMAHFALVSLSVTVNVNKL

f940.nt

ATGAGAAAGTATATTTTTATAATACTAATTGCAGTCTTGCTAATTGGTGTAAACATAAAAAAAATTGCGGCCGCAG
CCAATATTGATAGGCATACAAACTCCACTTTAGGAATAGATTTAAGTGTAGGAATCCCTATTTTTTACAACGACTT
ATCAAAAGCTTATCCTACCAATTTATATCCAGGAGGTATTGGGGCAATAAAATACCAGTACCATATTTTAAACAAT
TTAGCAATTGGACTTGAACTAAGGTATATGTTTAACTTTGATATTAACCATTCTTTTAATATATTAAATCCAGATT
CAAGTGTAGGTAAAATTTTTTATAGCGTGCCTATTACATTTTCAATAAATTATATATTTGATATAGGAGAATTATT

TABLE 1. Nucleotide and Amino Acid Sequences

TCAAATTCCAGTCTTCACAAATATAGGGTTTTCTCTTAATACATATGGAGATAGAAACAACAATATTACAAATTTA
AGAACTTTTGATGCACTCCCTACAATCTCTTTTGGATCTGGAATTTTATGGAACTTTAACTATAAATGGGCTTTTG
GAGCAACAGCATCTTGGTGGATGATGTTTGAATTTGGAAATTCTGCTAAAATGGCACATTTTGCACTTGTATCATT
ATCAGTTACAGTGAATGTAAATAAATTGTAG

t940.nt

GCCAATATTGATAGGCATACAAACTCCACTTTAGGAATAGATTTAAGTGTAGGAATCCCTATTTTTTACAACGACT
TATCAAAAGCTTATCCTACCAATTTATATCCAGGAGGTATTGGGGCAATAAAATACCAGTACCATATTTTAAACAA
TTTAGCAATTGGACTTGAACTAAGGTATATGTTTAACTTTGATATTAACCATTCTTTTAATATATTAAATCCAGAT
TCAAGTGTAGGTAAAATTTTTTATAGCGTGCCTATTACATTTTCAATAAATTATATATTTGATATAGGAGAATTAT
TTCAAATTCCAGTCTTCACAAATATAGGGTTTTCTCTTAATACATATGGAGATAGAAACAACAATATTACAAATTT
AAGAACTTTTGATGCACTCCCTACAATCTCTTTTGGATCTGGAATTTTATGGAACTTTAACTATAAATGGGCTTTT
GGAGCAACAGCATCTTGGTGGATGATGTTTGAATTTGGAAATTCTGCTAAAATGGCACATTTTGCACTTGTATCAT
TATCAGTTACAGTGAATGTAAATAAATTGTAG

f943.aa

MKNQFLNSYFQLITTIFLISSITIAAEEITSTLKVPNGFKVEIFLNNTIEKPRGITSDQDGNIFIGSGSTFAYFVT
KNRKIYTIAKTLQKPIGIDYWDNKLYISSVDKIYVVKNVKEEINKSIKSHKDYTWKMQIFALLPKNNSQMHSGRYI
KVDSKNNKLIVNIGSQHNVKIPPKKEAVILSINLKTKKEEIVAFGVRNSVGFDFHPISNEIYFSDNGQDGLGDNIP
PDEINVITEYKEHFGFPYVFGKNQKNYGFYNKAPKNTKFIPSIYELPAHVAPLGIHFYRGNNFPKEYINKLFIAEH
GSWNRSSPVGYKITTLDIDSKTRTARNYKTFLYGFLKHDKSKFGRPVDIITYYDGSILFTDDFGNKIYRVYYEKI

t943.aa

EITSTLKVPNGFKVEIFLNNTIEKPRGITSDQDGNIFIGSGSTFAYFVTKNRKIYTIAKTLQKPIGIDYWDNKLYI
SSVDKIYVVKNVKEEINKSIKSHKDYTWKMQIFALLPKNNSQMHSGRYIKVDSKNNKLIVNIGSQHNVKIPPKKEA
VILSINLKTKKEEIVAFGVRNSVGFDFHPISNEIYFSDNGQDGLGDNIPPDEINVITEYKEHFGFPYVFGKNQKNY
GFYNKAPKNTKFIPSIYELPAHVAPLGIHFYRGNNFPKEYINKLFIAEHGSWNRSSPVGYKITTLDIDSKTRTARN
YKTFLYGFLKHDKSKFGRPVDIITYYDGSILFTDDFGNKIYRVYYEKI

f943.nt

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CCAGATGAAATAAACGTAATAACCGAATATAAAGAACATTTTGGATTTCCCTATGTGTTTGGAAAAAATCAAAAAA
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TCCACTTGGAATACACTTTTACCGGGGAAATAACTTTCCAAAAGAATACATAAATAAATTATTCATAGCAGAACAC
GGCTCGTGGAACAGATCTTCTCCTGTTGGCTACAAAATAACAACACTAGACATTGATTCTAAAACCAGAACAGCAA

TABLE 1. Nucleotide and Amino Acid Sequences

GAAATTACAAGACTTTTTTATATGGATTTTTAAAGCACGACAAATCTAAATTTGGACGCCCTGTTGATATAATCAC
ATATTATGACGGTTCAATTCTTTTTACAGATGACTTTGGAAATAAAATATACAGAGTTTACTACGAAAAGATTTAA

t943.nt

GAAATAACAAGCACACTAAAAGTTCCTAATGGATTTAAAGTCGAAATTTTTTTAAACAATACAATTGAAAAACCTA
GAGGAATCACAAGCGATCAAGATGGAAATATATTCATAGGATCTGGAAGCACTTTTGCATACTTTGTAACAAAAAA
CAGAAAAATTTATACCATAGCAAAAACCCTGCAAAAACCTATTGGTATTGATTATTGGGATAATAAACTCTACATA
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AGATTCTAAAAATAACAAATTAATAGTAAATATAGGATCCCAGCACAATGTTAAAATTCCCCCAAAAAAAGAAGCA
GTAATCCTTAGTATTAATTTAAAAACAAAAAAAGAAGAAATAGTAGCTTTTGGAGTGAGAAACTCAGTTGGGTTTG
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TGAAATAAACGTAATAACCGAATATAAAGAACATTTTGGATTTCCCTATGTGTTTGGAAAAAATCAAAAAAATTAC
GGTTTTTATAACAAAGCACCCAAAAACACTAAGTTTATCCCATCTATTTACGAACTTCCCGCACATGTAGCTCCAC
TTGGAATACACTTTTACCGGGGAAATAACTTTCCAAAAGAATACATAAATAAATTATTCATAGCAGAACACGGCTC
GTGGAACAGATCTTCTCCTGTTGGCTACAAAATAACAACACTAGACATTGATTCTAAAACCAGAACAGCAAGAAAT
TACAAGACTTTTTTATATGGATTTTTAAAGCACGACAAATCTAAATTTGGACGCCCTGTTGATATAATCACATATT
ATGACGGTTCAATTCTTTTTACAGATGACTTTGGAAATAAAATATACAGAGTTTACTACGAAAAGATTTAA

f952.aa

MNYARFAVLIVLLFFYIWFFIILRMKRTNLFLLEKIQNGAKILDIRSPKEYSKSHYLKSINIPFNNLFAKKDKLGD
FESPIIVYGKSFNKSYEAKKVLKSMGFKNVFVAGTLKDMPQAKKEVG

t952.aa

RMKRTNLFLLEKIQNGAKILDIRSPKEYSKSHYLKSINIPFNNLFAKKDKLGDFESPIIVYGKSFNKSYEAKKVLK
SMGFKNVFVAGTLKDMPQAKKEVG

f952.nt

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AAAGAACTAATCTGTTTTTGTTAGAAAAAATCCAAAATGGAGCAAAAATTTTGGATATTCGGTCTCCCAAAGAATA
TAGCAAGTCTCATTATTTGAAGTCAATTAACATTCCTTTTAATAATTTATTTGCTAAAAAGGATAAATTAGGTGAT
TTTGAGTCCCCAATAATTGTTTATGGTAAAAGTTTTAATAAGTCTTACGAGGCTAAAAAAGTTTTAAAAAGCATGG
GATTTAAGAATGTGTTTGTTGCTGGAACCTTGAAAGACATGCCACAAGCAAAAAAAGAAGTTGGTTGA

t952.nt

AGGATGAAAAGAACTAATCTGTTTTTGTTAGAAAAAATCCAAAATGGAGCAAAAATTTTGGATATTCGGTCTCCCA
AAGAATATAGCAAGTCTCATTATTTGAAGTCAATTAACATTCCTTTTAATAATTTATTTGCTAAAAAGGATAAATT
AGGTGATTTTGAGTCCCCAATAATTGTTTATGGTAAAAGTTTTAATAAGTCTTACGAGGCTAAAAAAGTTTTAAAA
AGCATGGGATTTAAGAATGTGTTTGTTGCTGGAACCTTGAAAGACATGCCACAAGCAAAAAAAGAAGTTGGTTGA

TABLE 1. Nucleotide and Amino Acid Sequences

f378.aa

MIKKFLLFAMLNIFLTNKAHSNEEIIEISTEIQKEKYIPFLISRGKTQLEDLVKYTLEINPELDKNYVNTVAKTYI
DESLIEGVNYDIAYAQMLLETGALKFNGIVSKEQHNFSGIGATNNLTKGNSFSNITEGIKAHIQHLKAYASKQNIK
SNMVDPRFYLVKRGSAPTIYDLTGKWAKDKLYDKKLKKILLELLEYNNANKS

t378.aa

NEEIIEISTEIQKEKYIPFLISRGKTQLEDLVKYTLEINPELDKNYVNTVAKTYIDESLIEGVNYDIAYAQMLLET
GALKFNGIVSKEQHNFSGIGATNNLTKGNSFSNITEGIKAHIQHLKAYASKQNIKSNMVDPRFYLVKRGSAPTIYD
LTGKWAKDKLYDKKLKKILLELLEYNNANKS

f378.nt

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TCGAAATAAGTACTGAAATACAAAAGGAAAAATATATTCCCTTTTTAATAAGTAGAGGAAAAACTCAACTAGAAGA
CCTTGTAAAATATACTCTAGAAATAAATCCAGAGCTTGACAAAAACTATGTAAATACTGTTGCTAAAACCTATATA
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TCAATGGAATAGTTTCAAAAGAACAACACAATTTTTCAGGAATAGGCGCTACTAATAATCTTACAAAAGGAAATTC
TTTTTCCAATATTACAGAAGGAATTAAAGCTCATATTCAACATTTAAAAGCTTATGCTTCAAAACAAAATATCAAA
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AAGCTAA

t378.nt

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TAAAACCTATATAGACGAATCTTTGATTGAAGGGGTTAATTATGACATTGCCTATGCTCAAATGTTACTAGAAACA
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CAAAAGGAAATTCTTTTTCCAATATTACAGAAGGAATTAAAGCTCATATTCAACATTTAAAAGCTTATGCTTCAAA
ACAAAATATCAAATCAAATATGGTTGATCCTAGATTTTACCTTGTTAAAAGAGGATCTGCTCCAACAATATATGAT
TTGACTGGGAAATGGGCAAAAGACAAACTTTACGACAAAAAACTTAAAAAAATATTATTAGAACTATTAGAATATA
ATAATGCAAATAAAAGCTAA

f4.aa

MKLFRRNVMIKMPSSFTIIFSLIVFVTILTYVIPAGKFDKEFKQMGDGSKREIIVAGTYQYVDRGSRGFLHPIMTI
LTAMSKGMEHAVEVIVFVLIVGGAYGIIMKTGAIDVGIYFLIKKLGHKDKLLIPLLMFIFSIGGTVTGMSEETLPF
YFVMIPLIVALGYDSLVGAAIIALGAGVGTMASTVNPFATGIASAIASISLQDGFYFRIVLYFVSVLAAITYVCVY
ASKIKKDPSKSLVYSQKDEHYQYFVKKDGLSTGDNAQNALEFTFAHKLVLLLFGFMILILIFSIVNLGWWMQEMTM
LYLGVAIISAFICKLGETEMWDAFVKGSESLLTAALVIGLARGVMIVCDDGLITDTMLNAATNFLYNLPRPLFIIL
NEIIQIFIGFVVPSSSGHASLTMPIMAPLADFLSIPRASVVIAMQTASGLINLITPTSGVIMAVLGISRLSYGTWF
KFVLPLFMIEFFISILVIIANIYLSF

t4.aa

TABLE 1. Nucleotide and Amino Acid Sequences

KFDKEFKQMGDGSKREIIVAGTYQYVDRGSRGFLHPIMTILTAMSKGMEHAVEVIVFVLIVGGAYGIIMKTGAIDV
GIYFLIKKLGHKDKLLIPLLMFIFSIGGTVTGMSEETLPFYFVMIPLIVALGYDSLVGAAIIALGAGVGTMASTVN
PFATGIASAIASISLQDGFYFRIVLYFVSVLAAITYVCVYASKIKKDPSKSLVYSQKDEHYQYFVKKDGLSTGDNA
QNALEFTFAHKLVLLLFGFMILILIFSIVNLGWWMQEMTMLYLGVAIISAFICKLGETEMWDAFVKGSESLLTAAL
VIGLARGVMIVCDDGLITDTMLNAATNFLYNLPRPLFIILNEIIQIFIGFVVPSSSGHASLTMPIMAPLADFLSIP
RASVVIAMQTASGLINLITPTSGVIMAVLGISRLSYGTWFKFVLPLFMIEFFISILVIIANIYLSF

f4.nt

ATGAAATTATTTAGGAGAAACGTTATGATCAAAATGCCAAGTAGTTTTACAATAATATTTTCTTTAATTGTATTTG
TTACCATTTTAACGTATGTGATTCCTGCCGGTAAGTTTGATAAAGAATTTAAGCAAATGGGTGATGGATCTAAAAG
GGAAATAATTGTTGCTGGAACTTATCAATATGTAGATCGAGGCTCTAGGGGATTTTTACATCCTATTATGACTATT
TTAACCGCAATGTCAAAGGGGATGGAACATGCAGTTGAAGTTATTGTTTTTGTTTTAATTGTTGGGGGTGCTTATG
GGATTATTATGAAAACTGGAGCAATAGATGTGGGAATTTATTTTTTAATCAAGAAGTTGGGGCACAAAGATAAGTT
GCTTATTCCTTTGTTAATGTTTATTTTTTCAATTGGTGGAACTGTAACCGGAATGAGTGAAGAGACCCTTCCTTTT
TATTTTGTTATGATTCCCTTGATAGTAGCTTTGGGTTATGATAGTCTTGTTGGAGCGGCTATTATTGCTTTAGGAG
CTGGAGTGGGAACTATGGCTTCTACTGTAAATCCATTTGCGACAGGAATTGCATCTGCAATAGCTTCTATTAGCTT
GCAGGATGGATTTTATTTTAGAATTGTTCTTTATTTTGTATCAGTATTGGCTGCTATAACCTATGTTTGTGTTTAT
GCGTCTAAAATTAAAAAGGATCCCTCAAAATCGCTTGTGTATTCTCAAAAAGATGAACATTATCAATATTTTGTTA
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TTGTATCTTGGAGTTGCTATTATATCGGCTTTTATTTGTAAATTAGGTGAAACTGAAATGTGGGATGCGTTTGTGA
AAGGTTCTGAAAGTCTGCTAACCGCTGCTCTTGTTATTGGACTTGCTAGAGGTGTTATGATAGTATGTGATGATGG
GTTGATTACAGATACTATGTTAAATGCTGCTACTAATTTTTTATACAATCTTCCAAGACCCCTTTTTATCATATTG
AATGAAATTATTCAAATATTTATAGGATTTGTTGTTCCATCTTCATCAGGACATGCTAGTCTCACTATGCCAATAA
TGGCTCCTCTTGCCGATTTTTTGTCAATTCCAAGAGCTTCAGTTGTTATTGCCATGCAGACTGCATCTGGGCTTAT
TAATTTGATAACACCTACCAGCGGAGTTATAATGGCTGTATTGGGGATATCCAGATTGAGTTATGGTACGTGGTTT
AAGTTTGTTTTACCATTATTTATGATTGAGTTTTTTATCTCTATTTTAGTTATTATAGCTAACATTTATTTAAGTT
TTTAG

t4.nt

AAGTTTGATAAAGAATTTAAGCAAATGGGTGATGGATCTAAAAGGGAAATAATTGTTGCTGGAACTTATCAATATG
TAGATCGAGGCTCTAGGGGATTTTTACATCCTATTATGACTATTTTAACCGCAATGTCAAAGGGGATGGAACATGC
AGTTGAAGTTATTGTTTTTGTTTTAATTGTTGGGGGTGCTTATGGGATTATTATGAAAACTGGAGCAATAGATGTG
GGAATTTATTTTTTAATCAAGAAGTTGGGGCACAAAGATAAGTTGCTTATTCCTTTGTTAATGTTTATTTTTTCAA
TTGGTGGAACTGTAACCGGAATGAGTGAAGAGACCCTTCCTTTTTATTTTGTTATGATTCCCTTGATAGTAGCTTT
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CCATTTGCGACAGGAATTGCATCTGCAATAGCTTCTATTAGCTTGCAGGATGGATTTTATTTTAGAATTGTTCTTT
ATTTTGTATCAGTATTGGCTGCTATAACCTATGTTTGTGTTTATGCGTCTAAAATTAAAAAGGATCCCTCAAAATC
GCTTGTGTATTCTCAAAAAGATGAACATTATCAATATTTTGTTAAAAAAGATGGACTTTCTACCGGAGATAATGCT
CAGAATGCTCTTGAGTTTACTTTTGCTCATAAATTAGTTTTACTTTTATTTGGATTTATGATATTGATTTTGATAT
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CTAATTTTTTATACAATCTTCCAAGACCCCTTTTTATCATATTGAATGAAATTATTCAAATATTTATAGGATTTGT
TGTTCCATCTTCATCAGGACATGCTAGTCTCACTATGCCAATAATGGCTCCTCTTGCCGATTTTTTGTCAATTCCA
AGAGCTTCAGTTGTTATTGCCATGCAGACTGCATCTGGGCTTATTAATTTGATAACACCTACCAGCGGAGTTATAA
TGGCTGTATTGGGGATATCCAGATTGAGTTATGGTACGTGGTTTAAGTTTGTTTTACCATTATTTATGATTGAGTT
TTTTATCTCTATTTTAGTTATTATAGCTAACATTTATTTAAGTTTTTAG

TABLE 1. Nucleotide and Amino Acid Sequences

f43.aa

MKYFYFLFFLLIFNVYAQNVNSPALPSPPLLPEITENKPVERENSSKGENFSNVGLDGKYVNDTILYGLDSQVTSI
IKALKKSSDSQYNFSLKKRLEKTFNAELKREILELFISLKYSGGIDTANYILENYESKRYSNALFGLAISYLKEFD
DKEKLKKTLIDILENKEGNVVSIAAYYLGELNSLEYSKNMMEVFEKYSGNDGARREILIALGKMSAVDYQDRIYEI
SLDNYEGPSIKAAAIEALSYLASDKVTENADLYLQSNNNNLNVKLAIIASLSKDPSLKSKEILQGFLRDSDDNIRF
KAINAIKGHRDSSAKDILIYKLKSDPSLKVREASAKALIDMDLGNIEIKNIMFDFKIDNNFKISMFSYLLDKDSLK
ALSIALEIVNKENINRPSNVLRGVASMLAGKKGNFDNFYSKIIDSKNIDLRHLALKGAVYNKSSSLSDKLKKIKSE
TNSEYIKMLLKDY

t43.aa

LPSPPLLPEITENKPVERENSSKGENFSNVGLDGKYVNDTILYGLDSQVTSIIKALKKSSDSQYNFSLKKRLEKTF
NAELKREILELFISLKYSGGIDTANYILENYESKRYSNALFGLAISYLKEFDDKEKLKKTLIDILENKEGNVVSIA
AYYLGELNSLEYSKNMMEVFEKYSGNDGARREILIALGKMSAVDYQDRIYEISLDNYEGPSIKAAAIEALSYLASD
KVTENADLYLQSNNNNLNVKLAIIASLSKDPSLKSKEILQGFLRDSDDNIRFKAINAIKGHRDSSAKDILIYKLKS
DPSLKVREASAKALIDMDLGNIEIKNIMFDFKIDNNFKISMFSYLLDKDSLKALSIALEIVNKENINRPSNVLRGV
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f43.nt

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TTCTAATGTTGGTTTAGATGGTAAGTATGTTAACGATACAATTCTTTATGGGCTTGATAGTCAAGTGACAAGCATT
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t43.nt

CTTCCTAGTCCGCCTTTGTTGCCCGAAATTACAGAAAATAAGCCTGTTGAGAGAGAAAATTCTTCTAAGGGAGAGA
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CATTATAAAAGCTCTTAAAAAATCAAGCGATAGTCAATATAATTTTTCTCTTAAAAAAAGACTTGAGAAAACTTTT
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ATATTCTTGAAAATTATGAGAGTAAAAGATATTCAAACGCTTTATTTGGCTTGGCAATTTCGTATCTTAAGGAGTT

TABLE 1. Nucleotide and Amino Acid Sequences

TGATGATAAAGAAAAATTAAAAAAAACTCTTATTGACATTCTTGAAAATAAAGAGGGCAATGTGGTATCTATTGCA
GCTTATTATTTAGGAGAGCTTAATTCTCTTGAGTATTCTAAAAACATGATGGAAGTTTTTGAAAAATATTCTGGAA
ATGATGGGGCTAGAAGAGAAATACTTATTGCTCTTGGAAAAATGTCCGCTGTTGATTATCAGGATAGAATTTATGA
AATTTCGCTAGATAATTACGAGGGCCCATCAATTAAGGCTGCTGCAATCGAAGCGTTGTCATATCTTGCTTCAGAT
AAAGTAACTGAAAATGCTGATTTGTATCTTCAGAGTAATAACAATAATTTAAATGTTAAATTAGCTATTATTGCTT
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GTTTAAAGCTATTAATGCAATCAAAGGACATAGGGACTCTTCTGCAAAGGATATTTTGATTTATAAGCTTAAAAGC
GATCCATCTCTTAAAGTTAGGGAGGCTTCTGCTAAGGCCTTAATTGATATGGATCTTGGGAATATTGAGATAAAAA
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AAAAGCATTGTCAATTGCTTTAGAAATTGTTAATAAAGAAAATATTAATAGACCCTCAAATGTTTTAAGGGGCGTT
GCTTCAATGTTGGCTGGTAAAAAGGGTAATTTTGATAATTTTTATTCTAAAATCATTGACAGCAAAAATATTGATT
TAAGGCATTTAGCATTAAAAGGAGCTGTTTATAATAAATCTTCATCGCTTTCTGATAAGCTTAAAAAAATTAAAAG
TGAAACGAACTCCGAATATATTAAAATGCTTTTAAAAGATTATTGA

f50.aa

MKFVLNNLFKGCLICFFLFFSCLTTDRSIQDSHISDIVEKKKEAVIIDDNNVVLGSNEGKFKRDYLIGLKDNESFF
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DYKYSHASLRLAELKYLVKEKSDAISAFKEINEFSISGYDREIYGFLSNKLGVSHLNLESLGFLDNSVFDTFVFND
NIFVTNILGGLLRYNIKKNDCRVYLKDKKSIFLNGIRGFADYNGTIYIGGKNVVYYIDDVDGDLKQINVPGNADFS
NVQVLLAVKNGIFVGTLNSGLWFYDLKNWKNIPLGSNKISSLCFDSLKNLLLVGTVDKAIYSVNVDNLKKIEHLDF
FSKNDNEKNINFIKEYKDSYFVGTYGGGLFELNLNKNSYKKHVIANNIDVNYFMDMEIKDKKLLFATFDHGLLIYD
SENDNWDYFGPNNGLLNLNLIKVSRFENYVILGTINNGLVFVDENIKKQL

t50.aa

CLTTDRSIQDSHISDIVEKKKEAVIIDDNNVVLGSNEGKFKRDYLIGLKDNESFFLSDAFLKENNFYFKKARESYA
KKNIGLTNYYLNKIVTNENQHSRELLAKANLFFGYVNYENGFYDLSEYNFDLFLKDYKYSHASLRLAELKYLVKEK
SDAISAFKEINEFSISGYDREIYGFLSNKLGVSHLNLESLGFLDNSVFDTFVFNDNIFVTNILGGLLRYNIKKNDC
RVYLKDKKSIFLNGIRGFADYNGTIYIGGKNVVYYIDDVDGDLKQINVPGNADFSNVQVLLAVKNGIFVGTLNSGL
WFYDLKNWKNIPLGSNKISSLCFDSLKNLLLVGTVDKAIYSVNVDNLKKIEHLDFFSKNDNEKNINFIKEYKDSYF
VGTYGGGLFELNLNKNSYKKHVIANNIDVNYFMDMEIKDKKLLFATFDHGLLIYDSENDNWDYFGPNNGLLNLNLI
KVSRFENYVILGTINNGLVFVDENIKKQL

f50.nt

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TGTTGTTCTTGGGAGTAATGAGGGTAAATTTAAAAGAGACTATTTGATAGGATTAAAAGATAATGAATCTTTTTTT
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TTTGTTTTTTGGATATGTAAATTATGAGAATGGTTTTTATGATCTTTCCGAATATAATTTTGATCTATTTTTAAAA
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CTGCATTTAAAGAGATTAATGAATTTTCTATCTCAGGTTATGATAGAGAGATTTATGGCTTTTTAAGTAATAAACT
TGGAGTAAGTCATTTAAACTTAGAGTCTTTAGGATTTCTTGACAACAGCGTTTTTGATACATTTGTCTTTAATGAC
AATATATTTGTAACTAATATATTGGGAGGGCTTTTAAGATATAATATTAAAAAAAATGATTGTAGAGTCTATCTTA
AGGATAAAAAAAGCATTTTTTTAAATGGCATTAGGGGTTTTGCGGATTATAATGGAACAATTTATATTGGTGGTAA
AAATGTTGTTTATTATATAGATGATGTTGATGGGGATTTAAAGCAAATAAATGTTCCCGGTAATGCTGATTTTAGC
AATGTACAAGTTTTGCTTGCTGTTAAAAATGGAATATTTGTTGGCACTCTAAATTCTGGATTATGGTTTTATGATT
TAAAAAATTGGAAAAATATACCGCTTGGATCTAATAAAATTTCTTCACTCTGCTTTGATAGTTTAAAAAAATTTATT

TABLE 1. Nucleotide and Amino Acid Sequences

ATTAGTTGGAACAGTTGACAAGGCTATTTATAGTGTTAATGTCGATAATTTGAAAAAGATTGAACATTTGGATTTT
TTTAGCAAAAATGATAATGAAAAAAATATTAATTTTATAAAAGAATATAAAGATAGTTATTTTGTTGGAACATATG
GTGGGGGTCTTTTTGAATTAAATTTAAATAAAAATAGTTACAAAAAGCACGTTATTGCCAATAATATTGATGTTAA
TTATTTTATGGATATGGAGATTAAAGATAAAAAGCTATTGTTTGCAACCTTTGATCATGGGTTATTGATTTATGAT
TCTGAAAATGACAACTGGGATTATTTTGGACCCAATAATGGGCTTCTTAATTTGAATTTAATAAAAGTTTCTAGAT
TTGAAAATTATGTCATACTGGGCACTATTAATAACGGTTTGGTTTTTGTAGATGAAAATATTAAAAAACAGTTATG
A

t50.nt

TGCCTTACTACAGATAGATCTATTCAAGATTCTCATATTAGTGATATTGTAGAGAAGAAAAAAGAAGCAGTCATTA
TTGATGATAATAATGTTGTTCTTGGGAGTAATGAGGGTAAATTTAAAAGAGACTATTTGATAGGATTAAAAGATAA
TGAATCTTTTTTTCTTAGTGATGCTTTTTTAAAAGAAAATAATTTTTATTTTAAAAAAGCCAGGGAAAGTTATGCT
AAAAAAAATATTGGCTTGACAAATTATTATTTGAATAAAATAGTAACTAATGAGAATCAGCACAGCAGAGAATTGC
TAGCTAAAGCGAATTTGTTTTTTGGATATGTAAATTATGAGAATGGTTTTTATGATCTTTCCGAATATAATTTTGA
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TCTGATGCAATTTCTGCATTTAAAGAGATTAATGAATTTTCTATCTCAGGTTATGATAGAGAGATTTATGGCTTTT
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TGTCTTTAATGACAATATATTTGTAACTAATATATTGGGAGGGCTTTTAAGATATAATATTAAAAAAAATGATTGT
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AAAGTTTCTAGATTTGAAAATTATGTCATACTGGGCACTATTAATAACGGTTTGGTTTTTGTAGATGAAAATATTA
AAAAACAGTTATGA

f65.aa

MHIFKNVPFQINLILFLLVSVAKINASSKFYYAEQWYVIFNSQMKKKPENYKKNIFFLQKALKYPFGNPKYSLTKI
ETKEQWEKYKLLFKMHVNLLLVRQNLHLGDLFDTRNLYFFKTPEKDGIISNLEKSKKLYKLAINYYSEALKYHKKL
ENYTTVKLENDGITNWEDEYHKISLKELNYYDIIKKELLRIDETKAFFEQGPNYY

t65.aa

KINASSKFYYAEQWYVIFNSQMKKKPENYKKNIFFLQKALKYPFGNPKYSLTKIETKEQWEKYKLLFKMHVNLLLV
RQNLHLGDLFDTRNLYFFKTPEKDGIISNLEKSKKLYKLAINYYSEALKYHKKLENYTTVKLENDGITNWEDEYHK
ISLKELNYYDIIKKELLRIDETKAFFEQGPNYY

f65.nt

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TAAAAAAAATATATTTTTTCTTCAAAAAGCCTTAAAATACCCATTTGGAAATCCAAAATATTCTCTAACTAAAATA
GAAACCAAAGAACAGTGGGAAAAATATAAACTTCTTTTCAAAATGCATGTAAACTTGCTTCTAGTTAGGCAAAATT
TACATTTAGGAGATTTATTCGACACAAGAAATTTATATTTTTTCAAAACTCCAGAAAAAGATGGAATTATTTCCAA
TCTAGAAAAATCAAAAAAATTATATAAACTAGCTATTAATTACTACAGCGAAGCACTAAAATACCACAAAAAACTT
GAAAATTACACAACTGTTAAACTAGAAAACGATGGAATAACAAACTGGGAAGATGAATATCATAAAATTTCTCTTA

TABLE 1. Nucleotide and Amino Acid Sequences

AAGAGCTTAATTACTATGACATTATTAAAAAAGAACTACTAAGAATTGACGAAACTAAAGCATTTTTTGAACAAGG
GCCAAACTATTATTAA

t65.nt

KINASSKFYYAEQWYVIFNSQMKKKPENYKKNIFFLQKALKYPFGNPKYSLTKIETKEQWEKYKLLFKMHVNLLLV
RQNLHLGDLFDTRNLYFFKTPEKDGIISNLEKSKKLYKLAINYYSEALKYHKKLENYTTVKLENDGITNWEDEYHK
ISLKELNYYDIIKKELLRIDETKAFFEQGPNYY

f8.aa

MKNINRLILLILTTHTLLFSCALIADNKSKNLSTSEIILTQKTLLESSLIKNPSNVEYRIPISSIQEILNNNNDSF
LIKKTAAKIKISPQKLEEIKNYLNAYKNYLNNETEWIKFIDQSSVNGNLTIKIDTAFEKKTNFNHTNSDNENLTEL
IELQMHLEKEILNLIEQTFHDKNLGYIQLSHINSFFPQENINSITKEIIDGKEYIAPHIIANQLLKIKDKKYFEQF
MHFLKVENSKIKTIIEKQKISDLHNELYYSKQSPPRRRKRSTADSDNNNKYDIIPKIIDPNTGIEITPKNLRSILS
NGDIILIKPKIDWTEFFYFWQHVGIFDEEKYEATKKIAFNGIDSFDIKSIITSNQIKFDTASTQGSGYEKLSTYVQ
SRILKIFSPITDIRTIQKAINFGRSRYIDNNFGYMVPLISSNLWTDSFNLEEIHNKTYCSLMVDRIYKIAGLNVSR
NYEISGIITPGEINAAAYNFYMSYTIAGILPSVLPKRLIKPTLKEKFIGYNKEIVDAIELKKSKEKIFGRACNITN
LWCSGS

t8.aa

CALIADNKSKNLSTSEIILTQKTLLESSLIKNPSNVEYRIPISSIQEILNNNNDSFLIKKTAAKIKISPQKLEEIK
NYLNAYKNYLNNETEWIKFIDQSSVNGNLTIKIDTAFEKKTNFNHTNSDNENLTELIELQMHLEKEILNLIEQTFH
DKNLGYIQLSHINSFFPQENINSITKEIIDGKEYIAPHIIANQLLKIKDKKYFEQFMHFLKVENSKIKTIIEKQKI
SDLHNELYYSKQSPPRRRKRSTADSDNNNKYDIIPKIIDPNTGIEITPKNLRSILSNGDIILIKPKIDWTEFFYFW
QHVGIFDEEKYEATKKIAFNGIDSFDIKSIITSNQIKFDTASTQGSGYEKLSTYVQSRILKIFSPITDIRTIQKAI
NFGRSRYIDNNFGYMVPLISSNLWTDSFNLEEIHNKTYCSLMVDRIYKIAGLNVSRNYEISGIITPGEINAAAYNF
YMSYTIAGILPSVLPKRLIKPTLKEKFIGYNKEIVDAIELKKSKEKIFGRACNITNLWCSGS

f8.nt

ATGAAGAATATTAATAGATTAATATTATTAATATTAACTACACACACTTTATTATTCTCTTGTGCCTTAATTGCAG
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TCAAGAATATTAAAAATATTCTCACCAATAACAGACATAAGAACAATTCAAAAAGCTATTAATTTTGGAAGAAGTA
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AGAAATTCACAACAAAACCTATTGCTCTTTAATGGTTGATAGAATATATAAAATAGCAGGACTTAATGTATCAAGA

TABLE 1. Nucleotide and Amino Acid Sequences

AATTACGAAATTTCGGGAATAATTACTCCTGGAGAAATAAATGCAGCAGCTTACAATTTTTACATGTCTTATACGA
TTGCAGGAATACTTCCAAGCGTGCTTCCAAAAAGGCTCATTAAACCAACATTAAAAGAAAAATTCATTGGTTACAA
TAAAGAAATAGTAGATGCAATAGAATTAAAAAAATCGAAAGAAAAAATTTTTGGGAGAGCTTGCAACATTACAAAT
CTCTGGTGCTCAGGAAGTTAA

t8.nt

TGTGCCTTAATTGCAGATAATAAGTCAAAAAATTTAAGCACATCAGAAATCATATTAACACAAAAAACACTACTAG
AAAGCTCTTTAATAAAAAATCCTTCTAATGTAGAATATCGAATACCAATATCCAGTATCCAAGAAATTTTAAACAA
TAACAATGATTCTTTTTTAATAAAAAAAACAGCAGCAAAAATCAAAATAAGCCCTCAAAAACTTGAAGAAATAAAA
AACTATCTAAATGCTTATAAAAATTATCTAAATAATGAAACAGAATGGATAAAGTTTATAGATCAAAGTAGCGTCA
ATGGAAATTTAACAATTAAAATTGATACTGCTTTTGAAAAAAAAACAAATTTTAATCATACAAATTCAGATAATGA
AAATTTAACAGAACTAATAGAACTACAAATGCATCTGGAAAAAGAAATTTTAAACTTAATTGAGCAAACATTTCAT
GATAAAAATTTAGGATATATACAATTAAGTCACATCAACTCATTCTTTCCTCAAGAAAATATAAACTCAATAACAA
AAGAAATAATAGATGGAAAAGAATATATTGCACCGCACATAATAGCAAATCAATTATTAAAAATAAAAGATAAAAA
ATATTTTGAACAATTTATGCACTTTTTAAAAGTTGAAAACAGCAAAATAAAAACAATAATTGAAAAACAAAAAATT
TCAGATCTTCACAATGAACTGTATTATTCAAAACAATCCCCGCCCAGAAGAAGAAAAAGGTCAACTGCCGATTCCG
ATAATAACAATAAATACGATATAATACCAAAAATAATAGACCCAAATACAGGCATTGAAATAACTCCTAAAAATTT
AAGATCTATTTTATCAAATGGCGACATAATACTAATAAAACCAAAAATAGATTGGACAGAATTTTTTTATTTTTGG
CAACATGTGGGAATATTTGATGAAGAAAAATATGAAGCCACTAAAAAAATTGCATTCAATGGAATTGATAGCTTTG
ATATAAAATCAATAATTACAAGCAATCAAATCAAATTCGATACAGCATCTACTCAAGGTTCAGGATACGAAAAGCT
TTCAACATACGTACAATCAAGAATATTAAAAATATTCTCACCAATAACAGACATAAGAACAATTCAAAAAGCTATT
AATTTTGGAAGAAGTAGATACATTGACAATAACTTTGGATATATGGTTCCATTAATATCCTCTAATTTATGGACAG
ATTCATTCAATCTTGAAGAAATTCACAACAAAACCTATTGCTCTTTAATGGTTGATAGAATATATAAAATAGCAGG
ACTTAATGTATCAAGAAATTACGAAATTTCGGGAATAATTACTCCTGGAGAAATAAATGCAGCAGCTTACAATTTT
TACATGTCTTATACGATTGCAGGAATACTTCCAAGCGTGCTTCCAAAAAGGCTCATTAAACCAACATTAAAAGAAA
AATTCATTGGTTACAATAAAGAAATAGTAGATGCAATAGAATTAAAAAAATCGAAAGAAAAAATTTTTGGGAGAGC
TTGCAACATTACAAATCTCTGGTGCTCAGGAAGTTAA

f82.aa

MTRVFSKFFLFFCFSMLLFANSEDSNEKDIVSKDENPVFENEVLGYWVGYNDVSNIKNSIIYIYKYNGEVYGRILT
IIKDGKKYDAKNPSGDTVVGFENLAIEGLDFMWGLKYSSSSKKWDRGKIIDPKNGKIYNSEMRVDSKTGNLITKGK
VWIFGRSKIWTRAKDDEIPKLDLHNLVPAPPVKK

t82.aa

EDSNEKDIVSKDENPVFENEVLGYWVGYNDVSNIKNSIIYIYKYNGEVYGRILTIIKDGKKYDAKNPSGDTVVGFE
NLAIEGLDFMWGLKYSSSSKKWDRGKIIDPKNGKIYNSEMRVDSKTGNLITKGKVWIFGRSKIWTRAKDDEIPKLD
LHNLVPAPPVKK

f82nt

ATGACTAGAGTTTTTTCAAAGTTTTTTCTTTTTTTTTGTTTTTCAATGCTTTTATTTGCAAATTCAGAAGATTCAA
ATGAAAAGGACATTGTTAGCAAGGATGAAAACCCTGTTTTTGAAAATGAAGTTTTAGGATATTGGGTTGGTTATAA
TGATGTAAGTAACATAAAGAATTCTATTATCTATATTTATAAATATAATGGGGAAGTTTATGGCCGAATTTTAACT
ATAATAAAAGATGGCAAAAAGTATGATGCTAAAAATCCTTCAGGAGATACTGTAGTTGGGTTTGAAAATCTTGCAA
TAGAGGGTCTTGATTTTATGTGGGGTCTTAAGTATTCTTCTTCTTCTAAAAAGTGGGATAGGGGCAAAATAATAGA

TABLE 1. Nucleotide and Amino Acid Sequences

TCCTAAAAACGGTAAAATTTATAATTCTGAGATGCGTGTTGATAGTAAAACCGGAAATCTTATTACCAAGGGGAAA
GTTTGGATTTTTGGTAGAAGTAAAATTTGGACAAGAGCTAAAGATGATGAAATACCAAAATTAGATTTGCATAATC
TTGTTCCAGCGCCCCCTGTGAAAAAATAA

f82.nt

GAAGATTCAAATGAAAAGGACATTGTTAGCAAGGATGAAAACCCTGTTTTTGAAAATGAAGTTTTAGGATATTGGG
TTGGTTATAATGATGTAAGTAACATAAAGAATTCTATTATCTATATTTATAAATATAATGGGGAAGTTTATGGCCG
AATTTTAACTATAATAAAAGATGGCAAAAAGTATGATGCTAAAAATCCTTCAGGAGATACTGTAGTTGGGTTTGAA
AATCTTGCAATAGAGGGTCTTGATTTTATGTGGGGTCTTAAGTATTCTTCTTCTTCTAAAAAGTGGGATAGGGGCA
AAATAATAGATCCTAAAAACGGTAAAATTTATAATTCTGAGATGCGTGTTGATAGTAAAACCGGAAATCTTATTAC
CAAGGGGAAAGTTTGGATTTTTGGTAGAAGTAAAATTTGGACAAGAGCTAAAGATGATGAAATACCAAAATTAGAT
TTGCATAATCTTGTTCCAGCGCCCCCTGTGAAAAAATAA

f86.aa

MNKLMLMLITFATSLLAQTNKASTGLKTDQSFNNSLSESVKLKEIADIYPTNTNFLTGIGIVAGLAGKGDSIKQKD
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IASGITQPNNKLKGSGYTIDSVIINENQNINHSYNIILKKGNYTLINRIHKILTSKKINNKIKSDSTIEIEAKNIS
LLEEIENIKIETNPKILIDKKNGIILASENAKIGTFTFSIEKDNQNIFLSKNNKTTIQVNSMKLNEFILKNSNNLS
NKELIQIIQAAQKINKLNGELILEEIDGNQN

t86.aa

LKTDQSFNNSLSESVKLKEIADIYPTNTNFLTGIGIVAGLAGKGDSIKQKDLIIKILEENNIINEIGSNNIESKNI
ALVNVSLQVKGNTIKGSKHKACVASILDSKDLTNGILLKTNLKNKEGEIIAIASGITQPNNKLKGSGYTIDSVIIN
ENQNINHSYNIILKKGNYTLINRIHKILTSKKINNKIKSDSTIEIEAKNISLLEEIENIKIETNPKILIDKKNGII
LASENAKIGTFTFSIEKDNQNIFLSKNNKTTIQVNSMKLNEFILKNSNNLSNKELIQIIQAAQKINKLNGELILEE
IDGNQN

f86.nt

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ACTGGACTCAAAAGATTTAACAAATGGAATACTTTTAAAAACAAATCTTAAAAATAAAGAGGGGGAAATAATAGCA
ATTGCATCAGGAATTACACAGCCCAATAATAAATTAAAAGGATCTGGATATACTATAGATAGTGTAATAATAAATG
AGAATCAAAATATTAACCACAGTTATAATATAATTCTTAAAAAAGGAAATTATACATTAATAAATAGAATTCATAA
AATATTAACCTCTAAAAAAATCAACAACAAAATTAAATCAGACAGCACAATAGAAATAGAAGCAAAAAACATAAGC
CTATTAGAAGAGATTGAAAATATTAAAATAGAAACCAACCCCAAGATATTAATAGACAAAAAAAATGGTATTATTT
TAGCAAGTGAAAATGCAAAAATAGGAACTTTTACATTTTCCATTGAAAAAGACAATCAAAACATTTTTTTAAGTAA
AAATAACAAAACAACAATTCAAGTAAACTCAATGAAATTAAATGAATTTATATTAAAAAATTCCAACAATCTTAGC
AATAAAGAATTAATTCAAATAATTCAAGCTGCGCAAAAAATTAATAAATTAAATGGGGAACTTATCTTGGAGGAAA
TTGATGGAAACCAAAATTAA

t86.nt

TABLE 1. Nucleotide and Amino Acid Sequences

CTAAAAACAGATCAATCATTTAACAATAGCCTATCTGAAAGCGTAAAATTAAAAGAAATTGCGGATATTTATCCCA
CAAATACAAATTTTTTAACAGGTATTGGAATAGTAGCGGGACTTGCTGGAAAAGGAGACTCTATAAAACAAAAAGA
CCTTATAATTAAAATTTTAGAAGAAAACAATATAATAAATGAAATAGGCTCTAATAACATAGAAAGTAAAAATATT
GCACTAGTAAATGTCAGTCTCCAAGTAAAAGGTAATACAATCAAAGGTTCAAAACATAAAGCTTGCGTTGCATCAA
TACTGGACTCAAAAGATTTAACAAATGGAATACTTTTAAAAACAAATCTTAAAAATAAAGAGGGGGAAATAATAGC
AATTGCATCAGGAATTACACAGCCCAATAATAAATTAAAAGGATCTGGATATACTATAGATAGTGTAATAATAAAT
GAGAATCAAAATATTAACCACAGTTATAATATAATTCTTAAAAAAGGAAATTATACATTAATAAATAGAATTCATA
AAATATTAACCTCTAAAAAAATCAACAACAAAATTAAATCAGACAGCACAATAGAAATAGAAGCAAAAAACATAAG
CCTATTAGAAGAGATTGAAAATATTAAAATAGAAACCAACCCCAAGATATTAATAGACAAAAAAAATGGTATTATT
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AAAATAACAAAACAACAATTCAAGTAAACTCAATGAAATTAAATGAATTTATATTAAAAAATTCCAACAATCTTAG
CAATAAAGAATTAATTCAAATAATTCAAGCTGCGCAAAAAATTAATAAATTAAATGGGGAACTTATCTTGGAGGAA
ATTGATGGAAACCAAAATTAA

f90.aa

MCPITFTIPFFLAIFFAFSSSFVTDSSVSLLSRNTSLFSTLTPISLPIISGTLPAIVTLSKKYLSISLSFSKMIFI
KSLFEVIKLPIWLFIIFASGYFLNAFSIFLCISSFLSFMFI

t90.aa

SSFVTDSSVSLLSRNTSLFSTLTPISLPIISGTLPAIVTLSKKYLSISLSFSKMIFIKSLFEVIKLPIWLFIIFAS
GYFLNAFSIFLCISSFLSFMFI

f90.nt

ATGTGTCCTATTACTTTTACCATTCCATTTTTTCTAGCAATATTTTTTGCTTTTTCAAGCTCCTTTGTTACGGACT
CTTCTGTGTCTTTGCTATCAAGAAATACGTCTCTTTTTTCTACTTTAACTCCAATTTCTTTGCCTATTATTTCTGG
TACGCTTCCTGCAATAGTTACGCTGTCGAAAAAATATCTGTCAATCTCTTTAAGCTTTTCTAAAATGATTTTCATC
AAATCTTTATTTGAAGTGATTAAACTTCCCATATGGTTATTCATTATTTTTGCATCAGGATACTTTTTAAATGCTT
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t90.nt

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CTTTGCCTATTATTTCTGGTACGCTTCCTGCAATAGTTACGCTGTCGAAAAAATATCTGTCAATCTCTTTAAGCTT
TTCTAAAATGATTTTCATCAAATCTTTATTTGAAGTGATTAAACTTCCCATATGGTTATTCATTATTTTTGCATCA
GGATACTTTTTAAATGCTTTTTCGATTTTTTTGTGTATTTCTTCTTTTTTATCTTTTATGTTTATATGA

f469.aa

MANVALSSGFISQKIFGIIIIMVFLPTIIATPIINFLFKINKSGLKKELPIDQNTHICVSFEYDNLAKILIWDFKN
ELRKEGFFTQQIKNDSSQYINARKNNISFSIKREGSKITFECPNNHLIIIQDLFRETILNLEKITKEVETVSLRAK
KLDYSINYDKILSNINLNKRIKKENIILELKSSNKADVIRELLSVINIEIDKERIFQDLMEREKLITTALKEGFAI
PHLKTNLISKIHIAIGISHEGIDFNALDKNLSHVFILILCPAKDYVSYPRILASVVGKVDLYKKEILNAKTDKEIY
NIIVSZ

t469.aa

TABLE 1. Nucleotide and Amino Acid Sequences

VFLPTIIATPIINFLFKINKSGLKKELPIDQNTHICVSFEYDNLAKILIWDFKNELRKEGFFTQQIKNDSSQYINA
RKNNISFSIKREGSKITFECPNNHLIIIQDLFRETILNLEKITKEVETVSLRAKKLDYSINYDKILSNINLNKRIK
KENIILELKSSNKADVIRELLSVINIEIDKERIFQDLMEREKLITTALKEGFAIPHLKTNLISKIHIAIGISHEGI
DFNALDKNLSHVFILILCPAKDYVSYPRILASVVGKVDLYKKEILNAKTDKEIYNIIVSZ

f469.nt

ATGGCAAATGTAGCATTATCTTCAGGATTTATTAGCCAAAAAATATTTGGAATCATAATAATAATGGTGTTTTTGC
CAACAATCATTGCAACACCCATAATAAACTTTTTATTTAAAATAAATAAAAGTGGACTTAAAAAAGAACTCCCAAT
AGATCAAAATACACACATATGCGTATCATTTGAATATGATAATTTAGCCAAAATTCTTATATGGGACTTTAAAAAT
GAGTTAAGAAAAGAAGGATTTTTTACACAACAAATTAAAAATGATTCTTCACAATATATTAATGCAAGAAAAAACA
ATATATCCTTCTCAATAAAACGAGAAGGTAGCAAAATCACATTTGAATGCCCAAATAATCATTTAATTATAATACA
AGATCTTTTTAGAGAAACAATCTTAAACCTAGAAAAAATAACCAAAGAAGTTGAAACAGTCTCTTTAAGAGCAAAA
AAACTAGATTACTCAATAAATTACGATAAAATCCTTAGTAATATCAACCTAAATAAAAGAATAAAAAAGGAAAACA
TTATTCTAGAATTAAAATCAAGCAATAAGGCTGATGTAATAAGAGAGCTTCTAAGCGTAATAAACATTGAAATTGA
TAAAGAAAGAATATTCCAAGATTTAATGGAAAGAGAAAAGTTAATTACTACTGCACTAAAAGAAGGCTTTGCCATT
CCCCATTTAAAAACAAATTTAATATCAAAAATACATATTGCAATAGGAATAAGCCATGAGGGAATTGACTTTAATG
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TTTAGCATCTGTTGTGGGCAAAGTTGATCTGTACAAAAAAGAAATTTTAAATGCAAAAACAGATAAAGAAATTTAT
AATATAATAGTGAGCTAA

t469.nt

TTTTTGCCAACAATCATTGCAACACCCATAATAAACTTTTTATTTAAAATAAATAAAAGTGGACTTAAAAAAGAAC
TCCCAATAGATCAAAATACACACATATGCGTATCATTTGAATATGATAATTTAGCCAAAATTCTTATATGGGACTT
TAAAAATGAGTTAAGAAAAGAAGGATTTTTTACACAACAAATTAAAAATGATTCTTCACAATATATTAATGCAAGA
AAAAACAATATATCCTTCTCAATAAAACGAGAAGGTAGCAAAATCACATTTGAATGCCCAAATAATCATTTAATTA
TAATACAAGATCTTTTTAGAGAAACAATCTTAAACCTAGAAAAAATAACCAAAGAAGTTGAAACAGTCTCTTTAAG
AGCAAAAAAACTAGATTACTCAATAAATTACGATAAAATCCTTAGTAATATCAACCTAAATAAAAGAATAAAAAAG
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AAATTGATAAAGAAAGAATATTCCAAGATTTAATGGAAAGAGAAAAGTTAATTACTACTGCACTAAAAGAAGGCTT
TGCCATTCCCCATTTAAAAACAAATTTAATATCAAAAATACATATTGCAATAGGAATAAGCCATGAGGGAATTGAC
TTTAATGCTCTTGACAAGAACTTAAGTCATGTTTTTATATTAATACTGTGCCCAGCAAAAGATTACGTTAGCTACC
CTAGAATTTTAGCATCTGTTGTGGGCAAAGTTGATCTGTACAAAAAAGAAATTTTAAATGCAAAAACAGATAAAGA
AATTTATAATATAATAGTGAGCTAA

f477.aa

MEKPQGVSIVGAISGAMHVHLMAEHYGVPVVLHTDHCAKNLLPWVEGLLEYGEKYYSQHKKPLFSSHMLDLSEEPI
KENIEISKKFLERMAKIEMFLEIELGITGGEEDGVDNSDRALHELFSTPEDIYYGYSELLKVSPNFQIAAAFGNVH
GVYKPGNVKLTPKVLKDGQDYVISKTGVNMAKPVSYVFHGGSGSTIDEINEALSYGVVKMNIDTDTQWAAWEGVLN
YYKKNESRLQGQLGDGKDIDIPNKKFYDPRVWLREAEVSMKDRVKIACKNLNNINRNZ

t477.aa

MHVHLMAEHYGVPVVLHTDHCAKNLLPWVEGLLEYGEKYYSQHKKPLFSSHMLDLSEEPIKENIEISKKFLERMAK
IEMFLEIELGITGGEEDGVDNSDRALHELFSTPEDIYYGYSELLKVSPNFQIAAAFGNVHGVYKPGNVKLTPKVLK
DGQDYVISKTGVNMAKPVSYVFHGGSGSTIDEINEALSYGVVKMNIDTDTQWAAWEGVLNYYKKNESRLQGQLGDG
KDIDIPNKKFYDPRVWLREAEVSMKDRVKIACKNLNNINRNZ

f477.nt

ATGGAAAAACCACAAGGAGTTTCAATAGTTGGAGCTATTTCTGGTGCTATGCATGTTCATTTAATGGCAGAGCATT
ATGGTGTTCCTGTTGTTCTTCATACTGATCACTGTGCTAAAAATTTGCTTCCTTGGGTTGAAGGCCTTTTAGAATA
TGGAGAGAAATACTATAGTCAGCACAAAAAACCATTATTTTCTTCACATATGTTAGATTTATCAGAAGAACCTATT

TABLE 1. Nucleotide and Amino Acid Sequences

AAAGAAAATATTGAAATTTCTAAAAAATTCTTAGAAAGAATGGCAAAAATTGAAATGTTTTTGGAAATAGAGCTTG
GAATTACGGGTGGGGAAGAGGATGGAGTTGACAATTCAGATAGAGCTTTGCATGAACTATTTTCTACTCCTGAGGA
TATTTATTATGGATATTCAGAACTTTTAAAAGTTAGCCCAAATTTTCAGATTGCAGCAGCTTTTGGAAATGTTCAT
GGGGTATATAAACCGGGGAATGTTAAGCTTACTCCAAAAGTTTTAAAAGATGGTCAAGATTATGTCATATCAAAAA
CAGGAGTAAATATGGCTAAGCCAGTTTCTTATGTTTTTCATGGAGGGTCTGGATCTACAATTGATGAGATTAATGA
GGCGCTTTCTTATGGCGTTGTAAAGATGAATATTGACACAGATACACAGTGGGCTGCCTGGGAGGGTGTTTTAAAT
TATTACAAAAAAAATGAAAGTCGTTTGCAAGGTCAATTAGGAGATGGCAAGGATATTGATATTCCAAATAAGAAAT
TTTATGATCCAAGGGTTTGGTTAAGAGAAGCTGAAGTTTCTATGAAAGACCGTGTGAAGATTGCATGCAAAAATCT
TAATAATATTAATAGAAATTAA

t477.nt

ATGCATGTTCATTTAATGGCAGAGCATTATGGTGTTCCTGTTGTTCTTCATACTGATCACTGTGCTAAAAATTTGC
TTCCTTGGGTTGAAGGCCTTTTAGAATATGGAGAGAAATACTATAGTCAGCACAAAAAACCATTATTTTCTTCACA
TATGTTAGATTTATCAGAAGAACCTATTAAAGAAAATATTGAAATTTCTAAAAAATTCTTAGAAAGAATGGCAAAA
ATTGAAATGTTTTTGGAAATAGAGCTTGGAATTACGGGTGGGGAAGAGGATGGAGTTGACAATTCAGATAGAGCTT
TGCATGAACTATTTTCTACTCCTGAGGATATTTATTATGGATATTCAGAACTTTTAAAAGTTAGCCCAAATTTTCA
GATTGCAGCAGCTTTTGGAAATGTTCATGGGGTATATAAACCGGGGAATGTTAAGCTTACTCCAAAAGTTTTAAAA
GATGGTCAAGATTATGTCATATCAAAAACAGGAGTAAATATGGCTAAGCCAGTTTCTTATGTTTTTCATGGAGGGT
CTGGATCTACAATTGATGAGATTAATGAGGCGCTTTCTTATGGCGTTGTAAAGATGAATATTGACACAGATACACA
GTGGGCTGCCTGGGAGGGTGTTTTAAATTATTACAAAAAAAATGAAAGTCGTTTGCAAGGTCAATTAGGAGATGGC
AAGGATATTGATATTCCAAATAAGAAATTTTATGATCCAAGGGTTTGGTTAAGAGAAGCTGAAGTTTCTATGAAAG
ACCGTGTGAAGATTGCATGCAAAAATCTTAATAATATTAATAGAAATTAA

f488.aa

MPSSFPFLLVNGSSGIAVGMATNMAPHNLREICDAIVYMLDNENASIFDLLKIVKGPDFPTFGEIVYNDNLIKAYK
TGKGSVVIRARYHIEERAEDRNAIIVTEIPYTVNKSALLMKVALLAKEEKLEGLLDIRDESDREGIRIVLEVKRGF
DPHVIMNLLYEYTEFKKHFSINNLALVNGIPKQLNLEELLFEFIEHRKNIIERRIEFDLRKAKEKAHVLEGLNIAL
NNIDEVIKIIKSSKLAKDARERLVSNFGLSEIQANSVLDMRLQKLTALEIFKLEEELNILLSLIKDYEDILLNPVR
IINIIREETINLGLKFGDERRTKIIYDEEVLKTSMSDLMQKENIVVMLTKKGFLKRLSQNEYKLQGTGGKGLSSFD
LNDGDEIVIALCVNTHDYLFMISNEGKLYLINAYEIKDSSRASKGQNISELINLGDQEEILTIKNSKDLTDDAYLL
LTTASGKIARFESTDFKAVKSRGVIVIKLNDKDFVTSAEIVFKDEKVICLSKKGSAFIFNSRDVRLTNRGTQGVCG
MKLKEGDLFVKVLSVKENPYLLIVSENGYGKRLNMSKISELKRGATGYTSYKKSDKKAGSVVDAIAVSEDDEILLV
SKRSKALRTVAGKVSEQGKDARGIQVLFLDNDSLVSVSKFIKZ

t488.aa

MATNMAPHNLREICDAIVYMLDNENASIFDLLKIVKGPDFPTFGEIVYNDNLIKAYKTGKGSVVIRARYHIEERAE
DRNAIIVTEIPYTVNKSALLMKVALLAKEEKLEGLLDIRDESDREGIRIVLEVKRGFDPHVIMNLLYEYTEFKKHF
SINNLALVNGIPKQLNLEELLFEFIEHRKNIIERRIEFDLRKAKEKAHVLEGLNIALNNIDEVIKIIKSSKLAKDA
RERLVSNFGLSEIQANSVLDMRLQKLTALEIFKLEEELNILLSLIKDYEDILLNPVRIINIIREETINLGLKFGDE
RRTKIIYDEEVLKTSMSDLMQKENIVVMLTKKGFLKRLSQNEYKLQGTGGKGLSSFDLNDGDEIVIALCVNTHDYL
FMISNEGKLYLINAYEIKDSSRASKGQNISELINLGDQEEILTIKNSKDLTDDAYLLLTTASGKIARFESTDFKAV
KSRGVIVIKLNDKDFVTSAEIVFKDEKVICLSKKGSAFIFNSRDVRLTNRGTQGVCGMKLKEGDLFVKVLSVKENP
YLLIVSENGYGKRLNMSKISELKRGATGYTSYKKSDKKAGSVVDAIAVSEDDEILLVSKRSKALRTVAGKVSEQGK
DARGIQVLFLDNDSLVSVSKFIKZ

f488.nt

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AGAAGGACTTTTAGATATAAGAGATGAATCTGATCGAGAAGGTATTAGGATAGTTCTTGAAGTTAAAAGAGGATTT

TABLE 1. Nucleotide and Amino Acid Sequences

GATCCTCATGTTATTATGAATTTGCTTTATGAATATACTGAATTTAAAAAGCATTTTAGTATAAATAATTTAGCCC
TTGTTAATGGTATTCCCAAACAGTTAAATTTAGAAGAATTGTTATTTGAATTTATTGAGCATAGAAAAAATATTAT
CGAAAGACGTATTGAATTTGACTTGAGAAAGGCAAAAGAGAAAGCACATGTTCTTGAGGGATTAAATATTGCTTTA
AATAATATAGATGAGGTTATTAAGATTATTAAATCATCTAAATTAGCAAAAGATGCAAGGGAGAGGCTTGTTTCGA
ATTTTGGTCTTTCAGAGATTCAGGCCAATTCAGTTCTTGATATGAGGTTACAAAAACTTACAGCCCTTGAGATTTT
TAAGCTTGAAGAGGAGCTTAATATACTGTTAAGCTTAATAAAAGATTATGAAGATATTCTCTTGAATCCAGTAAGG
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GAAAGCTTTATTTAATCAATGCTTATGAAATAAAAGATTCTTCAAGAGCTTCAAAAGGTCAGAATATTAGTGAGCT
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AAAATGGGTATGGAAAAAGGTTAAACATGTCTAAAATATCTGAGCTTAAAAGAGGAGCCACTGGTTATACTAGTTA
TAAAAAATCTGATAAAAAAGCGGGTAGTGTTGTTGATGCTATAGCAGTTTCAGAGGATGATGAAATCTTGCTTGTA
AGTAAACGTTCAAAAGCTTTAAGAACAGTAGCTGGAAAAGTATCTGAACAAGGCAAAGATGCTAGAGGAATTCAAG
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t488.nt

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AGCATAGAAAAAATATTATCGAAAGACGTATTGAATTTGACTTGAGAAAGGCAAAAGAGAAAGCACATGTTCTTGA
GGGATTAAATATTGCTTTAAATAATATAGATGAGGTTATTAAGATTATTAAATCATCTAAATTAGCAAAAGATGCA
AGGGAGAGGCTTGTTTCGAATTTTGGTCTTTCAGAGATTCAGGCCAATTCAGTTCTTGATATGAGGTTACAAAAAC
TTACAGCCCTTGAGATTTTTAAGCTTGAAGAGGAGCTTAATATACTGTTAAGCTTAATAAAAGATTATGAAGATAT
TCTCTTGAATCCAGTAAGGATTATTAATATTATAAGAGAAGAAACTATTAATTTAGGTTTGAAATTTGGCGATGAA
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TTGTTATGCTTACAAAGAAAGGTTTCCTTAAAAGACTTTCACAAAATGAGTATAAATTGCAAGGTACGGGAGGAAA
AGGACTAAGTTCGTTTGATCTAAATGATGGAGATGAGATTGTTATTGCTTTGTGTGTCAATACTCATGATTATTTA
TTTATGATTTCAAATGAAGGAAAGCTTTATTTAATCAATGCTTATGAAATAAAAGATTCTTCAAGAGCTTCAAAAG
GTCAGAATATTAGTGAGCTTATTAATTTAGGAGATCAAGAAGAAATATTAACTATTAAGAATAGTAAAGATTTAAC
TGATGATGCTTATTTATTGCTTACAACTGCAAGTGGAAAGATAGCTAGATTCGAATCTACAGATTTTAAAGCAGTA
AAGTCACGAGGTGTTATTGTTATTAAACTGAATGATAAAGATTTTGTTACAAGTGCAGAGATTGTTTTTAAGGATG
AAAAAGTAATTTGTCTTTCTAAAAAGGGTAGTGCATTTATATTTAATTCAAGGGATGTTAGGCTTACTAATAGAGG
TACCCAAGGTGTTTGTGGAATGAAATTAAAAGAAGGTGATTTGTTTGTTAAAGTTTTATCGGTTAAAGAAAATCCT
TATCTTTTGATTGTTTCTGAAAATGGGTATGGAAAAAGGTTAAACATGTCTAAAATATCTGAGCTTAAAAGAGGAG
CCACTGGTTATACTAGTTATAAAAAATCTGATAAAAAAGCGGGTAGTGTTGTTGATGCTATAGCAGTTTCAGAGGA
TGATGAAATCTTGCTTGTAAGTAAACGTTCAAAAGCTTTAAGAACAGTAGCTGGAAAAGTATCTGAACAAGGCAAA
GATGCTAGAGGAATTCAAGTATTATTTCTTGATAATGACAGCTTGGTTTCTGTTTCAAAATTTATTAAATAA

f494.aa

MFALIRKIFMIYFLCITLAGFAMIFIDSKFTEQPNVKENQSKINQHTIEPNLIMFTSSIGGFLGVYVGIWIFNYDK
SNFYLNWGNLIILIYNIALIITVYSKSHS

t494.aa

TABLE 1. Nucleotide and Amino Acid Sequences

MIFIDSKFTEQPNVKENQSKINQHTIEPNLIMFTSSIGGFLGVYVGIWIFNYDKSNFYLNWGNLIILIYNIALIIT
VYSKSHS

f494.nt

ATGTTTGCATTAATTAGAAAAATATTTATGATCTATTTTTTATGCATTACTCTTGCAGGTTTTGCCATGATTTTTA
TTGACAGCAAATTTACCGAACAGCCTAATGTTAAAGAAAATCAAAGCAAAATTAATCAACATACAATTGAACCCAA
TTTAATCATGTTTACATCTTCTATAGGAGGATTTTTAGGTGTTTATGTTGGAATTTGGATCTTTAACTATGACAAA
AGCAATTTTTACCTAAATTGGGGAAATTTAATAATATTAATATACAACATAGCCCTAATTATCACTGTATACTCAA
AATCACATAGTTAG

t494.nt

ATGATTTTTATTGACAGCAAATTTACCGAACAGCCTAATGTTAAAGAAAATCAAAGCAAAATTAATCAACATACAA
TTGAACCCAATTTAATCATGTTTACATCTTCTATAGGAGGATTTTTAGGTGTTTATGTTGGAATTTGGATCTTTAA
CTATGACAAAAGCAATTTTTACCTAAATTGGGGAAATTTAATAATATTAATATACAACATAGCCCTAATTATCACT
GTATACTCAAAATCACATAGTTAG

f516.aa

MKKTPNTCIFLTLLIISNLNALANEEGNTNEKNDQPKQISNFFSPERGFIYSTGIGIGVGFFLNSNIKHLIFRPYY
TFSNNTFDFLIVAMILTRESLNIPKKMQYFKSYIGGGINWHIANLIKKTKYFSATIGIGGRFYLSTNFIEDIRFYE
KLPYVIEPYMFIEISSKKAIPLMGLDFKIDFLFLDTFNISFNFTIRYNFKDKNEMET

t516.aa

NEEGNTNEKNDQPKQISNFFSPERGFIYSTGIGIGVGFFLNSNIKHLIFRPYYTFSNNTFDFLIVAMILTRESLNI
PKKMQYFKSYIGGGINWHIANLIKKTKYFSATIGIGGRFYLSTNFIEDIRFYEKLPYVIEPYMFIEISSKKAIPLM
GLDFKIDFLFLDTFNISFNFTIRYNFKDKNEMET

f516.nt

ATGAAAAAAACTCCAAACACTTGTATTTTTCTTAACATTGCTTATCATTTCCAATTTAAATGCACTTGCAAATGAAG
AAGGCAATACTAATGAAAAAAATGATCAACCCAAACAAATCTCTAATTTTTTTAGCCCAGAAAGAGGGTTCATATA
TTCAACAGGAATTGGGATTGGAGTTGGATTTTTTCTAAATTCAAATATTAAACACCTTATCTTTAGACCTTATTAT
ACATTCTCTAATAATACTTTTGATTTTTTAATCGTTGCTATGATATTAACAAGGGAAAGCCTTAATATCCCCAAAA
AAATGCAATACTTTAAATCTTATATTGGAGGAGGAATAAACTGGCACATTGCAAACTTAATTAAAAAAACAAAATA
TTTTTCCGCCACCATTGGCATAGGTGGTCGTTTTTACCTATCTACAAACTTTATAGAAGACATTCGATTTTACGAA
AAATTGCCTTATGTAATAGAGCCTTATATGTTTATTGAAATTTCTTCTAAAAAGGCAATTCCTTTAATGGGGTTAG
ACTTTAAAATTGATTTTTTATTTTTAGATACATTTAACATTTCTTTTAATTTTACTATTAGATATAATTTTAAGGA
CAAAAACGAGATGGAAACATGA

t516.nt

AATGAAGAAGGCAATACTAATGAAAAAAATGATCAACCCAAACAAATCTCTAATTTTTTTAGCCCAGAAAGAGGGT
TCATATATTCAACAGGAATTGGGATTGGAGTTGGATTTTTTCTAAATTCAAATATTAAACACCTTATCTTTAGACC
TTATTATACATTCTCTAATAATACTTTTGATTTTTTAATCGTTGCTATGATATTAACAAGGGAAAGCCTTAATATC
CCCAAAAAAATGCAATACTTTAAATCTTATATTGGAGGAGGAATAAACTGGCACATTGCAAACTTAATTAAAAAAA
CAAAATATTTTTCCGCCACCATTGGCATAGGTGGTCGTTTTTACCTATCTACAAACTTTATAGAAGACATTCGATT
TTACGAAAAATTGCCTTATGTAATAGAGCCTTATATGTTTATTGAAATTTCTTCTAAAAAGGCAATTCCTTTAATG
GGGTTAGACTTTAAAATTGATTTTTTATTTTTAGATACATTTAACATTTCTTTTAATTTTACTATTAGATATAATT
TTAAGGACAAAAACGAGATGGAAACATGA

f517.aa

TABLE 1. Nucleotide and Amino Acid Sequences

MIPVVASGGILIALSIAFVGIGPDGPNFAEHPFYKQIADIGSIAFGMMLPVLAGFIAMAIADKPGLTPGLVGGVMS
GNVKAGFLGAIFAGFLAGYVARFLARRSVPEWLRPVMPIFVIPLISTIIVGFFMLYFGVYIGKFMGVLESGLKSLQ
SNSETFGVLGKIFLGLVLGSMITVDMGGPFNKVAFLFGVGLIPQVPEIMGMVAAAIPVPPMAMGLATFLAPKLFEN
EEKESGKIAFLISFIGISEGAIPFAASDPGRVIPSIVVGGAVSSIIAAFLGVANHAPHGGPIVLPVIDNKFGFIIA
IAVGVAVATALVIFLKSLKLKESE

t517.aa

DKPGLTPGLVGGVMSGNVKAGFLGAIFAGFLAGYVARFLARRSVPEWLRPVMPIFVIPLISTIIVGFFMLYFGVYI
GKFMGVLESGLKSLQSNSETFGVLGKIFLGLVLGSMITVDMGGPFNKVAFLFGVGLIPQVPEIMGMVAAAIPVPPM
AMGLATFLAPKLFENEEKESGKIAFLISFIGISEGAIPFAASDPGRVIPSIVVGGAVSSIIAAFLGVANHAPHGGP
IVLPVIDNKFGFIIAIAVGVAVATALVIFLKSLKLKESE

f517.nt

ATGATTCCTGTTGTTGCAAGTGGAGGAATTTTAATTGCTCTTAGCATTGCTTTTGTTGGGATTGGACCTGATGGGC
CTAATTTTGCTGAGCATCCATTTTATAAGCAGATTGCAGATATTGGTTCTATAGCTTTTGGGATGATGTTGCCCGT
GCTTGCTGGTTTTATTGCAATGGCAATTGCTGATAAGCCTGGTCTTACCCCCGGTCTTGTTGGTGGAGTAATGTCT
GGGAATGTAAAAGCAGGTTTCTTGGGCGCAATATTTGCGGGCTTTCTTGCAGGTTATGTTGCAAGGTTTTTAGCAA
GAAGATCTGTTCCTGAGTGGTTAAGACCTGTAATGCCTATATTTGTAATTCCGCTAATAAGCACCATTATTGTCGG
CTTTTTTATGCTGTATTTTGGTGTTTATATTGGAAAATTTATGGGGGTGCTTGAGAGTGGGCTTAAATCTTTACAG
AGTAATTCGGAAACTTTTGGCGTGTTGGGTAAAATTTTCTTAGGCTTAGTACTAGGTTCAATGATTACTGTTGATA
TGGGCGGACCTTTTAATAAAGTGGCATTTCTTTTTGGTGTAGGGCTAATTCCTCAAGTGCCAGAAATAATGGGAAT
GGTAGCAGCAGCAATTCCTGTTCCTCCTATGGCTATGGGGCTTGCAACCTTTTTAGCACCTAAATTGTTTGAAAAT
GAAGAAAAAGAATCTGGTAAAATAGCCTTTTTAATTTCATTTATTGGTATTAGCGAAGGAGCTATTCCTTTTGCTG
CTAGTGATCCCGGACGGGTAATCCCTTCGATAGTGGTAGGGGGAGCTGTATCAAGCATTATTGCCGCTTTTTTAGG
CGTTGCTAATCATGCTCCACACGGAGGACCAATAGTACTTCCTGTTATTGATAATAAATTTGGGTTTATTATTGCA
ATTGCTGTTGGAGTTGCGGTTGCAACAGCTTTGGTAATTTTTTTGAAATCTTTAAAATTAAAGGAATCTGAATGA

t517.nt

GATAAGCCTGGTCTTACCCCCGGTCTTGTTGGTGGAGTAATGTCTGGGAATGTAAAAGCAGGTTTCTTGGGCGCAA
TATTTGCGGGCTTTCTTGCAGGTTATGTTGCAAGGTTTTTAGCAAGAAGATCTGTTCCTGAGTGGTTAAGACCTGT
AATGCCTATATTTGTAATTCCGCTAATAAGCACCATTATTGTCGGCTTTTTTATGCTGTATTTTGGTGTTTATATT
GGAAAATTTATGGGGGTGCTTGAGAGTGGGCTTAAATCTTTACAGAGTAATTCGGAAACTTTTGGCGTGTTGGGTA
AAATTTTCTTAGGCTTAGTACTAGGTTCAATGATTACTGTTGATATGGGCGGACCTTTTAATAAAGTGGCATTTCT
TTTTGGTGTAGGGCTAATTCCTCAAGTGCCAGAAATAATGGGAATGGTAGCAGCAGCAATTCCTGTTCCTCCTATG
GCTATGGGGCTTGCAACCTTTTTAGCACCTAAATTGTTTGAAAATGAAGAAAAAGAATCTGGTAAAATAGCCTTTT
TAATTTCATTTATTGGTATTAGCGAAGGAGCTATTCCTTTTGCTGCTAGTGATCCCGGACGGGTAATCCCTTCGAT
AGTGGTAGGGGGAGCTGTATCAAGCATTATTGCCGCTTTTTTAGGCGTTGCTAATCATGCTCCACACGGAGGACCA
ATAGTACTTCCTGTTATTGATAATAAATTTGGGTTTATTATTGCAATTGCTGTTGGAGTTGCGGTTGCAACAGCTT
TGGTAATTTTTTTGAAATCTTTAAAATTAAAGGAATCTGAATGA

f519.aa

MIKIFKKIYILTLVLGMAHLSFASDNYMVRCSKEEDSTTCIAKLKEIKEKKNYDLFSMGIGIGDPIANIMITIPYI
NIDFGYGGFIGLKSNNFENYLNGGIDVIFKKQIGQYMKIGGGIGIGADWSKTSLIPPNEEEETDYERIGAVIRIPF
IMEYNFAKNLSIGFKIYPAVGPTILLTKPSILFEGIKFNFFGFGFIKFAFN

t519.aa

DNYMVRCSKEEDSTTCIAKLKEIKEKKNYDLFSMGIGIGDPIANIMITIPYINIDFGYGGFIGLKSNNFENYLNGG
IDVIFKKQIGQYMKIGGGIGIGADWSKTSLIPPNEEEETDYERIGAVIRIPFIMEYNFAKNLSIGFKIYPAVGPTI
LLTKPSILFEGIKFNFFGFGFIKFAFN

TABLE 1. Nucleotide and Amino Acid Sequences

f519.nt

ATGATAAAAATTTTTAAAAAAATATACATTTTAACATTAGTATTAGGTATGGCACACCTTTCTTTTGCATCTGACA
ATTATATGGTCAGATGCAGCAAGGAAGAAGATTCAACCACCTGTATCGCAAAGCTTAAAGAAATAAAAGAAAAAGAA
AAATTATGACTTATTTTCAATGGGCATTGGAATAGGAGATCCTATTGCAAATATTATGATTACAATTCCTTATATA
AATATTGATTTTGGATATGGAGGTTTTATTGGCCTTAAGTCAAACAATTTTGAAAATTATCTAAATGGTGGAATAG
ACGTTATTTTTAAAAAGCAAATTGGACAATATATGAAAATTGGCGGCGGCATTGGAATAGGTGCGGATTGGTCAAA
AACATCCCTTATACCCCCTAATGAAGAAGAAGAAACTGATTATGAGAGAATAGGCGCTGTTATAAGAATTCCTTTT
ATAATGGAATATAATTTTGCAAAAAATTTATCCATAGGATTCAAAATTTATCCTGCAGTAGGGCCAACAATATTAC
TAACAAAACCAAGCATTTTATTTGAAGGAATTAAATTCAATTTTTTTGGATTTGGATTCATAAAATTTGCATTTAA
TTAA

t519.nt

GACAATTATATGGTCAGATGCAGCAAGGAAGAAGATTCAACCACCTGTATCGCAAAGCTTAAAGAAATAAAAGAAA
AGAAAAATTATGACTTATTTTCAATGGGCATTGGAATAGGAGATCCTATTGCAAATATTATGATTACAATTCCTTA
TATAAATATTGATTTTGGATATGGAGGTTTTATTGGCCTTAAGTCAAACAATTTTGAAAATTATCTAAATGGTGGA
ATAGACGTTATTTTTAAAAAGCAAATTGGACAATATATGAAAATTGGCGGCGGCATTGGAATAGGTGCGGATTGGT
CAAAAACATCCCTTATACCCCCTAATGAAGAAGAAGAAACTGATTATGAGAGAATAGGCGCTGTTATAAGAATTCC
TTTTATAATGGAATATAATTTTGCAAAAAATTTATCCATAGGATTCAAAATTTATCCTGCAGTAGGGCCAACAATA
TTACTAACAAAACCAAGCATTTTATTTGAAGGAATTAAATTCAATTTTTTTGGATTTGGATTCATAAAATTTGCAT
TTAATTAA

f520.aa

MRMLLATIILILTTGLLAAQSKSKSMTEDDFDFDKLLAKEESVRRLFGIGFGVGYPLANITISVPYVDIDLGYGGF
VGLKPNNFLPYVVMGVDLLFKDEIHKNTMISGGIGIGADWSKGSPEKSNEKLEEEEENEAQQVASLQNRIGVVIRL
PLVIEYSFLKNIVIGFKAVATIGTTMLLGSPMSFEGARFNFLGTGFIKIYI

t520.aa

QSKSKSMTEDDFDFDKLLAKEESVRRLFGIGFGVGYPLANITISVPYVDIDLGYGGFVGLKPNNFLPYVVMGVDLL
FKDEIHKNTMISGGIGIGADWSKGSPEKSNEKLEEEEENEAQQVASLQNRIGVVIRLPLVIEYSFLKNIVIGFKAV
ATIGTTMLLGSPMSFEGARFNFLGTGFIKIYI

f520.nt

ATGAGAATGCTATTAGCAACAATAATACTTATATTAACAACGGGTTTATTAGCTGCACAATCCAAAAGCAAAAGTA
TGACTGAAGATGACTTTGATTTTGATAAACTTCTTGCAAAAGAAGAGTCTGTGCGCCGTTTATTTGGCATAGGTTT
TGGAGTTGGATATCCACTTGCAAACATTACAATATCTGTTCCATATGTAGACATAGACCTTGGGTACGGAGGATTC
GTAGGGCTTAAACCCAACAATTTCTTGCCCTATGTTGTGATGGGTGTAGATCTTCTATTTAAAGATGAAATACACA
AAAACACTATGATTTCTGGAGGCATTGGAATAGGTGCAGATTGGTCAAAAGGAAGTCCTGAAAAATCAAATGAAAA
ACTTGAAGAAGAGGAAGAAAATGAAGCACAACAAGTAGCTTCTCTTCAAAATAGAATAGGGGTTGTGATAAGATTG
CCTTTGGTAATAGAGTACAGCTTTCTTAAAAAATATTGTGATTGGATTTAAAGCTGTTGCTACTATTGGAACAACTA
TGCTACTTGGCAGCCCAATGTCATTTGAAGGAGCTAGATTTAATTTCTTAGGCACAGGCTTTATAAAAATATATAT
ATAG

t520.nt

CAATCCAAAAGCAAAAGTATGACTGAAGATGACTTTGATTTTGATAAACTTCTTGCAAAAGAAGAGTCTGTGCGCC
GTTTATTTGGCATAGGTTTTGGAGTTGGATATCCACTTGCAAACATTACAATATCTGTTCCATATGTAGACATAGA
CCTTGGGTACGGAGGATTCGTAGGGCTTAAACCCAACAATTTCTTGCCCTATGTTGTGATGGGTGTAGATCTTCTA
TTTAAAGATGAAATACACAAAAACACTATGATTTCTGGAGGCATTGGAATAGGTGCAGATTGGTCAAAAGGAAGTC
CTGAAAAATCAAATGAAAAACTTGAAGAAGAGGAAGAAAATGAAGCACAACAAGTAGCTTCTCTTCAAAATAGAAT
AGGGGTTGTGATAAGATTGCCTTTGGTAATAGAGTACAGCTTTCTTAAAAAATATTGTGATTGGATTTAAAGCTGTT

TABLE 1. Nucleotide and Amino Acid Sequences

GCTACTATTGGAACAACTATGCTACTTGGCAGCCCAATGTCATTTGAAGGAGCTAGATTTAATTTCTTAGGCACAG
GCTTTATAAAAATATATATATAG

f523.aa

MNIKINFFFTLPIGIFLGLFFPLGIYSSLSHAFIRLSYLSLIPFLIFSIPLGIENIIENKNFKKLFGKTIYYGILT
NLSGVAVSIIAATIYLPQRIPILEKTIQNTCFFEKEALLETFFPKNIFKIFTSSNPNLLSIYMISIIIGTSFYYAK
QKGRIARELMLSASNLFYHANGFIVNILNIGIIFITANYAANLKNFKDYPNYTNSITFFLAWTIIIILFVILPTISY
RLTKSFKMIYKGIFVSFQNIIFSGLAKDSYSPYVILIEDIKNERINIKKSIIINIPLINFVSKFGTIFVSVISFFI
ILKSYSSLPISIYEISYMSTLSFVFVFAFPHIPNSLIYIITMLCSTYTKGIELNVSNITPMLPILISLALLIDFAF
NIAIIHIINFKELKDQEKIN

t523.aa

IENIIENKNFKKLFGKTIYYGILTNLSGVAVSIIAATIYLPQRIPILEKTIQNTCFFEKEALLETFFPKNIFKIFT
SSNPNLLSIYMISIIIGTSFYYAKQKGRIARELMLSASNLFYHANGFIVNILNIGIIFITANYAANLKNFKDYPNY
TNSITFFLAWTIIIILFVILPTISYRLTKSFKMIYKGIFVSFQNIIFSGLAKDSYSPYVILIEDIKNERINIKKSII
INIPLINFVSKFGTIFVSVISFFIILKSYSSLPISIYEISYMSTLSFVFVFAFPHIPNSLIYIITMLCSTYTKGIE
LNVSNITPMLPILISLALLIDFAFNIAIIHIINFKELKDQEKIN

f523.nt

ATGAATATAAAAATCAATTTTTTTTTCACTTTGCCTATTGGAATCTTTTTAGGATTGTTTTTCCCTCTTGGAATTT
ATAGCTCCTTATCACATGCTTTTATAAGATTATCATACTTATCTCTTATTCCCTTTTTAATATTTTCAATTCCATT
AGGAATTGAAAATATTATTGAAAATAAAAACTTTAAAAAGCTTTTTGGTAAAACAATTTATTATGGAATTTTAACT
AACCTATCTGGAGTTGCTGTATCAATAATAGCTGCAACAATATATCTTCCGCAAAGAATTCCAATACTAGAAAAAA
CAATACAAAATACATGTTTTTTTGAAAAAGAAGCTTTACTAGAAACATTCTTTCCAAAAAATATTTTCAAAATATT
TACATCTAGCAATCCAAATCTACTAAGCATTTACATGATTTCAATAATAATAGGCACAAGTTTTTATTATGCAAAA
CAAAAAGGCAGAATAGCTAGAGAACTGATGCTAAGCGCATCCAATCTTTTTTACCATGCAAATGGGTTTATTGTAA
ACATATTAAATATAGGGATCATTTTTATAACAGCAAATTACGCTGCAAACTTAAAAAACTTCAAAGATTACCCAAA
TTATACAAACAGCATAACATTCTTTTTGGCATGGACAATTATAATTTTATTCGTAATATTGCCAACAATTAGTTAT
AGATTAACAAAAAGTTTTAAAATGATATATAAAGGCATTTTTGTATCATTTCAAAACATAATATTTTCAGGACTTG
CAAAAGATTCTTATTCCCCTTATGTGATATTAATAGAAGATATTAAAAACGAAAGAATAAATATAAAAAAATCCAT
AATTATAAACATACCTTTAATAAATTTTGTATCTAAATTTGGCACTATTTTTGTTTCAGTAATATCATTTTTTATA
ATTTTAAAATCATATTCTAGCTTACCCATTTCTATTTATGAAATAAGCTATATGAGCACTTTATCATTTGTTTTTG
TCTTTGCATTTCCTCATATACCAAATAGTTTAATTTATATAATTACAATGCTTTGCTCTACATATACAAAAGGAAT
AGAGCTAAATGTTTCAAACATAACACCAATGCTGCCGATATTAATCTCTTTGGCTTTACTAATCGACTTTGCTTTT
AACATTGCAATCATTCATATAATAAACTTCAAAGAATTAAAAGATCAAGAAAAAATTAATTAA

f523.nt

ATTGAAAATATTATTGAAAATAAAAACTTTAAAAAGCTTTTTGGTAAAACAATTTATTATGGAATTTTAACTAACC
TATCTGGAGTTGCTGTATCAATAATAGCTGCAACAATATATCTTCCGCAAAGAATTCCAATACTAGAAAAAAACAAT
ACAAAATACATGTTTTTTTGAAAAAGAAGCTTTACTAGAAACATTCTTTCCAAAAAATATTTTCAAAATATTTACA
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AAGGCAGAATAGCTAGAGAACTGATGCTAAGCGCATCCAATCTTTTTTACCATGCAAATGGGTTTATTGTAAACAT
ATTAAATATAGGGATCATTTTTATAACAGCAAATTACGCTGCAAACTTAAAAAACTTCAAAGATTACCCAAATTAT
ACAAACAGCATAACATTCTTTTTGGCATGGACAATTATAATTTTATTCGTAATATTGCCAACAATTAGTTATAGAT
TAACAAAAAGTTTTAAAATGATATATAAAGGCATTTTTGTATCATTTCAAAACATAATATTTTCAGGACTTGCAAA
AGATTCTTATTCCCCTTATGTGATATTAATAGAAGATATTAAAAACGAAAGAATAAATATAAAAAAATCCATAATT
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TAAAATCATATTCTAGCTTACCCATTTCTATTTATGAAATAAGCTATATGAGCACTTTATCATTTGTTTTTGTCTT
TGCATTTCCTCATATACCAAATAGTTTAATTTATATAATTACAATGCTTTGCTCTACATATACAAAAGGAATAGAG
CTAAATGTTTCAAACATAACACCAATGCTGCCGATATTAATCTCTTTGGCTTTACTAATCGACTTTGCTTTTAACA
TTGCAATCATTCATATAATAAACTTCAAAGAATTAAAAGATCAAGAAAAAATTAATTAA

TABLE 1. Nucleotide and Amino Acid Sequences

f526.aa

MKKEFIMLLLLLQTIMNLNSINTNTSTSIVKELQKNLYIFNSKEYQKDKDTLNEFINSININDKEILQSLEKIKNE
LFIISVFFNNKKGILIALNLGAEINFKYKISPISISIINNEFEITKILIDYGISLNQIDDTGYSPIFWAIYTNNEK
IFEFLKESGADLSFTLKNRKTPMQAAIETENIKLIKSLEKKKIYIDDNFKKKLKKLKNKEIVRILVK

t526.aa

NSINTNTSTSIVKELQKNLYIFNSKEYQKDKDTLNEFINSININDKEILQSLEKIKNELFIISVFFNNKKGILIAL
NLGAEINFKYKISPISISIINNEFEITKILIDYGISLNQIDDTGYSPIFWAIYTNNEKIFEFLKESGADLSFTLKN
RKTPMQAAIETENIKLIKSLEKKKIYIDDNFKKKLKKLKNKEIVRILVK

f526.nt

ATGAAAAAAGAATTCATTATGCTTTTACTGTTATTGCAAACAATAATGAATTTAAACTCAATAAATACTAATACAA
GTACTTCAATAGTAAAAGAATTGCAAAAAAATTTATATATTTTCAATAGCAAAGAATATCAAAAAGATAAAGACAC
TTTAAATGAATTTATAAATTCAATAAATATAAATGACAAAGAAATCTTACAAAGTTTAGAAAAAATCAAAAATGAG
CTTTTTATAATATCTGTTTTTTTCAACAATAAAAAAGGGATTTTAATTGCACTAAATCTTGGAGCAGAAATAAACT
TTAAATATAAAATATCTCCAATTTCAATTTCAATAATAAACAATGAATTTGAAATCACAAAAATATTGATAGATTA
CGGAATAAGCCTTAATCAAATAGATGATACAGGTTATTCTCCAATATTTTGGGCAATATATACTAATAACGAAAAA
ATATTTGAATTTTTAAAAGAAAGCGGAGCTGATTTAAGTTTCACACTTAAAAATAGAAAAACACCAATGCAAGCCG
CAATAGAAACAGAAAATATAAAACTAATTAAATCTCTGGAAAAGAAAAAAATTTACATTGACGACAATTTCAAAAA
AAAACTTAAAAAGCTTAAAAACAAAGAAATAGTTCGAATTTTAGTAAAATAG

t526.nt

AACTCAATAAATACTAATACAAGTACTTCAATAGTAAAAGAATTGCAAAAAAATTTATATATTTTCAATAGCAAAG
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TCACAAAAATATTGATAGATTACGGAATAAGCCTTAATCAAATAGATGATACAGGTTATTCTCCAATATTTTGGGC
AATATATACTAATAACGAAAAAATATTTGAATTTTTAAAAGAAAGCGGAGCTGATTTAAGTTTCACACTTAAAAAT
AGAAAAACACCAATGCAAGCCGCAATAGAAACAGAAAATATAAAACTAATTAAATCTCTGGAAAAGAAAAAAATTT
ACATTGACGACAATTTCAAAAAAAAACTTAAAAAGCTTAAAAACAAAGAAATAGTTCGAATTTTAGTAAAATAG

f544.aa

MTKNRIIWLLVLMVSSTFTATIISNYQNLMLSLVVLANFIPLLMDTSGNAGSQASALIIRELALGTVKVKDFFKVF
LKEICVSILVGAILASVNFLRIVFFVAPHHSDKLKIAFVVSSCLMVSLTVAKILGGLLPIVAKLLKLDPALMAGPL
ITTIADAITLIAYFNIAKWVLVSYAV

t544.aa

STFTATIISNYQNLMLSLVVLANFIPLLMDTSGNAGSQASALIIRELALGTVKVKDFFKVFLKEICVSILVGAILA
SVNFLRIVFFVAPHHSDKLKIAFVVSSCLMVSLTVAKILGGLLPIVAKLLKLDPALMAGPLITTIADAITLIAYFN
IAKWVLVSYAV

f544.nt

ATGACAAAAAATAGAATAATTTGGCTTTTAGTTCTTATGGTGTCTTCTACTTTTACAGCTACAATTATTTCAAATT
ATCAAAATTTAATGTTGTCTTTAGTGGTTTTAGCTAATTTTATTCCCCTTTTAATGGATACTTCAGGCAATGCCGG
CTCTCAGGCATCTGCGCTAATAATTCGTGAGCTTGCTCTTGGTACTGTCAAGGTAAAAGATTTTTTTAAAGTGTTT
TTAAAGGAAATATGTGTTAGCATTCTAGTGGGAGCAATTCTTGCTAGTGTTAATTTTTTAAGAATTGTCTTTTTTG
TAGCTCCACACCATTCTGATAAGCTGAAAATAGCTTTTGTAGTTTCATCTTGCTTGATGGTAAGTTTGACAGTAGC
AAAGATATTGGGAGGTCTTTTACCCATTGTTGCTAAACTTTTAAAGTTGGATCCAGCACTTATGGCAGGCCCTTTA

TABLE 1. Nucleotide and Amino Acid Sequences

ATCACTACAATTGCAGATGCTATTACTTTAATAGCTTATTTAATATAGCAAAATGGGTTTTAGTTAGCTATGCTG
TTTAA

t544.nt

TCTACTTTTACAGCTACAATTATTTCAAATTATCAAAATTTAATGTTGTCTTTAGTGGTTTTAGCTAATTTTATTC
CCCTTTTAATGGATACTTCAGGCAATGCCGGCTCTCAGGCATCTGCGCTAATAATTCGTGAGCTTGCTCTTGGTAC
TGTCAAGGTAAAAGATTTTTTTAAAGTGTTTTTAAAGGAAATATGTGTTAGCATTCTAGTGGGAGCAATTCTTGCT
AGTGTTAATTTTTTAAGAATTGTCTTTTTTGTAGCTCCACACCATTCTGATAAGCTGAAAATAGCTTTTGTAGTTT
CATCTTGCTTGATGGTAAGTTTGACAGTAGCAAAGATATTGGGAGGTCTTTTACCCATTGTTGCTAAACTTTTAAA
GTTGGATCCAGCACTTATGGCAGGCCCTTTAATCACTACAATTGCAGATGCTATTACTTTAATAGCTTATTTTAAT
ATAGCAAAATGGGTTTTAGTTAGCTATGCTGTTTAA

f545.aa

MTKNRIIWLLVLMVSSTFTATIISNYQNLMLSLVVLANFIPLLMDTSGNAGSQASALIIRELALGTVKVKDFFKVF
LKEICVSILVGAILASVNFLRIVFFVAPHHSDKLKIAFVVSSCLMVSLTVAKILGGLLPIVAKLLKLDPALMAGPL
ITTIADAITLIAYFNIAKWVLVSYAV

t545.aa

GSQASALIIRELALGTVKVKDFFKVFLKEICVSILVGAILASVNFLRIVFFVAPHHSDKLKIAFVVSSCLMVSLTV
AKILGGLLPIVAKLLKLDPALMAGPLITTIADAITLIAYFNIAKWVLVSYAV

f545.nt

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CTCTCAGGCATCTGCGCTAATAATTCGTGAGCTTGCTCTTGGTACTGTCAAGGTAAAAGATTTTTTTAAAGTGTTT
TTAAAGGAAATATGTGTTAGCATTCTAGTGGGAGCAATTCTTGCTAGTGTTAATTTTTTAAGAATTGTCTTTTTTG
TAGCTCCACACCATTCTGATAAGCTGAAAATAGCTTTTGTAGTTTCATCTTGCTTGATGGTAAGTTTGACAGTAGC
AAAGATATTGGGAGGTCTTTTACCCATTGTTGCTAAACTTTTAAAGTTGGATCCAGCACTTATGGCAGGCCCTTTA
ATCACTACAATTGCAGATGCTATTACTTTAATAGCTTATTTTAATATAGCAAAATGGGTTTTAGTTAGCTATGCTG
TTTAA

t545.nt

GGCTCTCAGGCATCTGCGCTAATAATTCGTGAGCTTGCTCTTGGTACTGTCAAGGTAAAAGATTTTTTTAAAGTGT
TTTTAAAGGAAATATGTGTTAGCATTCTAGTGGGAGCAATTCTTGCTAGTGTTAATTTTTTAAGAATTGTCTTTTT
TGTAGCTCCACACCATTCTGATAAGCTGAAAATAGCTTTTGTAGTTTCATCTTGCTTGATGGTAAGTTTGACAGTA
GCAAAGATATTGGGAGGTCTTTTACCCATTGTTGCTAAACTTTTAAAGTTGGATCCAGCACTTATGGCAGGCCCTT
TAATCACTACAATTGCAGATGCTATTACTTTAATAGCTTATTTTAATATAGCAAAATGGGTTTTAGTTAGCTATGC
TGTTTAA

f577.aa

MRIKNLILIAILLISPSCSTNKNIVVLTDNKTIPFYINQFNIENKANFIIKFRNNIDLQTIEKENAQIIISKNIGN
TNIANHFKSVKINYNPDYPILKHIFKQFNYKIIPLGFDIPILIYKNTHHIKKYINTKYLKEEYENFIKDGKFFISP
YVSENLFYVISQINNVRFSFEKNKLNYNENQILKMLEYFSSFLNTKQMDLQKDFFNKYGYLKLNKILLNKKSLLIA
GLSDITFYNSLSEQEKSQIKFSYLINDNNEIVISNPNFIGILETSVLTKKFINWILYKKTQKTLIGFNNQSQSNIC
FGFANGFTPYKELNLKIKHSIDGISPFIIDETQINSHSYVLSKKTIEKENLLINEWFFSKANNLKKNKN

t577.aa

NKNIVVLTDNKTIPFYINQFNIENKANFIIKFRNNIDLQTIEKENAQIIISKNIGNTNIANHFKSVKINYNPDYPI
LKHIFKQFNYKIIPLGFDIPILIYKNTHHIKKYINTKYLKEEYENFIKDGKFFISPYVSENLFYVISQINNVRFSF

TABLE 1. Nucleotide and Amino Acid Sequences

EKNKLNYNENQILKMLEYFSSFLNTKQMDLQKDFFNKYGYLKLNKILLNKKSLLIAGLSDITFYNSLSEQEKSQIK
FSYLINDNNEIVISNPNFIGILETSVLTKKFINWILYKKTQKTLIGFNNQSQSNICFGFANGFTPYKELNLKIKHS
IDGISPFIIDETQINSHSYVLSKKTIEKENLLINEWFFSKANNLKKNKN

f577.nt

ATGAGAATAAAAAATTTAATACTAATAGCAATTTTATTAATTAGCCCTAGCTGTTCAACAAATAAGAACATCGTTG
TACTAACTGACAATAAAACAATACCATTTTATATAAATCAATTTAATATAGAAAATAAAGCAAATTTTATAATTAA
GTTTAGAAATAATATTGATCTGCAAACAATAGAAAAAGAAAATGCACAAATAATTATTTCTAAAAACATTGGTAAC
ACAAATATTGCTAACCATTTTAAATCTGTAAAAATCAATTATAATCCAGATTATCCTATCTTAAAGCATATTTTCA
AGCAATTTAACTACAAAATTATTCCATTGGGCTTTGACATTCCTATTTTAATCTATAAAAATACACATCATATTAA
AAAATACATAAACACTAAATATCTAAAAGAAGAATACGAAAATTTCATTAAAGATGGAAAATTTTTTATATCGCCT
TATGTTTCTGAAAATTTATTTTATGTGATTTCTCAAATAAATAATGTGAGATTTTCTTTTGAAAAAAATAAATTAA
ATTATAATGAGAATCAAATTTTAAAAATGCTAGAATATTTCTCATCATTTTTAAATACAAAACAAATGGACTTGCA
AAAAGATTTCTTTAATAAATACGGCTACCTAAAGTTAAATAAAATATTGCTTAATAAAAAATCTCTTTTAATAGCA
GGATTGAGCGATATAACCTTCTACAATAGCTTAAGCGAACAAGAGAAGTCACAAATAAAATTTTCCTATTTAATAA
ACGATAACAATGAAATTGTTATCTCAAACCCAAATTTTATTGGCATTTTAGAAACATCTGTTTTAACTAAAAAATT
TATCAACTGGATATTGTATAAAAAAACTCAAAAAACCCTAATTGGATTTAACAATCAATCCCAATCAAATATATGT
TTTGGATTTGCCAATGGTTTTACCCCTTACAAAGAATTAAATTTAAAAATAAAACATTCAATTGATGGAATATCTC
CTTTTATTATTGACGAAACTCAAATCAATAGCCATTCCTATGTATTAAGCAAAAAAACAATTGAAAAAGAAAACTT
ACTAATAAATGAATGGTTTTTCTCTAAAGCTAATAATCTAAAAAAAAAATAAAAATTAA

t577.nt

AATAAGAACATCGTTGTACTAACTGACAATAAAACAATACCATTTTATATAAATCAATTTAATATAGAAAATAAAG
CAAATTTTATAATTAAGTTTAGAAATAATATTGATCTGCAAACAATAGAAAAAGAAAATGCACAAATAATTATTTC
TAAAAACATTGGTAACACAAATATTGCTAACCATTTTAAATCTGTAAAAATCAATTATAATCCAGATTATCCTATC
TTAAAGCATATTTTCAAGCAATTTAACTACAAAATTATTCCATTGGGCTTTGACATTCCTATTTTAATCTATAAAA
ATACACATCATATTAAAAAATACATAAACACTAAATATCTAAAAGAAGAATACGAAAATTTCATTAAAGATGGAAA
ATTTTTTATATCGCCTTATGTTTCTGAAAATTTATTTTATGTGATTTCTCAAATAAATAATGTGAGATTTTCTTTT
GAAAAAAATAAATTAAATTATAATGAGAATCAAATTTTAAAAATGCTAGAATATTTCTCATCATTTTTAAATACAA
AACAAATGGACTTGCAAAAAGATTTCTTTAATAAATACGGCTACCTAAAGTTAAATAAAATATTGCTTAATAAAAA
ATCTCTTTTAATAGCAGGATTGAGCGATATAACCTTCTACAATAGCTTAAGCGAACAAGAGAAGTCACAAATAAAA
TTTTCCTATTTAATAAACGATAACAATGAAATTGTTATCTCAAACCCAAATTTTATTGGCATTTTAGAAACATCTG
TTTTAACTAAAAAATTTATCAACTGGATATTGTATAAAAAAACTCAAAAAACCCTAATTGGATTTAACAATCAATC
CCAATCAAATATATGTTTTGGATTTGCCAATGGTTTTACCCCTTACAAAGAATTAAATTTAAAAATAAAACATTCA
ATTGATGGAATATCTCCTTTTATTATTGACGAAACTCAAATCAATAGCCATTCCTATGTATTAAGCAAAAAAACAA
TTGAAAAAGAAAACTTACTAATAAATGAATGGTTTTTCTCTAAAGCTAATAATCTAAAAAAAAAATAAAAATTAA

f584.aa

MIKTILLLVLYPVVVFSQISANQYFEGIYAKYQNIEDMQATINFTLKGLKQTGVLLYKFPDKFIINLDSNNQVFVS
DGEFLTVYVPSLGTSFNQQLLKGSSGGGLMKVLNSEYSVSYTNSPNLEDLDSSEPGKYIKLTFSRKLYKGAATINS
FIIAFAPDGIIRRITAFPTSGGREIVIDLTAVKFNVGILDSKFKYDPPKSSNKVDNFLYDIKKN

t584.aa

QISANQYFEGIYAKYQNIEDMQATINFTLKGLKQTGVLLYKFPDKFIINLDSNNQVFVSDGEFLTVYVPSLGTSFN
QQLLKGSSGGGLMKVLNSEYSVSYTNSPNLEDLDSSEPGKYIKLTFSRKLYKGAATINSFIIAFAPDGIIRRITAF
PTSGGREIVIDLTAVKFNVGILDSKFKYDPPKSSNKVDNFLYDIKKN

f584.nt

ATGATAAAAACAATACTTTTATTAGTTTTGTATCCTGTTGTTGTGTTTTCTCAAATATCTGCAAATCAATATTTTG
AAGGAATTTATGCTAAATATCAAAATATAGAGGACATGCAAGCAACAATTAATTTTACTTTAAAGGGGTTAAAGCA

TABLE 1. Nucleotide and Amino Acid Sequences

AACAGGTGTTTTGCTTTATAAGTTTCCAGACAAGTTTATTATCAATTTAGATTCAAATAATCAAGTTTTTGTAAGT
GATGGTGAATTTTTGACAGTTTATGTTCCATCTCTTGGGACTTCTTTTAATCAGCAATTATTAAAGGGTAGTAGTG
GGGGAGGTCTTATGAAAGTTTTAAATAGTGAGTATAGCGTATCTTATACCAATTCTCCAAATTTAGAAGATCTCGA
TTCATCTGAGCCTGGAAAATATATTAAATTAACCTTTTCTAGAAAGCTTTACAAGGGGGCTGCTACTATTAATTCT
TTTATTATTGCTTTTGCTCCGGATGGAATAATTAGAAGAATTACTGCTTTTCCTACTAGTGGTGGGCGCGAAATAG
TTATTGATTTGACTGCTGTGAAGTTTAATGTTGGAATTCTTGATAGCAAATTTAAATATGATCCTCCAAAATCTTC
AAATAAGGTAGATAATTTTTTATATGATATTAAAAAAAATTAA

t584.nt

CAAATATCTGCAAATCAATATTTTGAAGGAATTTATGCTAAATATCAAAATATAGAGGACATGCAAGCAACAATTA
ATTTTACTTTAAAGGGGTTAAAGCAAACAGGTGTTTTGCTTTATAAGTTTCCAGACAAGTTTATTATCAATTTAGA
TTCAAATAATCAAGTTTTTGTAAGTGATGGTGAATTTTTGACAGTTTATGTTCCATCTCTTGGGACTTCTTTTAAT
CAGCAATTATTAAAGGGTAGTAGTGGGGGAGGTCTTATGAAAGTTTTAAATAGTGAGTATAGCGTATCTTATACCA
ATTCTCCAAATTTAGAAGATCTCGATTCATCTGAGCCTGGAAAATATATTAAATTAACCTTTTCTAGAAAGCTTTA
CAAGGGGGCTGCTACTATTAATTCTTTTATTATTGCTTTTGCTCCGGATGGAATAATTAGAAGAATTACTGCTTTT
CCTACTAGTGGTGGGCGCGAAATAGTTATTGATTTGACTGCTGTGAAGTTTAATGTTGGAATTCTTGATAGCAAAT
TTAAATATGATCCTCCAAAATCTTCAAATAAGGTAGATAATTTTTTATATGATATTAAAAAAAATTAA

f596.aa

MKERCLYLLVFVALCVNNLFSDDYLIYDFDLSLNEFLEVSTRKDNLEPMVDSNRILLFYPPKKEIRKIFAAFDFDQ
YSKKYLFKKNEHGVFFVKVNIPHGTSSIKYRLIVDGVWTNDEYNKNVVYNEDLIPFSKIEIAKEKSSYISLRNPIQ
SYDNNEIEIFYIGRPGQIVTIAGSFNNFNPFLNRLIEKEDNKGIYTIKLKNLPKDRIYYYFIDSGNKVIDKNNVNR
INLYFVEGIDNKIDFEVSYFDHK

t596.aa

DDYLIYDFDLSLNEFLEVSTRKDNLEPMVDSNRILLFYPPKKEIRKIFAAFDFDQYSKKYLFKKNEHGVFFVKVNI
PHGTSSIKYRLIVDGVWTNDEYNKNVVYNEDLIPFSKIEIAKEKSSYISLRNPIQSYDNNEIEIFYIGRPGQIVTI
AGSFNNFNPFLNRLIEKEDNKGIYTIKLKNLPKDRIYYYFIDSGNKVIDKNNVNRINLYFVEGIDNKIDFEVSYFD
HK

f596.nt

ATGAAAGAAAGGTGTTTGTATTTATTGGTTTTTGTAGCTTTATGTGTTAACAATCTTTTTTCAGATGATTATTTAA
TTTATGACTTTGATTTAAGTTTAAATGAATTTCTAGAAGTTTCAACAAGAAAAGACAATCTTGAGCCTATGGTTGA
TTCCAATCGTATATTATTGTTTTATCCTCCTAAAAAAGAAATTAGAAAAATTTTTGCTGCCTTTGACTTTGATCAG
TATTCTAAGAAATATTTATTCAAAAAAAATGAGCATGGAGTTTTTTTTGTTAAAGTTAATATTCCTCATGGCACAA
GCAGTATAAAATATAGGCTTATTGTAGACGGTGTTTGGACTAATGACGAGTATAATAAAAATGTAGTTTATAATGA
GGATTTAATCCCATTTTCTAAAATTGAGATCGCTAAAGAGAAGTCCAGCTATATTTCTTTGAGAAATCCAATACAA
TCATATGATAACAATGAAATTGAAATTTTTTACATAGGTCGTCCTGGACAAATAGTTACAATAGCTGGTAGTTTTA
ACAATTTTAATCCTTTTTTAAATAGGCTTATTGAGAAAGAGGACAATAAGGGAATTTATACTATTAAGCTTAAAAA
TTTACCCAAGGATAGAATTTATTATTATTTTATTGATTCTGGTAACAAAGTAATAGATAAAAATAATGTTAATAGA
ATTAATTTATATTTTGTTGAGGGAATTGATAATAAAATAGATTTCGAAGTTTCCTATTTTGATCATAAGTAA

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GATGATTATTTAATTTATGACTTTGATTTAAGTTTAAATGAATTTCTAGAAGTTTCAACAAGAAAAGACAATCTTG
AGCCTATGGTTGATTCCAATCGTATATTATTGTTTTATCCTCCTAAAAAAGAAATTAGAAAAATTTTTGCTGCCTT
TGACTTTGATCAGTATTCTAAGAAATATTTATTCAAAAAAAATGAGCATGGAGTTTTTTTTGTTAAAGTTAATATT
CCTCATGGCACAAGCAGTATAAAATATAGGCTTATTGTAGACGGTGTTTGGACTAATGACGAGTATAATAAAAATG
TAGTTTATAATGAGGATTTAATCCCATTTTCTAAAATTGAGATCGCTAAAGAGAAGTCCAGCTATATTTCTTTGAG
AAATCCAATACAATCATATGATAACAATGAAATTGAAATTTTTTACATAGGTCGTCCTGGACAAATAGTTACAATA
GCTGGTAGTTTTAACAATTTTAATCCTTTTTTAAATAGGCTTATTGAGAAAGAGGACAATAAGGGAATTTATACTA
TTAAGCTTAAAAATTTACCCAAGGATAGAATTTATTATTATTTTATTGATTCTGGTAACAAAGTAATAGATAAAAA

TABLE 1. Nucleotide and Amino Acid Sequences

TAATGTTAATAGAATTAATTTATATTTTGTTGAGGGAATTGATAATAAAATAGATTTCGAAGTTTCCTATTTTGAT
CATAAGTAA

f598.aa

MRQRVMIAMALSCHPSLLIADEPTTALDVTIQEQILLLIKNLSKKFNTSTIFITHDLAVVAEICDTVSVMYQGKIV
EEGTVEEIFNNPKHPYTIGLLKSILTLEHDPNKKLYSTKENPMKITKTSTEEF

t598.aa

EPTTALDVTIQEQILLLIKNLSKKFNTSTIFITHDLAVVAEICDTVSVMYQGKIVEEGTVEEIFNNPKHPYTIGLL
KSILTLEHDPNKKLYSTKENPMKITKTSTEEF

f598.nt

ATGAGACAAAGAGTTATGATTGCCATGGCTCTTAGCTGTCATCCATCCTTATTAATAGCAGATGAACCAACAACAG
CCCTTGATGTTACAATCCAAGAGCAAATATTATTATTAATCAAAAACCTATCTAAAAAATTCAATACTTCTACCAT
ATTTATAACTCATGATCTTGCGGTTGTTGCTGAAATTTGTGATACAGTATCTGTAATGTATCAAGGAAAAATTGTA
GAAGAAGGAACAGTAGAGGAAATATTTAACAATCCTAAGCATCCTTACACCATTGGGCTTTTAAAATCAATTCTTA
CGCTAGAACACGATCCAAATAAAAAGCTTTATTCAACAAAAGAAAACCCTATGAAGATCACAAAAACCAGCACCGA
GGAGTTTTAA

t598.nt

GAACCAACAACAGCCCTTGATGTTACAATCCAAGAGCAAATATTATTATTAATCAAAAACCTATCTAAAAAATTCA
ATACTTCTACCATATTTATAACTCATGATCTTGCGGTTGTTGCTGAAATTTGTGATACAGTATCTGTAATGTATCA
AGGAAAAATTGTAGAAGAAGGAACAGTAGAGGAAATATTTAACAATCCTAAGCATCCTTACACCATTGGGCTTTTA
AAATCAATTCTTACGCTAGAACACGATCCAAATAAAAAGCTTTATTCAACAAAAGAAAACCCTATGAAGATCACAA
AAACCAGCACCGAGGAGTTTTAA

f600.aa

MAIMERSIIGLFIALAFVSWLTVARVVRGQVQSLSSSEFIQAAKTLGATNQRIILKHLIPNSIGMIVIFTTIRVPS
FIMAEAFLSFLGLGISAPMTSWGELVQNGIATFVEYPWKVFIPAIVMTIFLLFMNFLGDGLRDAFDPKDSI

t600.aa

RVVRGQVQSLSSSEFIQAAKTLGATNQRIILKHLIPNSIGMIVIFTTIRVPSFIMAEAFLSFLGLGISAPMTSWGE
LVQNGIATFVEYPWKVFIPAIVMTIFLLFMNFLGDGLRDAFDPKDSI

f600.nt

ATGGCAATAATGGAAAGAAGTATAATCGGCTTATTCATAGCACTTGCATTTGTATCATGGTTAACAGTAGCTCGAG
TTGTACGAGGCCAAGTACAATCACTATCAAGTTCGGAATTTATACAAGCAGCCAAAACCCTTGGTGCAACAAATCA
AAGAATAATCTTAAAACACTTGATCCCTAATAGCATTGGAATGATAGTTATATTCACAACAATAAGGGTTCCAAGC
TTTATTATGGCTGAAGCATTTTTATCCTTTTTAGGACTTGGAATTTCAGCTCCAATGACAAGCTGGGGAGAATTAG
TGCAAAATGGAATTGCTACATTTGTTGAATATCCATGGAAAGTTTTTATTCCAGCTATAGTTATGACAATATTTCT
ATTATTTATGAACTTTTTAGGTGATGGGCTAAGGGATGCTTTTGATCCAAAAGATAGCATCTAA

t600.nt

CGAGTTGTACGAGGCCAAGTACAATCACTATCAAGTTCGGAATTTATACAAGCAGCCAAAACCCTTGGTGCAACAA
ATCAAAGAATAATCTTAAAACACTTGATCCCTAATAGCATTGGAATGATAGTTATATTCACAACAATAAGGGTTCC
AAGCTTTATTATGGCTGAAGCATTTTTATCCTTTTTAGGACTTGGAATTTCAGCTCCAATGACAAGCTGGGGAGAA

TABLE 1. Nucleotide and Amino Acid Sequences

TTAGTGCAAAATGGAATTGCTACATTTGTTGAATATCCATGGAAAGTTTTTATTCCAGCTATAGTTATGACAATAT
TTCTATTATTTATGAACTTTTTAGGTGATGGGCTAAGGGATGCTTTTGATCCAAAAGATAGCATCTAA

f603.aa

MLKFTLKKILGIIPTLLVIIFLCFFVMRMAPGSPFDSEKPIDPQVKARLMEKYHLDKPFYIQAFYYITNALRGDLG
PSLKKKDLTVSQYIKLGFPKSLTLGVISLIISLSIGIPIGILAAIYKNTYVDYIITSIAILGISIPLFVIGPILQY
FFAIKWGLLYTSGWITERGGFSNLILPIITLSMPNVAIFARIIRGSMLEIIQSDFIRTARAKGLSFKKIVIKHMLR
GAMLPVVSYIGPAFAAIISGSVVIEKIFRIAGMGMFITESALNRDYPVLMGGLLVYSIILLISILISDIIYKILDP
RV

t603.aa

SPFDSEKPIDPQVKARLMEKYHLDKPFYIQAFYYITNALRGDLGPSLKKKDLTVSQYIKLGFPKSLTLGVISLIIS
LSIGIPIGILAAIYKNTYVDYIITSIAILGISIPLFVIGPILQYFFAIKWGLLYTSGWITERGGFSNLILPIITLS
MPNVAIFARIIRGSMLEIIQSDFIRTARAKGLSFKKIVIKHMLRGAMLPVVSYIGPAFAAIISGSVVIEKIFRIAG
MGMFITESALNRDYPVLMGGLLVYSIILLISILISDIIYKILDPRV

f603.nt

ATGTTAAAGTTTACTTTAAAGAAAATATTAGGAATAATACCAACTTTACTGGTAATAATTTTTTTATGCTTTTTTG
TAATGAGAATGGCTCCTGGAAGTCCATTTGATTCTGAAAAACCTATTGATCCTCAAGTAAAAGCAAGATTGATGGA
AAAATATCACCTTGACAAGCCTTTTTATATTCAAGCTTTTTATTACATTACAAACGCTCTCAGGGGAGATCTGGGA
CCTTCTTTGAAAAAGAAAGACCTTACAGTTAGTCAATACATAAAATTAGGATTTCCAAAATCACTTACACTAGGAG
TAATATCCCTTATTATATCACTATCAATAGGAATACCAATAGGTATATTAGCTGCCATTTATAAAAATACTTATGT
GGATTATATAATAACATCAATAGCAATATTGGGGATTTCAATACCATTATTCGTAATAGGGCCAATTTTACAATAT
TTTTTTGCAATTAAATGGGGTTTGCTTTATACCTCTGGATGGATTACAGAAAGAGGAGGATTTTCAAATTTAATTC
TACCCATAATAACTCTTAGCATGCCCAACGTAGCTATTTTCGCAAGAATAATCAGAGGATCAATGCTAGAAATAAT
ACAAAGCGACTTTATAAGAACTGCGCGTGCAAAAGGGCTAAGCTTCAAAAAGATAGTTATAAAGCATATGTTAAGA
GGAGCAATGTTGCCTGTAGTAAGCTATATAGGTCCAGCATTTGCTGCTATAATATCTGGAAGCGTGGTTATTGAAA
AAATATTTAGAATTGCTGGAATGGGAATGTTTATAACAGAATCCGCACTAAACAGAGATTACCCAGTATTAATGGG
CGGATTGTTAGTATATTCAATAATACTGCTTATTTCTATATTAATATCAGATATTATATATAAAATATTAGATCCA
AGAGTATAA

t603.nt

AGTCCATTTGATTCTGAAAAACCTATTGATCCTCAAGTAAAAGCAAGATTGATGGAAAAATATCACCTTGACAAGC
CTTTTTATATTCAAGCTTTTTATTACATTACAAACGCTCTCAGGGGAGATCTGGGACCTTCTTTGAAAAAGAAAGA
CCTTACAGTTAGTCAATACATAAAATTAGGATTTCCAAAATCACTTACACTAGGAGTAATATCCCTTATTATATCA
CTATCAATAGGAATACCAATAGGTATATTAGCTGCCATTTATAAAAATACTTATGTGGATTATATAATAACATCAA
TAGCAATATTGGGGATTTCAATACCATTATTCGTAATAGGGCCAATTTTACAATATTTTTTTGCAATTAAATGGGG
TTTGCTTTATACCTCTGGATGGATTACAGAAAGAGGAGGATTTTCAAATTTAATTCTACCCATAATAACTCTTAGC
ATGCCCAACGTAGCTATTTTCGCAAGAATAATCAGAGGATCAATGCTAGAAATAATACAAAGCGACTTTATAAGAA
CTGCGCGTGCAAAAGGGCTAAGCTTCAAAAAGATAGTTATAAAGCATATGTTAAGAGGAGCAATGTTGCCTGTAGT
AAGCTATATAGGTCCAGCATTTGCTGCTATAATATCTGGAAGCGTGGTTATTGAAAAAATATTTAGAATTGCTGGA
ATGGGAATGTTTATAACAGAATCCGCACTAAACAGAGATTACCCAGTATTAATGGGCGGATTGTTAGTATATTCAA
TAATACTGCTTATTTCTATATTAATATCAGATATTATATATAAAATATTAGATCCAAGAGTATAA

f607.aa

MKYIKIALMLIIFSLIACISNAKKEKIVFRVSNLSEPSSLDPQLSTDLYGSNIITNLFLGLAVKDSQTGKYKPGLA
KSWNISEDGIIYTFNLREDIVWSDGVAITAEEIKKSYLRILNKKTAAMYANLIKSTIKNAQEYFDETVPESELGIK
AIDSKTLEITLTSPKPYFPDMLTHSAYIPVPMHIVEKYGENWTNPENIVVSGAYKLKERSINDKIVIEKNEKYYNA
KNVEIDEVIFYPTEGSVAYNMYINGELDFLQGAEKNNLEEIKIRDDYYSGLKNGMAYIAFNTTIKPLDNLKVRQAI
SLAIDRETLTKVVLKGSSDPTRNLTPKFDDYSYGKNLILFDPENAKKLLAEAGYPDGKGFPTLKYKISEGRPTTAE

TABLE 1. Nucleotide and Amino Acid Sequences

FLQEQFKKILNINLEIENEEWTTFLGSRRTGNYQMSSVGWIGDYFDPLTFLDSLFTTENHFLGAYKYSNKEYDALI
KKSNFELDPIKRQDILRQAEEIIAEKDFPMAPLYIPKSHYLFRNDKWTGWVPNIAESYLYEDIKTKK

t607.aa

CISNAKKEKIVFRVSNLSEPSSLDPQLSTDLYGSNIITNLFLGLAVKDSQTGKYKPGLAKSWNISEDGIIYTFNLR
EDIVWSDGVAITAEEIKKSYLRILNKKTAAMYANLIKSTIKNAQEYFDETVPESELGIKAIDSKTLEITLTSPKPY
FPDMLTHSAYIPVPMHIVEKYGENWTNPENIVVSGAYKLKERSINDKIVIEKNEKYYNAKNVEIDEVIFYPTEGSV
AYNMYINGELDFLQGAEKNNLEEIKIRDDYYSGLKNGMAYIAFNTTIKPLDNLKVRQAISLAIDRETLTKVVLKGS
SDPTRNLTPKFDDYSYGKNLILFDPENAKKLLAEAGYPDGKGFPTLKYKISEGRPTTAEFLQEQFKKILNINLEIE
NEEWTTFLGSRRTGNYQMSSVGWIGDYFDPLTFLDSLFTTENHFLGAYKYSNKEYDALIKKSNFELDPIKRQDILR
QAEEIIAEKDFPMAPLYIPKSHYLFRNDKWTGWVPNIAESYLYEDIKTKK

f607.nt

ATGAAATATATAAAAATAGCCTTAATGCTAATAATTTTTTCTTTAATAGCATGTATTAGTAATGCTAAAAAAGAAA
AAATAGTTTTCAGAGTATCAAACTTAAGCGAGCCATCATCACTTGATCCTCAACTCTCAACAGACCTTTACGGTAG
CAACATTATTACAAACCTATTCTTAGGCCTAGCGGTAAAAGATTCTCAAACTGGAAAATATAAACCAGGACTTGCA
AAAAGTTGGAATATTTCTGAAGATGGAATTATTTACACATTTAACCTAAGAGAAGATATAGTTTGGAGCGATGGAG
TTGCCATTACTGCCGAGGAGATAAAAAAATCATACCTAAGAATTTTAAATAAAAAAACAGCTGCAATGTATGCTAA
TTTAATAAAATCTACAATAAAAAATGCACAAGAATATTTCGATGAGACAGTGCCTGAATCTGAGCTTGGCATAAAG
GCTATTGACAGCAAAACCTTAGAGATAACATTAACATCTCCAAAGCCTTATTTTCCTGATATGCTAACACACTCAG
CATACATACCAGTTCCAATGCATATTGTTGAAAAATATGGAGAAAATTGGACAAATCCTGAAAATATAGTTGTTAG
TGGCGCATACAAACTTAAAGAAAGATCAATTAACGATAAAATCGTAATAGAAAAAAATGAAAAATACTATAATGCA
AAAAATGTAGAAATTGATGAAGTAATATTTTACCCAACAGAAGGTAGCGTGGCTTACAATATGTACATAAACGGTG
AACTCGATTTTCTACAAGGAGCAGAAAAGAATAATTTAGAAGAAATTAAAATAAGAGATGATTATTATTCTGGGTT
AAAAAACGGAATGGCATACATAGCATTCAATACAACAATAAAACCACTAGACAATTTAAAAGTTAGACAAGCCATC
TCCCTTGCCATTGACAGAGAAACTTTAACTAAAGTAGTTTTAAAGGGAAGTTCAGATCCAACAAGAAATCTAACTC
CAAAATTTGATGATTATTCTTATGGAAAAAATTTAATACTATTTGATCCTGAGAATGCAAAAAAACTTTTAGCTGA
AGCTGGATATCCGGATGGGAAAGGATTCCCCACATTAAAATATAAAATATCGGAGGGAAGACCAACAACAGCAGAA
TTTTTGCAAGAACAATTTAAAAAAATACTAAACATTAACTTAGAAATCGAGAATGAAGAATGGACAACATTCCTAG
GAAGCAGAAGAACTGGAAATTACCAAATGTCAAGCGTGGGGTGGATAGGAGATTATTTTGATCCCTTAACATTCTT
AGACAGCTTATTTACAACAGAAAATCATTTTTTAGGAGCGTACAAATATTCAAACAAAGAGTATGATGCTTTAATA
AAAAAATCTAATTTTGAACTTGATCCAATAAAAAGACAAGACATTTTAAGACAAGCTGAAGAGATAATAGCAGAAA
AAGACTTTCCTATGGCACCTTTATATATACCCAAATCTCATTATCTTTTCAGAAATGATAAATGGACAGGGTGGGT
ACCAAATATCGCAGAAAGCTATTTATATGAAGATATTAAAACTAAAAAATAA

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TGTATTAGTAATGCTAAAAAAGAAAAAATAGTTTTCAGAGTATCAAACTTAAGCGAGCCATCATCACTTGATCCTC
AACTCTCAACAGACCTTTACGGTAGCAACATTATTACAAACCTATTCTTAGGCCTAGCGGTAAAAGATTCTCAAAC
TGGAAAATATAAACCAGGACTTGCAAAAAGTTGGAATATTTCTGAAGATGGAATTATTTACACATTTAACCTAAGA
GAAGATATAGTTTGGAGCGATGGAGTTGCCATTACTGCCGAGGAGATAAAAAAATCATACCTAAGAATTTTAAATA
AAAAAACAGCTGCAATGTATGCTAATTTAATAAAATCTACAATAAAAAATGCACAAGAATATTTCGATGAGACAGT
GCCTGAATCTGAGCTTGGCATAAAGGCTATTGACAGCAAAACCTTAGAGATAACATTAACATCTCCAAAGCCTTAT
TTTCCTGATATGCTAACACACTCAGCATACATACCAGTTCCAATGCATATTGTTGAAAAATATGGAGAAAATTGGA
CAAATCCTGAAAATATAGTTGTTAGTGGCGCATACAAACTTAAAGAAAGATCAATTAACGATAAAATCGTAATAGA
AAAAAATGAAAAATACTATAATGCAAAAAATGTAGAAATTGATGAAGTAATATTTTACCCAACAGAAGGTAGCGTG
GCTTACAATATGTACATAAACGGTGAACTCGATTTTCTACAAGGAGCAGAAAAGAATAATTTAGAAGAAATTAAAA
TAAGAGATGATTATTATTCTGGGTTAAAAAACGGAATGGCATACATAGCATTCAATACAACAATAAAACCACTAGA
CAATTTAAAAGTTAGACAAGCCATCTCCCTTGCCATTGACAGAGAAACTTTAACTAAAGTAGTTTTAAAGGGAAGT
TCAGATCCAACAAGAAATCTAACTCCAAAATTTGATGATTATTCTTATGGAAAAAATTTAATACTATTTGATCCTG
AGAATGCAAAAAAACTTTTAGCTGAAGCTGGATATCCGGATGGGAAAGGATTCCCCACATTAAAATATAAAATATC
GGAGGGAAGACCAACAACAGCAGAATTTTTGCAAGAACAATTTAAAAAAATACTAAACATTAACTTAGAAATCGAG
AATGAAGAATGGACAACATTCCTAGGAAGCAGAAGAACTGGAAATTACCAAATGTCAAGCGTGGGGTGGATAGGAG
ATTATTTTGATCCCTTAACATTCTTAGACAGCTTATTTACAACAGAAAATCATTTTTTAGGAGCGTACAAATATTC

TABLE 1. Nucleotide and Amino Acid Sequences

AAACAAAGAGTATGATGCTTTAATAAAAAAATCTAATTTTGAACTTGATCCAATAAAAAGACAAGACATTTTAAGA
CAAGCTGAAGAGATAATAGCAGAAAAAGACTTTCCTATGGCACCTTTATATATACCCAAATCTCATTATCTTTTCA
GAAATGATAAATGGACAGGGTGGGTACCAAATATCGCAGAAAGCTATTTATATGAAGATATTAAAACTAAAAAATA
A

f611.aa

MKKIFLFLFISFYLFGFEDSSLKIGIDDVYVEAHEEGFHLFIRKKPAIKSVILTESFEIPDKKKDVATYSFRTLSY
NKVNGDEIRILNGRVIKNKELLSLTSSTPVPNKKFGEAFHILIPKKLKYGFPNFSTRSGDIDLEVLKSKKEPFWFS
IRSFEKKYNDYLGRYQDNAYELLFKDDQNQGKIEFNELKDTFTKFSDEVVIANNGIDIVDKINKILKNSEDSVYDL
DLVLVVDVTDSMKSNIEILKEHLFSIIEPQLQKFKSYRIGLVFYKDYLEDFLTKAFDFNTIPYLNNILKYVNVGGG
GDYPEAVFEGIDAAVTQFDWRAERRFIIVIGDAPPHEYPRGSIVYKDVINSAKEKDITIYGIIFQ

t611.aa

FEDSSLKIGIDDVYVEAHEEGFHLFIRKKPAIKSVILTESFEIPDKKKDVATYSFRTLSYNKVNGDEIRILNGRVI
KNKELLSLTSSTPVPNKKFGEAFHILIPKKLKYGFPNFSTRSGDIDLEVLKSKKEPFWFSIRSFEKKYNDYLGRYQ
DNAYELLFKDDQNQGKIEFNELKDTFTKFSDEVVIANNGIDIVDKINKILKNSEDSVYDLDLVLVVDVTDSMKSNI
EILKEHLFSIIEPQLQKFKSYRIGLVFYKDYLEDFLTKAFDFNTIPYLNNILKYVNVGGGGDYPEAVFEGIDAAVT
QFDWRAERRFIIVIGDAPPHEYPRGSIVYKDVINSAKEKDITIYGIIFQ

f611.nt

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TTGATGATGTTTATGTTGAGGCTCATGAAGAGGGATTTCATCTTTTTATTAGAAAAAAACCTGCAATCAAATCAGT
AATATTGACAGAGTCTTTTGAAATTCCTGATAAGAAAAAAGATGTGGCTACTTATTCATTTCGTACATTAAGTTAT
AATAAGGTTAATGGAGATGAAATTCGGATTTTAAATGGAAGAGTTATTAAGAATAAAGAACTTTTATCATTGACAT
CTTCCACCCCTGTTCCTAATAAAAAGTTTGGAGAAGCTTTTCATATATTGATTCCAAAAAAATTAAAATATGGATT
TCCAAATTTTTCAACAAGAAGTGGTGATATTGACTTAGAAGTATTAAAAAGTAAAAAAGAGCCCTTTTGGTTTTCT
ATAAGATCTTTTGAGAAAAAATATAATGATTATTTGGGCAGATATCAAGACAATGCTTATGAATTGCTTTTCAAGG
ATGATCAAAATCAGGGAAAAATTGAATTTAATGAATTAAAAGATACTTTTACAAAATTTTCAGATGAGGTTGTTAT
TGCTAATAATGGCATTGATATTGTTGATAAAATAAACAAAATTTTAAAAAACTCAGAAGATTCAGTTTATGATTTA
GATTTAGTGCTTGTTGTTGATGTTACTGATAGTATGAAAAGCAATATTGAGATTCTAAAAGAGCATTTGTTTTCAA
TAATAGAACCTCAACTTCAAAAGTTTAAATCCTACAGAATAGGTCTTGTTTTTTATAAAGACTATCTTGAAGATTT
TTTAACCAAAGCTTTTGATTTTAATACTATTCCTTATTTAAATAATATTCTTAAGTATGTTAATGTTGGTGGCGGT
GGGGATTATCCAGAAGCTGTTTTTGAGGGGATTGATGCTGCTGTGACCCAATTTGATTGGCGGGCAGAAAGAAGGT
TTATTATTGTTATAGGAGATGCACCTCCTCATGAGTATCCAAGAGGGTCTATTGTTTATAAAGATGTTATCAATTC
TGCAAAGGAAAAAGATATTACAATTTATGGAATAATATTTCAGTAA

t611.nt

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TACTTATTCATTTCGTACATTAAGTTATAATAAGGTTAATGGAGATGAAATTCGGATTTTAAATGGAAGAGTTATT
AAGAATAAAGAACTTTTATCATTGACATCTTCCACCCCTGTTCCTAATAAAAAGTTTGGAGAAGCTTTTCATATAT
TGATTCCAAAAAAATTAAAATATGGATTTCCAAATTTTTCAACAAGAAGTGGTGATATTGACTTAGAAGTATTAAA
AAGTAAAAAAGAGCCCTTTTGGTTTTCTATAAGATCTTTTGAGAAAAAATATAATGATTATTTGGGCAGATATCAA
GACAATGCTTATGAATTGCTTTTCAAGGATGATCAAAATCAGGGAAAAATTGAATTTAATGAATTAAAAGATACTT
TTACAAAATTTTCAGATGAGGTTGTTATTGCTAATAATGGCATTGATATTGTTGATAAAATAAACAAAATTTTAAA
AAACTCAGAAGATTCAGTTTATGATTTAGATTTAGTGCTTGTTGTTGATGTTACTGATAGTATGAAAAGCAATATT
GAGATTCTAAAAGAGCATTTGTTTTCAATAATAGAACCTCAACTTCAAAAGTTTAAATCCTACAGAATAGGTCTTG
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TCTTAAGTATGTTAATGTTGGTGGCGGTGGGGATTATCCAGAAGCTGTTTTTGAGGGGATTGATGCTGCTGTGACC
CAATTTGATTGGCGGGCAGAAAGAAGGTTTATTATTGTTATAGGAGATGCACCTCCTCATGAGTATCCAAGAGGGT
CTATTGTTTATAAAGATGTTATCAATTCTGCAAAGGAAAAAGATATTACAATTTATGGAATAATATTTCAGTAA

TABLE 1. Nucleotide and Amino Acid Sequences

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MIFFRNSFMALIFSFSILSISYFFGDFFQFSYIKMISWRFILFLIMATGIATCAKSNSLNLGNEGQIYFGAFLVYI
FSSFFGLTYFNFVFLILLSSFFVGLLGLIPFFITFFFGLNKALTGLLISYGNQRLVDGFILNMLKTGSFSNQTKRI
NSLFALDSSLIYLFLLGVSVWLFYVFIHKKTIYGLQLEILSNKKKIDIFFNINEFKYKFFAVFGSAFLNGLAGSMF
VVFFRPYLVLGLTSGLGWSSLIVAVISGFNYVYVLFFSLLFSILIEFNNFLNINYDFKYEFIGLCQSIAIFISLFL
IKARKK

t617.aa

AKSNSLNLGNEGQIYFGAFLVYIFSSFFGLTYFNFVFLILLSSFFVGLLGLIPFFITFFFGLNKALTGLLISYGNQ
RLVDGFILNMLKTGSFSNQTKRINSLFALDSSLIYLFLLGVSVWLFYVFIHKKTIYGLQLEILSNKKKIDIFFNIN
EFKYKFFAVFGSAFLNGLAGSMFVVFFRPYLVLGLTSGLGWSSLIVAVISGFNYVYVLFFSLLFSILIEFNNFLNI
NYDFKYEFIGLCQSIAIFISLFLIKARKK

f617.nt

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ATTTTTTTCAATTTTCTTATATTAAAATGATATCTTGGCGCTTTATTTTATTTTTAATTATGGCTACGGGGATTGC
TACTTGTGCCAAGAGTAATTCATTAAATCTTGGGAATGAAGGTCAGATTTATTTTGGGGCATTTTTAGTTTATATA
TTTTCAAGTTTTTTTGGATTAACCTATTTTAATTTTGTATTTTTGATACTTTTAAGTTCTTTTTTTGTAGGACTTT
TGGGGCTTATCCCCTTTTTTATTACTTTTTTCTTCGGATTAAATAAAGCCTTAACAGGTCTTTTAATATCTTATGG
AAATCAAAGATTGGTGGATGGATTTATTTTAAATATGTTAAAAACAGGTAGTTTTTCTAATCAGACAAAAAGGATT
AATAGTTTGTTTGCTTTAGATTCATCACTTATTTACTTGTTTTTGCTTGGTGTATCAGTTTGGCTTTTTTATGTTT
TTATTCACAAAAAAACTATTTATGGTCTTCAGCTTGAAATATTAAGCAATAAAAAAAAGATAGACATTTTTTTCAA
TATAAATGAATTTAAATATAAGTTTTTCGCTGTATTTGGCAGTGCTTTTTTAAATGGTCTTGCAGGTTCTATGTTT
GTAGTGTTTTTTAGACCATATTTGGTTTTAGGGCTAACTTCAGGACTTGGTTGGAGTAGTCTAATTGTTGCTGTAA
TTTCAGGATTTAATTATGTTTATGTATTATTTTTTAGCTTATTGTTTTCAATATTAATTGAATTTAATAATTTTCT
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ATTAAAGCTAGGAAAAAGTAG

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GCCAAGAGTAATTCATTAAATCTTGGGAATGAAGGTCAGATTTATTTTGGGGCATTTTTAGTTTATATATTTTCAA
GTTTTTTTGGATTAACCTATTTTAATTTTGTATTTTTGATACTTTTAAGTTCTTTTTTTGTAGGACTTTTGGGGCT
TATCCCCTTTTTTATTACTTTTTTCTTCGGATTAAATAAAGCCTTAACAGGTCTTTTAATATCTTATGGAAATCAA
AGATTGGTGGATGGATTTATTTTAAATATGTTAAAAACAGGTAGTTTTTCTAATCAGACAAAAAGGATTAATAGTT
TGTTTGCTTTAGATTCATCACTTATTTACTTGTTTTTGCTTGGTGTATCAGTTTGGCTTTTTTATGTTTTTATTCA
CAAAAAAACTATTTATGGTCTTCAGCTTGAAATATTAAGCAATAAAAAAAAGATAGACATTTTTTTCAATATAAAT
GAATTTAAATATAAGTTTTTCGCTGTATTTGGCAGTGCTTTTTTAAATGGTCTTGCAGGTTCTATGTTTGTAGTGT
TTTTTAGACCATATTTGGTTTTAGGGCTAACTTCAGGACTTGGTTGGAGTAGTCTAATTGTTGCTGTAATTTCAGG
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AATTATGACTTTAAGTATGAATTTATTGGGCTTTGTCAATCAATTGCTATTTTTATCTCTTTATTTTTGATTAAAG
CTAGGAAAAAGTAG

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MVVEINSLRTCYLLVLLLLVAYGLVVFYTSSFFLSLELTGNPNFLFFTRLNYLFLSFMVFLVFERISLNFLKKSIF
PVLIITLFLIMATFLSPSISGAKRWIFFQGVSIQPSEIFKISFTIYLSAYLSKFDPRKNNGISYWIKPMLIFAIFW
VLIILQNDYSTAIYFAILFFIVLFVSNMAFSYVFAIVVTFLPVSAIFLMLEPYRVSRIFAFLNPYDDPSGKGYQII
ASLNALKSGGILGKGLGMGEVKLGKLPEANSDFIFSVLGEELGFLGVLFAISLFFLFFYFGYFIAIHSNSRFKFFI
AFISSLAIFLQSMMNILIAIGLLPPTGINLPFFSSGGSSIIVTMALSGLISNVSKNLSNN

t631.aa

TABLE 1. Nucleotide and Amino Acid Sequences

RISLNFLKKSIFPVLIITLFLIMATFLSPSISGAKRWIFFQGVSIQPSEIFKISFTIYLSAYLSKFDPRKNNGISY
WIKPMLIFAIFWVLIILQNDYSTAIYFAILFFIVLFVSNMAFSYVFAIVVTFLPVSAIFLMLEPYRVSRIFAFLNP
YDDPSGKGYQIIASLNALKSGGILGKGLGMGEVKLGKLPEANSDFIFSVLGEELGFLGVLFAISLFFLFFYFGYFI
AIHSNSRFKFFIAFISSLAIFLQSMMNILIAIGLLPPTGINLPFFSSGGSSIIVTMALSGLISNVSKNLSNN

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ATGGTTGTAGAGATAAATTCACTTAGGACATGTTATTTGCTTGTTTTGCTGCTATTGGTAGCCTATGGCCTTGTAG
TTTTTTATACTTCTTCCTTTTTTCTAAGCTTAGAATTGACAGGTAATCCAAATTTTTTATTTTTCACAAGACTTAA
TTATCTTTTTTTAAGTTTTATGGTTTTTCTTGTTTTTGAAAGGATTTCTTTAAATTTTTTAAAAAAATCAATATTT
CCTGTATTGATTATAACTCTTTTTTTAATTATGGCAACTTTTTTATCTCCAAGTATTTCTGGAGCAAAGAGATGGA
TATTCTTTCAAGGTGTTAGCATTCAACCTTCTGAGATTTTTAAAATATCTTTTACTATTTATCTTTCAGCTTATTT
GAGCAAGTTTGACCCAAGAAAAAACAATGGTATTTCATACTGGATAAAGCCAATGTTGATTTTTGCAATTTTTTGG
GTGTTAATAATTTTGCAAAACGATTATTCAACAGCTATTTATTTTGCCATTCTTTTTTTTATTGTTTTGTTTGTTT
CTAATATGGCATTTAGCTATGTTTTTGCTATTGTGGTTACTTTTTTACCAGTTTCTGCTATATTCTTGATGCTTGA
ACCTTATAGGGTTTCTAGAATTTTTGCCTTTCTCAATCCTTACGATGATCCTTCTGGCAAAGGTTACCAGATAATA
GCATCTCTTAATGCTTTAAAAAGTGGAGGAATTTTAGGTAAAGGGCTGGGAATGGGAGAGGTAAAACTTGGAAAAT
TACCAGAGGCCAATTCGGATTTTATTTTTTCAGTTCTTGGAGAAGAATTAGGATTTTTAGGGGTTTTGTTTGCTAT
AAGCTTGTTTTTTTTGTTTTTTTACTTTGGTTATTTTATAGCTATTCATTCTAATAGTAGGTTTAAATTTTTTATT
GCATTTATTTCAAGTCTTGCAATTTTTCTTCAAAGCATGATGAATATTTTAATTGCAATCGGTCTTTTGCCTCCTA
CAGGGATAAATTTACCATTTTTTTCATCTGGGGGATCTTCTATTATTGTTACCATGGCATTGTCTGGCCTTATTTC
AAATGTTTCAAAAAATTTAAGTAATAATTGA

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AGGATTTCTTTAAATTTTTTAAAAAAATCAATATTTCCTGTATTGATTATAACTCTTTTTTTAATTATGGCAACTT
TTTTATCTCCAAGTATTTCTGGAGCAAAGAGATGGATATTCTTTCAAGGTGTTAGCATTCAACCTTCTGAGATTTT
TAAAATATCTTTTACTATTTATCTTTCAGCTTATTTGAGCAAGTTTGACCCAAGAAAAAACAATGGTATTTCATAC
TGGATAAAGCCAATGTTGATTTTTGCAATTTTTTGGGTGTTAATAATTTTGCAAAACGATTATTCAACAGCTATTT
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TACGATGATCCTTCTGGCAAAGGTTACCAGATAATAGCATCTCTTAATGCTTTAAAAAGTGGAGGAATTTTAGGTA
AAGGGCTGGGAATGGGAGAGGTAAAACTTGGAAAATTACCAGAGGCCAATTCGGATTTTATTTTTTCAGTTCTTGG
AGAAGAATTAGGATTTTTAGGGGTTTTGTTTGCTATAAGCTTGTTTTTTTTGTTTTTTTACTTTGGTTATTTTATA
GCTATTCATTCTAATAGTAGGTTTAAATTTTTTATTGCATTTATTTCAAGTCTTGCAATTTTTCTTCAAAGCATGA
TGAATATTTTAATTGCAATCGGTCTTTTGCCTCCTACAGGGATAAATTTACCATTTTTTTCATCTGGGGGATCTTC
TATTATTGTTACCATGGCATTGTCTGGCCTTATTTCAAATGTTTCAAAAAATTTAAGTAATAATTGA

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MKVNNFLSFFFRAFFLLFLIVILFFFVLFFIDFIGMYNTKRYFPEFVRTKLLGETSLVFDHNSNIILDEARLVKER
EAIDIKNQQIEKLKEDLKLKEDSLNKLEFELKQKQKDLDLKQKIIDDIINKYNDEEANILQTAVYLMNMPPEDAVK
RLEDLNPELAISYMRKIEELSKKEGRLSIVPYWLSLMDSKKAAILIRKMSVSSLE

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IDFIGMYNTKRYFPEFVRTKLLGETSLVFDHNSNIILDEARLVKEREAIDIKNQQIEKLKEDLKLKEDSLNKLEFE
LKQKQKDLDLKQKIIDDIINKYNDEEANILQTAVYLMNMPPEDAVKRLEDLNPELAISYMRKIEELSKKEGRLSIV
PYWLSLMDSKKAAILIRKMSVSSLE

f647.nt

ATGAAAGTGAATAATTTTTTATCGTTCTTTTTTAGGGCATTTTTTTTGTTATTTTTAATTGTTATTTTATTTTTCT
TTGTATTATTCTTTATTGATTTTATTGGAATGTATAATACTAAAAGATATTTCCCCGAATTTGTAAGAACCAAGTT
GTTAGGAGAAACTTCTCTGGTCTTTGATCATAATTCTAATATAATTCTTGATGAAGCTAGACTTGTGAAGGAAAGA
GAAGCTATTGATATTAAGAATCAGCAGATTGAAAAGCTTAAAGAAGATCTAAAGTTAAAAGAAGACAGTTTAAATA

TABLE 1. Nucleotide and Amino Acid Sequences

AGCTTGAATTTGAGCTTAAGCAAAAGCAGAAAGATTTAGATTTAAAACAAAAAATAATAGATGACATTATAAATAA
ATATAATGATGAGGAAGCAAATATTTTGCAAACAGCTGTATATTTAATGAATATGCCACCAGAAGATGCTGTTAAG
CGGCTTGAAGATTTAAATCCCGAGCTTGCAATATCTTATATGCGGAAAATTGAAGAGCTTTCCAAAAAAGAAGGTC
GTTTATCAATTGTTCCTTATTGGTTATCTCTTATGGATTCTAAAAAAGCTGCTATATTGATTAGAAAAATGTCTGT
TAGTTCATTGGAGTAG

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ATTGATTTTATTGGAATGTATAATACTAAAAGATATTTCCCCGAATTTGTAAGAACCAAGTTGTTAGGAGAAACTT
CTCTGGTCTTTGATCATAATTCTAATATAATTCTTGATGAAGCTAGACTTGTGAAGGAAAGAGAAGCTATTGATAT
TAAGAATCAGCAGATTGAAAAGCTTAAAGAAGATCTAAAGTTAAAAGAAGACAGTTTAAATAAGCTTGAATTTGAG
CTTAAGCAAAAGCAGAAAGATTTAGATTTAAAACAAAAAATAATAGATGACATTATAAATAAATATAATGATGAGG
AAGCAAATATTTTGCAAACAGCTGTATATTTAATGAATATGCCACCAGAAGATGCTGTTAAGCGGCTTGAAGATTT
AAATCCCGAGCTTGCAATATCTTATATGCGGAAAATTGAAGAGCTTTCCAAAAAAGAAGGTCGTTTATCAATTGTT
CCTTATTGGTTATCTCTTATGGATTCTAAAAAAGCTGCTATATTGATTAGAAAAATGTCTGTTAGTTCATTGGAGT
AG

f653.aa

MLTYGDMVTLLLVFFVTMFSLNDIIFQENVIRIMSASFTGAGFFKGGKTLDFSKLSYLSNSFMSLPSTVRNKQASQ
TAKNKSMIEFIEKIQSKNIVVRQEERGIVISLAADAFFDSASADVKLEENRDSIQKIASFIGFLSPRGYNFKIEGH
TDNIDTDVNGPWKSNWELSAARSVNMLEHILNYLDQSDVKRIENNFEVSGFGGSRPIATDDTPEGRAYNRRIDILI
TTDASLSFPKEIKQ

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NDIIFQENVIRIMSASFTGAGFFKGGKTLDFSKLSYLSNSFMSLPSTVRNKQASQTAKNKSMIEFIEKIQSKNIVV
RQEERGIVISLAADAFFDSASADVKLEENRDSIQKIASFIGFLSPRGYNFKIEGHTDNIDTDVNGPWKSNWELSAA
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f653.nt

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ACTACAGATGCATCTTTAAGTTTCCCTAAGGAAATTAAGCAGTAA

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AATGATATTATTTTTCAAGAAAATGTGATAAGAATAATGTCTGCTTCTTTCACGGGTGCTGGATTTTTCAAGGGCG
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ACAAGCATCTCAGACTGCTAAAAATAAATCCATGATTGAATTTATTGAGAAGATTCAGTCTAAAAATATTGTAGTT
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TTGAAGAGAATAGAGATTCTATTCAAAAAATAGCATCTTTTATTGGCTTTTTAAGTCCTAGAGGCTATAATTTTAA
AATAGAAGGGCATACAGATAATATTGATACTGATGTAAATGGACCTTGGAAAAGCAATTGGGAACTTTCGGCTGCT
AGATCTGTTAATATGCTGGAACATATTTTGAACTATTTAGATCAATCTGATGTTAAAAGAATTGAAAATAATTTTG
AAGTATCTGGTTTTGGTGGAAGTAGGCCTATTGCAACAGACGATACCCCTGAGGGTAGGGCTTATAATAGAAGAAT
TGATATATTAATTACTACAGATGCATCTTTAAGTTTCCCTAAGGAAATTAAGCAGTAA

f664.aa

TABLE 1. Nucleotide and Amino Acid Sequences

MRMSVYTMGFAYIRSIMGYVVLFFFASLAVNFFVNIIQVGFFITFKSLEPRWDKISFNFSRWAKNSFFSAGAFFNL
FKSLLKVVIICLIYYFIIENNIGKISKLSEYTLQSGISIVLVIAYKICFFSVMFLAIVGVFDYLFQRSQYIESLKM
TKEEVKQERKEMEGDPLLRSRIKERMRVILSTNLRVAIPQADVVITNPEHFAVAIKWDSETMLAPKVLAKGQDEIA
LTIKKIARENNVPLMENKLLARALYANVKVNEEIPREYWEIVSKILVRVYSITKKFN

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FVNIIQVGFFITFKSLEPRWDKISFNFSRWAKNSFFSAGAFFNLFKSLLKVVIICLIYYFIIENNIGKISKLSEYT
LQSGISIVLVIAYKICFFSVMFLAIVGVFDYLFQRSQYIESLKMTKEEVKQERKEMEGDPLLRSRIKERMRVILST
NLRVAIPQADVVITNPEHFAVAIKWDSETMLAPKVLAKGQDEIALTIKKIARENNVPLMENKLLARALYANVKVNE
EIPREYWEIVSKILVRVYSITKKFN

f664.nt

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CATCTTTAGCTGTTAATTTTTTTGTTAATATTATTCAAGTAGGCTTTTTTATTACTTTTAAATCTTTGGAGCCAAG
GTGGGATAAAATTAGTTTTAATTTTTCCAGATGGGCAAAAAATTCTTTTTTTTTCAGCAGGGGCTTTTTTCAATTTG
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CTAAGCTTTCGGAGTATACACTTCAATCTGGAATTTCTATTGTGTTAGTGATTGCCTATAAGATATGTTTTTTTC
AGTAATGTTTTTGGCAATTGTAGGGGTGTTTGATTATTTGTTTCAAAGATCTCAGTACATTGAGAGTTTGAAAATG
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CTAATGTTAAGGTTAATGAAGAGATTCCAAGAGAATATTGGGAGATTGTTTCAAAAATTCTTGTGAGAGTATATTC
TATTACTAAAAAGTTTAATTAG

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TTTGTTAATATTATTCAAGTAGGCTTTTTTATTACTTTTAAATCTTTGGAGCCAAGGTGGGATAAAATTAGTTTTA
ATTTTTCCAGATGGGCAAAAAATTCTTTTTTTTTCAGCAGGGGCTTTTTTCAATTTGTTTAAAAGTTTGTTAAAAGT
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CTTCAATCTGGAATTTCTATTGTGTTAGTGATTGCCTATAAGATATGTTTTTTTCAGTAATGTTTTTGGCAATTG
TAGGGGTGTTTGATTATTTGTTTCAAAGATCTCAGTACATTGAGAGTTTGAAAATGACAAAAGAAGAGGTAAAGCA
GGAAAGAAAGGAAATGGAAGGTGATCCTTTACTTCGATCTAGAATAAAAGAGAGAATGAGGGTTATTTTAAGTACC
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ATAGCGAAACAATGTTAGCTCCAAAGGTGCTTGCAAAAGGTCAAGATGAAATAGCTCTCACAATTAAAAAAATTGC
AAGAGAAAATAATGTTCCTTTAATGGAAAATAAGCTCCTTGCAAGAGCTCTTTATGCTAATGTTAAGGTTAATGAA
GAGATTCCAAGAGAATATTGGGAGATTGTTTCAAAAATTCTTGTGAGAGTATATTCTATTACTAAAAAGTTTAATT
AG

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MFTLSFVLINFIITGILILMLEFNFLKVDFKGNILLAGIFMGLMQGLGALPGISRSGITIFSASVIGFNRKSAFEI
SFLSLIPIVFGAILLKHKEFYDIFMVLNFFEINLGALVAFVVGIFSINFFFKMLNNKKLYYFSIYLFALSIIVCYF
VRI

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ITGILILMLEFNFLKVDFKGNILLAGIFMGLMQGLGALPGISRSGITIFSASVIGFNRKSAFEISFLSLIPIVFGA
ILLKHKEFYDIFMVLNFFEINLGALVAFVVGIFSINFFFKMLNNKKLYYFSIYLFALSIIVCYFVRI

f680.nt

TABLE 1. Nucleotide and Amino Acid Sequences

ATGTTTACATTGTCTTTCGTTTTAATTAATTTTATTATAACAGGGATTTTAATCTTGATGCTAGAATTTAATTTTT
TAAAAGTTGATTTTAAAGGTAATATTTTGTTAGCAGGAATTTTTATGGGGCTGATGCAAGGCTTGGGTGCGCTTCC
AGGAATCTCTCGTTCAGGAATTACGATCTTTTCGGCATCGGTTATTGGATTTAATAGAAAAAGTGCATTTGAAATT
TCATTTTTATCTTTAATTCCAATAGTTTTTGGAGCGATTTTATTAAAACATAAAGAATTTTATGATATTTTTATGG
TTTTAAATTTTTTTGAAATAAACTTAGGAGCATTAGTTGCTTTTGTTGTTGGTATTTTCTCAATAAATTTCTTTTT
TAAAATGCTTAATAACAAAAAACTGTATTATTTTTCTATATATTTATTTGCACTTTCAATTATAGTTTGTTATTTT
GTTAGAATATGA

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ATAACAGGGATTTTAATCTTGATGCTAGAATTTAATTTTTTAAAAGTTGATTTTAAAGGTAATATTTTGTTAGCAG
GAATTTTTATGGGGCTGATGCAAGGCTTGGGTGCGCTTCCAGGAATCTCTCGTTCAGGAATTACGATCTTTTCGGC
ATCGGTTATTGGATTTAATAGAAAAAGTGCATTTGAAATTTCATTTTTATCTTTAATTCCAATAGTTTTTGGAGCG
ATTTTATTAAAACATAAAGAATTTTATGATATTTTTATGGTTTTAAATTTTTTTGAAATAAACTTAGGAGCATTAG
TTGCTTTTGTTGTTGGTATTTTCTCAATAAATTTCTTTTTTAAAATGCTTAATAACAAAAAACTGTATTATTTTTC
TATATATTTATTTGCACTTTCAATTATAGTTTGTTATTTTGTTAGAATATGA

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MIVLLISIGCANAVHIINEIFKLIKKEQLSKESIKATIKKLKTPILLTSFTTAFGFLSLTTSSINAYKTMGIFMSI
GVIISMIISLTVLPGIITLIPFAKKKSFEKEKENKLNKISFLERLAKLNTQITKSILKRKYTSSIMVLIIILGISFV
GLLKIEINFDEKDYFKESTSVKKTLNLMQKEMGGISIFKIEIEGRPGEFKNAKAMQILDLITDKLDAFSAKTQSSS
INGILKFTNFKIKKESPLEYKLPENKIILNKLINLIDKSDWTKDNKRMYINDDWSLISIIVRIEDNSTEGIKKFEK
YAINTINEYMKNNKYHFSGVYDKVLIAKTMVKEQVINIITTLGSITLLLMFFFKSIKTGIIIAIPVAWSVFLNFAV
MRLFGITLNPATATIASVSMGVGVDYSIHFFNTFILQYQKNQIYKTALLESIPNVFNGIFANSISVGIGFLTLTFS
SYKIISTLGAIIAFTMLTTSLASLTLLPLLIYLFKPRVKLASNNNFKKLKQZ

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YKTMGIFMSIGVIISMIISLTVLPGIITLIPFAKKKSFEKEKENKLNKISFLERLAKLNTQITKSILKRKYTSSIM
VLIIILGISFVGLLKIEINFDEKDYFKESTSVKKTLNLMQKEMGGISIFKIEIEGRPGEFKNAKAMQILDLITDKLD
AFSAKTQSSSINGILKFTNFKIKKESPLEYKLPENKIILNKLINLIDKSDWTKDNKRMYINDDWSLISIIVRIEDN
STEGIKKFEKYAINTINEYMKNNKYHFSGVYDKVLIAKTMVKEQVINIITTLGSITLLLMFFFKSIKTGIIIAIPV
AWSVFLNFAVMRLFGITLNPATATIASVSMGVGVDYSIHFFNTFILQYQKNQIYKTALLESIPNVFNGIFANSISV
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f688.nt

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TABLE 1. Nucleotide and Amino Acid Sequences

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ATAA

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CCTTGAAAGACTTGCCAAACTAAATACGCAAATAACAAAATCTATATTAAAAAGAAAATATACATCCTCTATAATG
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AAGAAAGCACAAGTGTAAAAAAAACATTAAACCTAATGCAAAAAGAAATGGGGGAATATCGATTTTCAAAATAGA
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GCATTTTCTGCAAAAACTCAATCTAGTTCTATTAATGGCATTTTAAAATTTACAAATTTTAAAATTAAAAAAGAAT
CCCCACTAGAGTATAAACTGCCTGAAAATAAAATTATACTAAACAAACTAATAAATTTGATAGATAAAAGCGATTG
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TCAAATCTACAAAACTGCACTTCTTGAATCAATACCCAATGTATTTAATGGAATATTTGCAAATTCTATTTCTGTT
GGAATAGGATTTTTAACTCTAACATTTTCGTCTTATAAAATAATATCAACTCTTGGAGCAATAATTGCTTTTACAA
TGCTAACGACATCTCTTGCATCACTAACTCTTCTTCCATTATTAATTTATTTATTTAAACCTAGAGTAAAGCTAGC
CTCAAACAACAATTTTAAAAAATTAAAACAATAA

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VPIIGPIIGAILGATIYEFTLKNNKD

t704.aa

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PKWIEMDPGLENTQGIMATFPAVPGFLPGFIDQIFGTFLLMFLISVVGDFTKKHSDNPFIPFIVGAVVLSIGISFG
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f704.nt

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ACTAA

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TABLE 1. Nucleotide and Amino Acid Sequences

AAAACTTTTACATTACATTGTAGCACAAATATTAGGAGCTTTTACAGGTGCATTAATGACACTTGTCGTATTTTAT
CCTAAATGGATAGAAATGGATCCTGGCTTAGAAAATACTCAAGGAATAATGGCAACTTTCCCTGCTGTTCCTGGAT
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ATCACGGATTTAACAATCTAAGTATAGTTATTGTACCAATAATTGGCCCAATAATTGGAGCAATTTTGGGAGCTAC
AATTTACGAATTTACACTAAAAAATAACAAAG
ACTAA

f707.aa

MRRLFLLYILCSFVFLNLFAQGSSSYIDKQKELAIFYYEVGQRYINVGKIKKGKLFQAKALKIYPDLKKGFDIKLA
VKELDARIKDDNPKVVMLEDIKLEEIPGIVHEKIEINDFTNAPKIEYIAQRERSKNQDKIIKFQFGKFARALISRN
FDLFDSVIADKVNVMGQFESKNDFISTLSSASSKADADELEYLSVDDYYDLKSLKISKSNDTSFAVNVNAKKNDVT
KNFPFWKERQTLIFTTEDDNNWFLSSINZ

t707.aa

MRRLFLLYILCSFVFLNLFAQGSSSYIDKQKELAIFYYEVGQRYINVGKIKKGKLFQAKALKIYPDLKKGFDIKLA
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FDLFDSVIADKVNVMGQFESKNDFISTLSSASSKADADELEYLSVDDYYDLKSLKISKSNDTSFAVNVNAKKNDVT
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CCATAAATTGA

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AAAAAATGATGTTACTAAAAATTTTCCATTTTGGAAAGAACGTCAAACTTTAATTTTTACTACAGAGGATGATAAT
AATTGGTTTTTGTCTTCCATAAATTGA

f709.aa

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YAANFVGNEILYFDVNNNVNALVKDGFSYLKSPYDVIEANNLLYVTLYSSDEIGVYDKVLGVKRKSIGNKGTKDGE
LLAPQYMAIDKRNYIYVSEWGNKRVSKFGLEGDFILHFGSRTSGYKGLLGPTGVTYLNENIYVADSLRNTIEVFDT

TABLE 1. Nucleotide and Amino Acid Sequences

SGNHLYSVFTSIEGIEGLSSDFVGNNVIVSSKDGVYKYSIAKKTITKILKADKMNSKISSSILDANNQMIVSDFNN
AKVSVYKSDASLYDSLNVDVRRIIRLGGPKIYVELNVSSKSGLPVVGLKSENFSISNENYYIVNPKVAYNVNASKD
INIAVVFDKSSYMKKYDTDQIVGLNALMELSKNKNFSFINATSVPIIDNIESLTNSIRNTSSLGPYSTDAVKTDVS
LKLAGSGLMSKSSRRAVVYFSGGILNRKAFEKYSLDTIVSYYKNNDIRFYLILFGNDPINSKLQYLVNETGGAVIP
FSSYEGVSKVYDLILEQKTGTYLLEYYYPGPQEPNKYFNLSVEANINQQTGRGEFAYFIN

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QGIVTNKDAQEEFKWALNSYNNGIYDDALLSFKKILSFDPNNLDYHFWTGNVYYRLGYVEEALMEWRNLKDQGYKV
PYLRHLISTIEQRRGIFSNYELNFKKLVKVASLDNSIYKRPHGYQITSLRADKYGGYYAANFVGNEILYFDVNNNV
NALVKDGFSYLKSPYDVIEANNLLYVTLYSSDEIGVYDKVLGVKRKSIGNKGTKDGELLAPQYMAIDKRNYIYVSE
WGNKRVSKFGLEGDFILHFGSRTSGYKGLLGPTGVTYLNENIYVADSLRNTIEVFDTSGNHLYSVFTSIEGIEGLS
SDFVGNNVIVSSKDGVYKYSIAKKTITKILKADKMNSKISSSILDANNQMIVSDFNNAKVSVYKSDASLYDSLNVD
VRRIIRLGGPKIYVELNVSSKSGLPVVGLKSENFSISNENYYIVNPKVAYNVNASKDINIAVVFDKSSYMKKYDTD
QIVGLNALMELSKNKNFSFINATSVPIIDNIESLTNSIRNTSSLGPYSTDAVKTDVSLKLAGSGLMSKSSRRAVVY
FSGGILNRKAFEKYSLDTIVSYYKNNDIRFYLILFGNDPINSKLQYLVNETGGAVIPFSSYEGVSKVYDLILEQKT
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f709.nt

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AACTTGTAAAAGTTGCTTCTCTTGATAATTCTATTTATAAAAGGCCACATGGGTACCAGATTACATCTTTAAGGGC
TGATAAGTACGGCGGATATTACGCTGCTAACTTTGTAGGCAATGAAATATTGTATTTTGATGTTAATAACAATGTT

TABLE 1. Nucleotide and Amino Acid Sequences

AATGCTTTAGTTAAAGATGGCTTTAGTTATTTAAAATCACCTTATGATGTTATTGAAGCTAATAATCTGCTTTATG
TGACTCTTTATTCAAGTGATGAAATTGGTGTTTATGACAAAGTTCTTGGAGTTAAAAGGAAATCTATTGGGAATAA
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DIQTLVGAMLLTLGIGIQNIPEGAAISLPLRRGNVALAKCFNYGQMSGLVEIVGGLMGAYAVYSFTRILPFALAFS
AGAMIYVSIEQLIPEAKRKDIDNKVPSIFGVIGFTLMMFLDVSLGZ

t730.aa

AVFFFRKVDNKIMDAMLGFSAGIMIAASFFSLIQPAIERAEELGYITWVPAVFGFLVGAFFIYIVDVFVPDLDKLT
FIDEDLTKHGKKDFLLFTAVTLHNFPEGLAVGVAFGALASNPDIQTLVGAMLLTLGIGIQNIPEGAAISLPLRRGN
VALAKCFNYGQMSGLVEIVGGLMGAYAVYSFTRILPFALAFSAGAMIYVSIEQLIPEAKRKDIDNKVPSIFGVIGF
TLMMFLDVSLGZ

f730.nt

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CAAGTATATTTGGTGTTATTGGTTTTACATTAATGATGTTTCTCGATGTTTCACTAGGTTAA

t730.nt

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TABLE 1. Nucleotide and Amino Acid Sequences

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f197.aa

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NNMDFGHSEANTNYFKKAVEDYRQNQLKFIGWYSNLSEGISAEVAIRSKQSEKKAFAIIVPVYSPEDKLVCGYLAG
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DRILLSEMGEDCYYAMLPISSKLGEKSGVLIARLPYKDIYGVISSLRFQYILYSVLGIIALSIVLSIRIDRIISFR
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SEGSSKQSDQIAQFKMALDQVGEVVQSSASSSEQLSSMSDKMLEKSKELRKSVLFFKIKDSKIENPENDDYDFRLI
DCPENSFKDENQNLKSNGISTSNASGHNNYSLDIESESSVRTINKRVDPKKAIDIADKDLNFDDDFSEF

t197.aa

VLCGYLEDYYKQLTRAQVRRAAFSLQSFLDTLHVIINGAASNLALETISEFAMSENRGKDFSESELIDLRKNPKFV
IDSVKVSKKYRQYLYNFMANLKNDTLFEEFAFFDFEGRVIVSTRHENNMDFGHSEANTNYFKKAVEDYRQNQLKFI
GWYSNLSEGISAEVAIRSKQSEKKAFAIIVPVYSPEDKLVCGYLAGYLLNDIVADSFDRFRFGFYKRGNFIYVDPN
NIAVNPFEEYNETSRVSSKFLNVLKDVFSKPPFPSNIASEVSVYTIDRILLSEMGEDCYYAMLPISSKLGEKSGVL
IARLPYKDIYGVISSLRFQYILYSVLGIIALSIVLSIRIDRIISFRLNAIRVLVQDMVKGNLDKDYALDDDENTLD
ELGMLSLQVVKMKKAISVAISSVLRNISYVNKASLEVASSSQNLSSSALQQASALEEMSANVEQIASGVNMSANNS
YETEQIALKTNENSQIGGRAVEESVIAMQDIVEKVSVIEEIARKTNLLALNAAIEAARAGDEGKGFAVVASEIRKL
ADLSKISALEIGELVEDNSKVATEAGVIFKEMLPEIEETANLVKKISEGSSKQSDQIAQFKMALDQVGEVVQSSAS
SSEQLSSMSDKMLEKSKELRKSVLFFKIKDSKIENPENDDYDFRLIDCPENSFKDENQNLKSNGISTSNASGHNNY
SLDIESESSVRTINKRVDPKKAIDIADKDLNFDDDFSEF

f197.nt

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AGCTTTTTCTTTGCAATCTTTTTTAGACACCCTGCATGTCATAATCAATGGTGCAGCTTCTAATTTGGCACTTGAA
ACCATATCAGAATTTGCAATGTCTGAGAATAGAGGAAAAGATTTCTCTGAGTCGGAATTGATAGATTTAAGAAAAA
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AGAGTGGAGTACTTATTGCTAGGCTTCCTTATAAGGATATTTACGGAGTAATATCTAGTCTAAGATTTCAGTATAT
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GCGCCAATAATTCTTATGAAACAGAACAAATAGCTTTAAAGACGAATGAAAATTCTCAGATAGGTGGTAGGGCCGT
TGAAGAATCTGTTATTGCTATGCAAGACATTGTGGAGAAAGTTAGTGTTATTGAAGAGATAGCTAGAAAAAACCAAT
TTACTTGCTTTGAATGCGGCTATTGAAGCTGCAAGAGCAGGAGATGAGGGAAAGGGATTTGCTGTTGTGGCCAGTG

TABLE 1. Nucleotide and Amino Acid Sequences

AGATTAGAAAGTTGGCTGATTTGAGTAAAATTTCTGCTCTTGAGATTGGAGAGTTAGTTGAAGATAACTCTAAGGT
AGCAACTGAAGCGGGAGTGATCTTTAAAGAAATGCTACCCGAAATTGAAGAAACGGCTAATCTTGTTAAGAAGATT
TCAGAAGGTAGCTCTAAGCAAAGCGATCAGATTGCTCAATTTAAAATGGCTTTAGATCAGGTTGGAGAAGTTGTTC
AATCTTCAGCTTCAAGCAGTGAGCAGCTTTCTAGTATGTCCGATAAAATGTTAGAAAAGTCTAAGGAACTTAGAAA
ATCTGTATTATTTTTCAAAATTAAAGATTCTAAAATTGAAAATCCAGAAAATGATGATTATGATTTCAGGTTAATA
GATTGTCCTGAAAATTCTTTTAAAGATGAAAATCAAAATTTGAAAAGCAATGGAATTTCTACTTCAAATGCCAGTG
GGCATAATAATTATTCTTTAGATATTGAGAGCGAATCTTCTGTAAGAACTATTAATAAGCGAGTTGATCCTAAAAA
AGCTATCGATATTGCTGATAAGGATTTAAATTTTGATGATGATTTTTCAGAGTTTTAG

t197.nt

GTTTTATGCGGTTATTTAGAAGATTATTATAAGCAGCTTACAAGGGCGCAAGTAAGAAGAGCAGCTTTTTCTTTGC
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TGCAATGTCTGAGAATAGAGGAAAAGATTTCTCTGAGTCGGAATTGATAGATTTAAGAAAAAAATCCAAAATTTGTT
ATTGACTCTGTAAAGGTGAGCAAAAAAATATCGACAATACTTATACAATTTTATGGCCAATCTTAAAAATGATACCC
TTTTTGAAGAATTCGCTTTTTTTGATTTTGAAGGGAGAGTAATTGTTAGCACAAGACATGAGAATAATATGGATTT
TGGTCATTCTGAGGCTAATACCAATTATTTTAAAAAAGCTGTTGAGGATTATAGGCAAAACCAATTAAAATTTATA
GGTTGGTATTCAAATCTTTCTGAAGGAATATCCGCAGAAGTTGCTATTAGGTCTAAACAAAGCGAAAAAAAGGCTT
TTGCAATAATTGTACCTGTATATTCCCCAGAAGATAAACTTGTTTGTGGGTATTTGGCCGGATATTTGCTTAATGA
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AATATAGCAGTTAATCCTTTTGAAGAATATAATGAAACCAGCAGGGTTAGTTCTAAATTTTTGAATGTTCTTAAAG
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AGTTCTAGTTCAAGATATGGTTAAGGGCAATTTAGATAAAGATTATGCTCTTGATGATGATGAAAATACTCTTGAT
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ATATTAGCTATGTAAATAAGGCAAGTTTAGAAGTTGCCAGTTCAAGTCAAAATTTAAGCTCTAGTGCATTGCAACA
GGCATCTGCTCTTGAAGAAATGTCAGCTAATGTTGAGCAAATAGCCTCAGGTGTCAACATGAGCGCCAATAATTCT
TATGAAACAGAACAAATAGCTTTAAAGACGAATGAAAATTCTCAGATAGGTGGTAGGGCCGTTGAAGAATCTGTTA
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TGCGGCTATTGAAGCTGCAAGAGCAGGAGATGAGGGAAAGGGATTTGCTGTTGTGGCCAGTGAGATTAGAAAGTTG
GCTGATTTGAGTAAAATTTCTGCTCTTGAGATTGGAGAGTTAGTTGAAGATAACTCTAAGGTAGCAACTGAAGCGG
GAGTGATCTTTAAAGAAATGCTACCCGAAATTGAAGAAACGGCTAATCTTGTTAAGAAGATTTCAGAAGGTAGCTC
TAAGCAAAGCGATCAGATTGCTCAATTTAAAATGGCTTTAGATCAGGTTGGAGAAGTTGTTCAATCTTCAGCTTCA
AGCAGTGAGCAGCTTTCTAGTATGTCCGATAAAATGTTAGAAAAGTCTAAGGAACTTAGAAAATCTGTATTATTTT
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TTCTTTTAAAGATGAAAATCAAAATTTGAAAAGCAATGGAATTTCTACTTCAAATGCCAGTGGGCATAATAATTAT
TCTTTAGATATTGAGAGCGAATCTTCTGTAAGAACTATTAATAAGCGAGTTGATCCTAAAAAAGCTATCGATATTG
CTGATAAGGATTTAAATTTTGATGATGATTTTTCAGAGTTTTAG

f200.aa

MTISKNVFSKFILKFLNSSAFVSVFALFVGFLIVGLVVMGLGHSPFRMYFIILEIIFSSPKHLGYVLSYSAPLIFT
GLSIGISLKAGLFNIGVEGQFILGSIVALIASVLLDLPPILHVITIFIITFLASGSLGILIGYLKAKFNISEVISG
IMFNWILFHLNNIILDFSFIKRDNSDFSKPIKESAYIDFLASWKLSPEGLAYRSSHPFVNELLKAPLHFGIILGII
FAILIWFLLNKTIIGFKINATGSNIEASRCMGINVKAVLIFSMFLSAAVAGLAGAIQLMGVNKAIFKLSYMQGIGF
NGIAASLMGNNSPIGIIFSSILFSILLYGSSRVQSLMGLPSSIVSLMMGIIVLVISASYFLNKIVLKGVKRVKYNN
ILD

t200.aa

LVVMGLGHSPFRMYFIILEIIFSSPKHLGYVLSYSAPLIFTGLSIGISLKAGLFNIGVEGQFILGSIVALIASVLL
DLPPILHVITIFIITFLASGSLGILIGYLKAKFNISEVISGIMFNWILFHLNNIILDFSFIKRDNSDFSKPIKESA
YIDFLASWKLSPEGLAYRSSHPFVNELLKAPLHFGIILGIIFAILIWFLLNKTIIGFKINATGSNIEASRCMGINV

TABLE 1. Nucleotide and Amino Acid Sequences

KAVLIFSMFLSAAVAGLAGAIQLMGVNKAIFKLSYMQGIGFNGIAASLMGNNSPIGIIFSSILFSILLYGSSRVQS
LMGLPSSIVSLMMGIIVLVISASYFLNKIVLKGVKRVKYNNILD

f200.nt

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TTTAGCTTCAGGCAGTTTAGGAATTTTAATCGGATATTTAAAAGCCAAATTCAATATTAGCGAAGTGATTTCAGGA
ATAATGTTTAATTGGATATTATTTCATTTAAATAATATAATTTTAGATTTTAGTTTTATTAAAAGAGATAATAGTG
ATTTTTCAAAACCCATTAAAGAAAGCGCATATATTGATTTTTTAGCTTCTTGGAAGCTCTCACCAGAAGGTCTTGC
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TTTGCTATTTTAATATGGTTTTTACTTAATAAAACTATTATTGGATTTAAAATAAATGCCACAGGAAGTAATATTG
AAGCTTCAAGATGTATGGGTATTAATGTAAAAGCTGTGCTAATTTTTTTCAATGTTTCTCTCAGCAGCTGTTGCAGG
TCTTGCTGGTGCTATTCAACTTATGGGTGTTAATAAAGCTATATTTAAGCTTTCTTATATGCAAGGAATTGGTTTT
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TGCTTTATGGAAGCAGTAGAGTTCAAAGTTTAATGGGCCTTCCATCTTCAATTGTATCTTTGATGATGGGAATAAT
TGTTCTTGTAATTTCTGCTAGCTATTTTTTAAATAAAATTGTTTTAAAAGGTGTTAAGCGTGTCAAATATAATAAT
ATTCTTGATTAG

t200.nt

GGGCTAGTGGTGATGGGGCTTGGTCATTCTCCTTTTAGAATGTATTTTATAATATTAGAAATTATTTTTTCTTCTC
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AGCGGGTCTTTTTAATATTGGGGTTGAAGGCCAGTTTATACTAGGATCTATTGTTGCTTTAATAGCATCAGTTTTA
CTTGATTTGCCTCCAATTTTACATGTAATTACTATTTTTATTATTACTTTTTTAGCTTCAGGCAGTTTAGGAATTT
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GTGTTAATAAAGCTATATTTAAGCTTTCTTATATGCAAGGAATTGGTTTTAATGGGATAGCTGCTTCTCTTATGGG
AAACAATTCGCCAATTGGCATAATATTTTCTAGCATTCTTTTTTCTATATTGCTTTATGGAAGCAGTAGAGTTCAA
AGTTTAATGGGCCTTCCATCTTCAATTGTATCTTTGATGATGGGAATAATTGTTCTTGTAATTTCTGCTAGCTATT
TTTTAAATAAAATTGTTTTAAAAGGTGTTAAGCGTGTCAAATATAATAATATTCTTGATTAG

f208.aa

MVKKFSIFLKAIIIFSIFELLIEELSIILFLPYKIRFALIFLGFLFDTIFIFIFLYKITKAYLSQRLEIYVRNNLF
FDIIHCLIPLAFYSSYQLKNIIVAHETILNPIMLSLFKLRFLRLLRFNDLIIEIYYNSKEKNLILIAFARTFSMSL
LIPFTFFIIISSSKIVNSIPEKQEFNIIKNISIINEKAYIKEKYPFILIIKEKDDIIYSKSDEIFVYYSPSEYRVI
EMEKTKFYIDKYLQRKSDSILGIFLFTLFASFTIFLMNFYKFFKASFLNPIILMTKILQDPLEYRKIQIPFTLSEE
KVYELAKSFNNLLLKEKLNSKRKSKIPLEIEKVKKIINKNQEIK

t208.aa

IIIFSIFELLIEELSIILFLPYKIRFALIFLGFLFDTIFIFIFLYKITKAYLSQRLEIYVRNNLFFDIIHCLIPLA
FYSSYQLKNIIVAHETILNPIMLSLFKLRFLRLLRFNDLIIEIYYNSKEKNLILIAFARTFSMSLLIPFTFFIIIS
SSKIVNSIPEKQEFNIIKNISIINEKAYIKEKYPFILIIKEKDDIIYSKSDEIFVYYSPSEYRVIEMEKTKFYIDK
YLQRKSDSILGIFLFTLFASFTIFLMNFYKFFKASFLNPIILMTKILQDPLEYRKIQIPFTLSEEKVYELAKSFNN
LLLKEKLNSKRKSKIPLEIEKVKKIINKNQEIK

f208.nt

TABLE 1. Nucleotide and Amino Acid Sequences

ATGGTAAAAAAATTTTCAATTTTCTTAAAAGCAATAATAATTTTTTCAATATTTGAACTTTTAATCGAAGAACTCT
CAATAATTCTTTTTTTACCATACAAAATACGATTTGCACTAATATTTCTTGGGTTTCTATTTGACACAATTTTTAT
TTTCATTTTTTATACAAAATAACCAAGGCCTACCTTTCCCAAAGATTAGAAATCTACGTCAGAAACAATCTATTC
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GGAAAAAGATGACATAATATACTCAAAATCAGACGAAATATTTGTTTACTACAGTCCCAGTGAATATAGAGTAATA
GAAATGGAGAAAACAAAATTTTATATAGATAAATATTTGCAAAGAAAAAGCGATTCTATTCTTGGAATTTTTCTAT
TTACATTGTTTGCATCATTTACTATTTTTTTAATGAATTTTTATAAATTTTTTAAAGCAAGCTTTTTAAATCCTAT
TATTTTAATGACAAAAATTTTACAAGACCCATTAGAATATCGAAAAATTCAAATTCCTTTTACTTTAAGCGAAGAA
AAAGTATATGAACTTGCAAAATCATTTAACAATCTCTTGCTAAAAGAAAAACTAAACTCAAAGCGAAAAAGCAAAA
TACCTTTAGAAATTGAAAAAGTAAAAAAAATAATTAATAAAAACCAGGAAATAAAATGA

t208.nt

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CCTTTCCCAAAGATTAGAAATCTACGTCAGAAACAATCTATTCTTCGATATAATCCACTGCCTTATTCCTTTAGCG
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TTAATAAAAACCAGGAAATAAAATGA

f210.aa

MKIQIIIMLLALLDFPLNARLLDISIEKRADEEIKKYSSYNLILEKEYYTNFPTSEIEKNIYKLTEHFVKSIMLNK
TNYSLLNSNYKEANKYLIQSELIDKKFLKYKIFKIKNINGIFKSHSLIYTKKGFYKLELYIENNAEPLKIFNLNIT
YFLKNLDKISNEMIFFPREKREVNMIQKTTIAADSSSKPRGINYDTGIPFNVLIVDDSVFTVKQLTQIFTSEGFNI
IDTAADGEEAVIKYKNHYPNIDIVTLDITMPKMDGITCLSNIMEFDKNARVIMISALGKEQLVKDCLIKGAKTFIV
KPLDRAKVLQRVMSVFVK

t210.aa

RLLDISIEKRADEEIKKYSSYNLILEKEYYTNFPTSEIEKNIYKLTEHFVKSIMLNKTNYSLLNSNYKEANKYLIQ
SELIDKKFLKYKIFKIKNINGIFKSHSLIYTKKGFYKLELYIENNAEPLKIFNLNITYFLKNLDKISNEMIFFPRE
KREVNMIQKTTIAADSSSKPRGINYDTGIPFNVLIVDDSVFTVKQLTQIFTSEGFNIIDTAADGEEAVIKYKNHYP
NIDIVTLDITMPKMDGITCLSNIMEFDKNARVIMISALGKEQLVKDCLIKGAKTFIVKPLDRAKVLQRVMSVFVK

f210.nt

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TTGAAAAAAGAGCAGATGAAGAAATAAAAAAATATTCGTCTTATAATTTAATTTTAGAAAAAGAATACTATACCAA
TTTTCCAACAAGCGAAATAGAAAAAAATATTTATAAACTAACAGAACATTTTGTAAAAAGCATAATGCTCAATAAA
ACTAACTACAGCTTATTAAATTCAAACTACAAAGAAGCAAATAAAATATCTAATTCAAAGCGAACTCATTGATAAAA
AATTTTTAAAATATAAAATATTTAAAATCAAAAATATAAATGGAATTTTTAAAAGCCATTCACTAATATATACAAA

TABLE 1. Nucleotide and Amino Acid Sequences

AAAAGGATTTTACAAATTAGAACTTTACATAGAAAATAATGCAGAACCTCTAAAAATATTTAACCTTAACATTACT
TATTTTTTAAAGAATTTAGATAAAATAAGTAATGAAATGATTTTTTTCCCAAGGGAATGA

t210.nt

AGACTTTTGGACATTTCAATTGAAAAAAGAGCAGATGAAGAAATAAAAAAATATTCGTCTTATAATTTAATTTTAG
AAAAAGAATACTATACCAATTTTCCAACAAGCGAAATAGAAAAAAATATTTATAAACTAACAGAACATTTTGTAAA
AAGCATAATGCTCAATAAAACTAACTACAGCTTATTAAATTCAAACTACAAAGAAGCAAATAAATATCTAATTCAA
AGCGAACTCATTGATAAAAAATTTTTAAAATATAAAATATTTAAAATCAAAAATATAAATGGAATTTTTAAAAGCC
ATTCACTAATATATACAAAAAAAGGATTTTACAAATTAGAACTTTACATAGAAAATAATGCAGAACCTCTAAAAAT
ATTTAACCTTAACATTACTTATTTTTTAAAGAATTTAGATAAAATAAGTAATGAAATGATTTTTTTCCCAAGGGAA
TGA

f22.aa

MLKTLTKIITISCLIVGCASLPYTPPKQNLNYLMELLPGANLYAHVNLIKNRSIYNSLSPKYKSVLGLISNLYFSY
KKENNDFALLIMGNFPKDIFWGIHKNRNTESIGNIFTNPKWKLKNSNIYIIPNKARTSIAITQKDITAKDNNMLTT
KYIGEIEKNEMFFWIQDPTLLLPNQIVSSKNLIPFSSGTLSINSLNQEEYIFKSLIKTNNPPILKILSKKLIPTVL
TNMTNLTISSHIKTTIKDQNTVEIEFNIQKSSVESLIEKLASNIQT

t22.aa

PYTPPKQNLNYLMELLPGANLYAHVNLIKNRSIYNSLSPKYKSVLGLISNLYFSYKKENNDFALLIMGNFPKDIFW
GIHKNRNTESIGNIFTNPKWKLKNSNIYIIPNKARTSIAITQKDITAKDNNMLTTKYIGEIEKNEMFFWIQDPTLL
LPNQIVSSKNLIPFSSGTLSINSLNQEEYIFKSLIKTNNPPILKILSKKLIPTVLTNMTNLTISSHIKTTIKDQNT
VEIEFNIQKSSVESLIEKLASNIQT

f22.nt

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CAGGTCTATTTATAACTCTTTAAGCCCTAAATATAAATCAGTTCTTGGGCTTATAAGCAATTTATACTTTAGCTAT
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ACAAACATGACAAACCTCACAATATCAAGCCACATAAAGACCACAATAAAAGACCAAAATACGGTTGAAATAGAAT
TTAATATTCAAAAATCTAGTGTTGAAAGCCTTATAGAAAAACTAGCTTCAAATATTCAAACCTAA

t22.nt

CCTTACACTCCTCCAAAACAAAATCTAAATTACTTAATGGAACTTTTACCTGGCGCAAATTTATACGCCCATGTAA
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ATACTTTAGCTATAAAAAAGAAAATAACGATTTTGCTCTACTAATAATGGGTAATTTCCCAAAAGATATTTTCTGG
GGAATTCATAAAAATAGAAATACAGAATCAATAGGCAATATATTTACAAATCCAAAATGGAAACTTAAAAATTCAA
ATATATACATTATTCCAAACAAAGCTAGAACTAGCATTGCAATAACCCAAAAAGATATAACCGCAAAAGACAATAA
TATGCTAACAACAAAATATATTGGGGAAATAGAAAAAAATGAAATGTTTTTTTGGATTCAAGATCCAACATTATTG
CTCCCAAACCAAATAGTAAGCAGCAAAAATTTAATTCCCTTTAGCAGTGGAACTTTGTCTATAAACAGCTTAAATC
AAGAAGAATATATTTTTAAATCCTTAATCAAAACAAATAATCCACCAATACTAAAAATATTGTCAAAAAAGTTAAT
TCCAACCGTCTTGACAAACATGACAAACCTCACAATATCAAGCCACATAAAGACCACAATAAAAGACCAAAATACG
GTTGAAATAGAATTTAATATTCAAAAATCTAGTGTTGAAAGCCTTATAGAAAAACTAGCTTCAAATATTCAAACCT
AA

f221.aa

TABLE 1. Nucleotide and Amino Acid Sequences

MGITVFYLFSIFASFVLGSSMDSVKENVLKSTIFYYDVEEVEFPYARKQTLQFIAKTHLKYAVFNFDKNKMFSYTF
VFDKKLISQYAIFIEVKKKFGEATLVTPLNYLWDLGDSIIVLNKNILRITLKSYISNYNK

t221.aa

SMDSVKENVLKSTIFYYDVEEVEFPYARKQTLQFIAKTHLKYAVFNFDKNKMFSYTFVFDKKLISQYAIFIEVKKK
FGEATLVTPLNYLWDLGDSIIVLNKNILRITLKSYISNYNK

f221.nt

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ACAATTTATTGCTAAAACCCATTTAAAATATGCTGTTTTTAATTTTGACAAAAATAAAATGTTTTCGTACACTTTT
GTTTTTGATAAAAAATTAATATCTCAGTATGCAATTTTTATTGAGGTAAAGAAAAAGTTTGGCGAGGCTACACTAG
TAACGCCTTTGAATTATTTATGGGATCTTGGTGATTCTATTATTGTTTTAAATAAAAATATTTTAAGAATTACTTT
AAAATCTTATATTTCAAATTATAATAAATGA

t221.nt

AGCATGGATTCTGTTAAAGAGAATGTTCTCAAGAGCACTATTTTTTATTATGATGTTGAAGAAGTTGAATTTCCTT
ATGCTAGGAAGCAGACTTTACAATTTATTGCTAAAACCCATTTAAAATATGCTGTTTTTAATTTTGACAAAAATAA
AATGTTTTCGTACACTTTTGTTTTTGATAAAAAATTAATATCTCAGTATGCAATTTTTATTGAGGTAAAGAAAAAG
TTTGGCGAGGCTACACTAGTAACGCCTTTGAATTATTTATGGGATCTTGGTGATTCTATTATTGTTTTAAATAAAA
ATATTTTAAGAATTACTTTAAAATCTTATATTTCAAATTATAATAAATGA

f253.aa

MYMENIEVRGQPNFFGLIPFFVFIIIYLGTGIYLGVIGVEMAFYQLPASVAMFFASIVCFLVFKGKFSDKIHIFIK
GAAQYDIILMCLIFMLSGAFSSLCKEIGCVETVANLGIKYINPNWIVSGIFFVTCFLSFSAGTSVGSIVAIAPIAF
NIAVKSGINPNLIAASVMCGAMFGDNLSLISDTTIVSSRTQGSSILDVFISSSFYAFPSAILTFFSFFFLSENLSN
ATNFLHESSIDLVKTVPYLMIIFFSLAGMNVFIVLFLGILSICLISVLYGNLYFLDVMKNINKGFLNMADLIFLSI
LTGGVSFAVIHNGGFKWLLIKLKSLIRGKSSAEFSIGAFVSIVDVFLANNTIAILICGKVAKKIAFENNISVQRSA
SILDMFSCIFQGIIPYGAQMIILVNFSNGLVSPISILPFLVYFGFLLFFVILSILGLDIKKVFLFFLKK

t253.aa

LVFKGKFSDKIHIFIKGAAQYDIILMCLIFMLSGAFSSLCKEIGCVETVANLGIKYINPNWIVSGIFFVTCFLSFS
AGTSVGSIVAIAPIAFNIAVKSGINPNLIAASVMCGAMFGDNLSLISDTTIVSSRTQGSSILDVFISSSFYAFPSA
ILTFFSFFFLSENLSNATNFLHESSIDLVKTVPYLMIIFFSLAGMNVFIVLFLGILSICLISVLYGNLYFLDVMKN
INKGFLNMADLIFLSILTGGVSFAVIHNGGFKWLLIKLKSLIRGKSSAEFSIGAFVSIVDVFLANNTIAILICGKV
AKKIAFENNISVQRSASILDMFSCIFQGIIPYGAQMIILVNFSNGLVSPISILPFLVYFGFLLFFVILSILGLDIK
KVFLFFLKK

f253.nt

ATGTATATGGAAAATATTGAAGTAAGAGGGCAGCCAAATTTTTTTGGGCTTATTCCTTTTTTTGTTTTTATTATTA
TCTATTTAGGCACGGGGATTTATTTGGGAGTTATTGGTGTAGAAATGGCCTTTTATCAACTGCCGGCTAGTGTTGC
AATGTTTTTTGCTTCCATTGTTTGTTTTTTGGTATTTAAAGGAAAATTTTCCGACAAAATTCACATATTTATTAAA
GGAGCAGCTCAGTACGATATTATACTAATGTGTCTTATTTTTATGCTTTCGGGAGCTTTCTCTTCTCTTTGTAAAG
AAATAGGCTGCGTTGAAACTGTAGCAAATTTGGGAATTAAATATATTAATCCTAATTGGATTGTTTCTGGTATATT
TTTTGTAACCTGCTTTCTTTCTTTTTCTGCCGGCACTTCTGTTGGATCTATCGTTGCAATTGCTCCTATTGCTTTT
AATATTGCTGTTAAAAGCGGCATTAATCCGAATTTAATAGCAGCATCTGTAATGTGTGGAGCTATGTTTGGAGATA
ATCTTTCTTTAATATCAGATACAACTATTGTTTCTAGTCGAACTCAAGGTAGTAGCATCTTAGATGTTTTTATTAG
TAGCAGTTTTTATGCTTTTCCATCCGCCATACTAACTTTTTTTTCTTTTTTTCTTTCTTTCTGAAAATTTGTCCAAT
GCCACAAACTTTTTACACGAAAGTTCAATAGATTTAGTGAAAACTGTGCCTTATTTAATGATTATATTTTTCTCTT

TABLE 1. Nucleotide and Amino Acid Sequences

TAGCTGGAATGAATGTTTTTATAGTTCTTTTTTTAGGTATTCTTTCTATATGTCTTATTAGCGTTTTGTATGGTAA
TTTATACTTTCTAGATGTAATGAAAAACATTAATAAAGGGTTTTTAAATATGGCGGATTTGATTTTTCTTTCAATT
TTAACAGGGGGAGTTTCTTTTGCCGTGATTCATAATGGAGGCTTTAAATGGCTACTTATTAAATTAAAATCCTTGA
TTAGAGGAAAAAGTTCAGCGGAATTTTCTATTGGGGCTTTTGTTTCAATAGTTGATGTTTTTCTTGCTAATAACAC
AATTGCCATACTTATTTGCGGCAAAGTAGCAAAAAAGATAGCTTTTGAAAATAACATCAGTGTTCAAAGAAGTGCT
TCTATTTTAGATATGTTCTCTTGTATTTTTCAAGGCATTATTCCTTATGGTGCGCAAATGATTATTTTAGTGAATT
TTTCAAATGGACTTGTGTCGCCAATTAGTATTTTGCCATTTTTAGTTTATTTTGGATTTTTATTGTTTTTTGTTAT
TTTATCTATTTTGGGCCTTGATATAAAAAAAGTTTTTTTATTTTTTTTAAAAAAAATAA

t253.nt

TTGGTATTTAAAGGAAAATTTTCCGACAAAATTCACATATTTATTAAAGGAGCAGCTCAGTACGATATTATACTAA
TGTGTCTTATTTTTATGCTTTCGGGAGCTTTCTCTTCTCTTTGTAAAGAAATAGGCTGCGTTGAAACTGTAGCAAA
TTTGGGAATTAAATATATTAATCCTAATTGGATTGTTTCTGGTATATTTTTTGTAACCTGCTTTCTTTCTTTTTCT
GCCGGCACTTCTGTTGGATCTATCGTTGCAATTGCTCCTATTGCTTTTAATATTGCTGTTAAAAGCGGCATTAATC
CGAATTTAATAGCAGCATCTGTAATGTGTGGAGCTATGTTTGGAGATAATCTTTCTTTAATATCAGATACAACTAT
TGTTTCTAGTCGAACTCAAGGTAGTAGCATCTTAGATGTTTTTATTAGTAGCAGTTTTTATGCTTTTCCATCCGCC
ATACTAACTTTTTTTTCTTTTTTCTTTCTTTCTGAAAATTTGTCCAATGCCACAAACTTTTTACACGAAAGTTCAA
TAGATTTAGTGAAAACTGTGCCTTATTTAATGATTATATTTTTCTCTTTAGCTGGAATGAATGTTTTTATAGTTCT
TTTTTTAGGTATTCTTTCTATATGTCTTATTAGCGTTTTGTATGGTAATTTATACTTTCTAGATGTAATGAAAAAC
ATTAATAAAGGGTTTTTAAATATGGCGGATTTGATTTTTCTTTCAATTTTAACAGGGGGAGTTTCTTTTGCCGTGA
TTCATAATGGAGGCTTTAAATGGCTACTTATTAAATTAAAATCCTTGATTAGAGGAAAAAGTTCAGCGGAATTTTC
TATTGGGGCTTTTGTTTCAATAGTTGATGTTTTTCTTGCTAATAACACAATTGCCATACTTATTTGCGGCAAAGTA
GCAAAAAAGATAGCTTTTGAAAATAACATCAGTGTTCAAAGAAGTGCTTCTATTTTAGATATGTTCTCTTGTATTT
TTCAAGGCATTATTCCTTATGGTGCGCAAATGATTATTTTAGTGAATTTTTCAAATGGACTTGTGTCGCCAATTAG
TATTTTGCCATTTTTAGTTTATTTTGGATTTTTATTGTTTTTTGTTATTTTATCTATTTTGGGCCTTGATATAAAA
AAAGTTTTTTTATTTTTTTTAAAAAAAATAA

f265.aa

MRKCFVSLSLLLIFFACSSNVEIELNDDISGIVSIFVNVNREFEKIRKELLTTLVGEEIANMPLFPVDEIKKYFKN
GEEKLGLKLLSIKTQGDSINLVVKFDNLIKILGDYMKKPDISVFKIEKKDGKNIIELNINLENATKNINENKEYIS
DALAALLPSDEIPMSAKEYKDVLVYFLSDFTSKASELIDNSKLNLVVKTSRNVQEQFGFKQINSNTLRFEMDMVKG
LSLETPIKLRLV
Y

t265.aa

SNVEIELNDDISGIVSIFVNVNREFEKIRKELLTTLVGEEIANMPLFPVDEIKKYFKNGEEKLGLKLLSIKTQGDS
INLVVKFDNLIKILGDYMKKPDISVFKIEKKDGKNIIELNINLENATKNINENKEYISDALAALLPSDEIPMSAKE
YKDVLVYFLSDFTSKASELIDNSKLNLVVKTSRNVQEQFGFKQINSNTLRFEMDMVKGLSLETPIKLRLVY

f265.nt

ATGAGAAAGTGTTTTGTTAGCTTGAGTTTATTGTTGATTTTTTTTGCTTGTAGCTCTAATGTTGAAATTGAGTTAA
ATGATGATATTAGTGGTATTGTTTCAATATTTGTTAATGTTAATAGAGAATTTGAAAAAATTAGAAAAGAACTCTT
AACAACTTTGGTGGGAGAAGAAATTGCAAATATGCCTCTTTTTCCTGTAGATGAAATAAAAAAATACTTTAAAAAT
GGAGAGGAAAAGCTTGGGCTTAAGCTTTTGAGTATTAAAACCCAAGGAGATTCTATTAATTTAGTTGTTAAGTTTG
ATAATTTAATTAAAATTTTAGGCGATTATATGAAAAAACCCGATATATCTGTGTTTAAGATAGAAAAAAAAGATGG
TAAAAATATTATTGAACTTAATATTAATTTGGAAAACGCTACTAAGAATATTAATGAAAATAAAGAATATATTAGT
GATGCACTTGCTGCTCTTTTGCCATCGGATGAGATCCCAATGTCTGCCAAAGAATATAAAGATGTTTTGGTTTATT
TTTTATCGGATTTTACTTCCAAAGCAAGTGAACTTATTGACAATTCCAAACTTAATCTTGTAGTTAAGACTTCTAG
AAATGTTCAAGAACAATTTGGATTCAAACAAATTAACTCAAACACACTGCGGTTTGAGATGGATATGGTTAAAGGA
TTAAGTCTTGAAACACCAATAAAACTTAGATTAGTTTATTGA

t265.nt

TABLE 1. Nucleotide and Amino Acid Sequences

TCTAATGTTGAAATTGAGTTAAATGATGATATTAGTGGTATTGTTTCAATATTTGTTAATGTTAATAGAGAATTTG
AAAAAATTAGAAAAGAACTCTTAACAACTTTGGTGGGAGAAGAAATTGCAAATATGCCTCTTTTTCCTGTAGATGA
AATAAAAAAATACTTTAAAAATGGAGAGGAAAAGCTTGGGCTTAAGCTTTTGAGTATTAAAACCCAAGGAGATTCT
ATTAATTTAGTTGTTAAGTTTGATAATTTAATTAAAATTTTAGGCGATTATATGAAAAAACCCGATATATCTGTGT
TTAAGATAGAAAAAAAAGATGGTAAAAATATTATTGAACTTAATATTAATTTGGAAAACGCTACTAAGAATATTAA
TGAAAATAAAGAATATATTAGTGATGCACTTGCTGCTCTTTTGCCATCGGATGAGATCCCAATGTCTGCCAAAGAA
TATAAAGATGTTTTGGTTTATTTTTTATCGGATTTTACTTCCAAAGCAAGTGAACTTATTGACAATTCCAAACTTA
ATCTTGTAGTTAAGACTTCTAGAAATGTTCAAGAACAATTTGGATTCAAACAAATTAACTCAAACACACTGCGGTT
TGAGATGGATATGGTTAAAGGATTAAGTCTTGAAACACCAATAAAACTTAGATTAGTTTATTGA

f269.aa

MNIRKLLFCIFFMNISFLLFAGDYKGLDFKIKFFNQSIYRVNSNVFIEVSLSNASESVLTLEIGDINSFGFDFDVT
DTTNIKVKRPIEYVKKRSKNVAIPVRNMSLRPNEKFSVVINLNQFVKFSKDGVYFVKGIFFPDISDPSKKKESNII
TLFLNDGFDENPGSIDLVNLSENNDIQDILKKKKLSPDEIVKYLLKALQLGKKEKFFLYLDIEGLLLNDKGKAYLY
KQKLSPIPNKNVVEEYKEYLWNSNNSDISKAPNKFSIIETTYSDTSGKVIADLYFDDGQFYISKRYTFFFKKYDYY
WIIYDYIVQNTGIKEK

t269.aa

GDYKGLDFKIKFFNQSIYRVNSNVFIEVSLSNASESVLTLEIGDINSFGFDFDVTDTTNIKVKRPIEYVKKRSKNV
AIPVRNMSLRPNEKFSVVINLNQFVKFSKDGVYFVKGIFFPDISDPSKKKESNIITLFLNDGFDENPGSIDLVNLS
ENNDIQDILKKKKLSPDEIVKYLLKALQLGKKEKFFLYLDIEGLLLNDKGKAYLYKQKLSPIPNKNVVEEYKEYLW
NSNNSDISKAPNKFSIIETTYSDTSGKVIADLYFDDGQFYISKRYTFFFKKYDYYWIIYDYIVQNTGIKEK

f269.nt

ATGAATATTAGAAAATTGCTTTTTTTGTATCTTTTTTATGAATATTTCTTTTCTTTTGTTTGCGGGAGATTACAAGG
GCCTTGATTTTAAAATCAAGTTTTTTAATCAATCTATTTATCGTGTCAATAGTAATGTTTTTATTGAAGTTTCTCT
TAGTAATGCGTCTGAGAGTGTTTTAACTTTAGAAATAGGCGATATTAATTCTTTTGGCTTTGATTTTGATGTTACT
GATACCACCAATATTAAAGTTAAAAGACCTATTGAATATGTTAAAAAGAGATCTAAAAATGTTGCAATTCCTGTTA
GAAATATGAGCTTGAGACCTAATGAAAAATTTTCTGTAGTTATTAACTTAAATCAATTTGTTAAGTTTAGTAAAGA
TGGAGTTTATTTTGTTAAGGGTATTTTTTTCCCAGACATTTCAGATCCATCTAAGAAAAAAGAATCCAATATTATT
ACGCTTTTTTTGAATGATGGTTTTGATGAAAATCCAGGTAGCATAGACCTTGTTAATTTGTCTGAAAATAATGATA
TTCAAGATATCTTGAAAAAGAAAAAATTATCTCCCGATGAAATTGTTAAATATTTGTTAAAGGCATTGCAGCTTGG
GAAAAAAGAAAAGTTCTTTTTATATCTTGATATTGAAGGTTTGTTATTAAATGACAAGGGCAAGGCATACCTTTAT
AAGCAAAAGTTATCACCTATTCCCAATAAAAATGTAGTTGAAGAGTATAAAGAATATTTGTGGAATTCTAATAATT
CGGATATTTCAAAAGCACCAAATAAATTTTCTATTATTGAAACTACTTATTCTGATACTTCTGGCAAGGTGATTGC
TGATTTATATTTTGACGATGGGCAATTTTATATTTCCAAAAGATATACTTTCTTCTTTAAAAAATATGATTATTAT
TGGATAATTTATGATTACATTGTTCAAAATACTGGCATTAAGGAAAAGTAA

t269.nt

GGAGATTACAAGGGCCTTGATTTTAAAATCAAGTTTTTTAATCAATCTATTTATCGTGTCAATAGTAATGTTTTTA
TTGAAGTTTCTCTTAGTAATGCGTCTGAGAGTGTTTTAACTTTAGAAATAGGCGATATTAATTCTTTTGGCTTTGA
TTTTGATGTTACTGATACCACCAATATTAAAGTTAAAAGACCTATTGAATATGTTAAAAAGAGATCTAAAAATGTT
GCAATTCCTGTTAGAAATATGAGCTTGAGACCTAATGAAAAATTTTCTGTAGTTATTAACTTAAATCAATTTGTTA
AGTTTAGTAAAGATGGAGTTTATTTTGTTAAGGGTATTTTTTTCCCAGACATTTCAGATCCATCTAAGAAAAAAGA
ATCCAATATTATTACGCTTTTTTTGAATGATGGTTTTGATGAAAATCCAGGTAGCATAGACCTTGTTAATTTGTCT
GAAAATAATGATATTCAAGATATCTTGAAAAAGAAAAAATTATCTCCCGATGAAATTGTTAAATATTTGTTAAAGG
CATTGCAGCTTGGGAAAAAAGAAAAGTTCTTTTTATATCTTGATATTGAAGGTTTGTTATTAAATGACAAGGGCAA
GGCATACCTTTATAAGCAAAAGTTATCACCTATTCCCAATAAAAATGTAGTTGAAGAGTATAAAGAATATTTGTGG
AATTCTAATAATTCGGATATTTCAAAAGCACCAAATAAATTTTCTATTATTGAAACTACTTATTCTGATACTTCTG
GCAAGGTGATTGCTGATTTATATTTTGACGATGGGCAATTTTATATTTCCAAAAGATATACTTTCTTCTTTAAAAA
ATATGATTATTATTGGATAATTTATGATTACATTGTTCAAAATACTGGCATTAAGGAAAAGTAA

TABLE 1. Nucleotide and Amino Acid Sequences

f29.aa

MNWLSFFYVLLFLLIFPFELQSNNKENIENLIKLHMLYDLTNNLSKELETINKIKNFDLEQHYLLITKYYLKIKKY
KEANDFLKKINQKKIKNQKIKNEIISLKLRINEDNINEEEIKKILNNEKNIDVKIIYQIFSLIKFKNKKLANKIKN
IILTNYPKSIYSYKIKRNE

t29.aa

NNKENIENLIKLHMLYDLTNNLSKELETINKIKNFDLEQHYLLITKYYLKIKKYKEANDFLKKINQKKIKNQKIKN
EIISLKLRINEDNINEEEIKKILNNEKNIDVKIIYQIFSLIKFKNKKLANKIKNIILTNYPKSIYSYKIKRNE

f29.nt

ATGAACTGGCTATCCTTTTTTTATGTTTTATTATTTTTATTAATTTTTCCTTTTGAATTACAGAGTAATAATAAAG
AAAATATAGAAAATTTAATAAAGCTACATATGCTTTATGATTTAACCAATAACCTGTCAAAAGAATTAGAAACAAT
AAATAAAATTAAAAATTTTGACTTAGAACAACATTATCTGCTAATTACAAAATATTATCTAAAAATAAAAAAATAT
AAAGAAGCTAATGATTTTTTAAAAAAAATAAACCAAAAAAAGATCAAAAATCAAAAAATAAAAAACGAAATCATTT
CGCTAAAATTAAGAATAAATGAAGATAATATTAATGAAGAAGAAATCAAAAAAATTTTAAATAACGAAAAAAATAT
AGATGTCAAAATAATTTATCAAATATTCAGTCTTATAAAATTTAAAAATAAAAAATTAGCAAATAAAATTAAAAAC
ATAATACTAACAAACTATCCCAAAAGCATTTATTCTTATAAAATAAAAAGAAATGAATAA

t29.nt

AATAATAAAGAAAATATAGAAAATTTAATAAAGCTACATATGCTTTATGATTTAACCAATAACCTGTCAAAAGAAT
TAGAAACAATAAATAAAATTAAAAATTTTGACTTAGAACAACATTATCTGCTAATTACAAAATATTATCTAAAAAT
AAAAAAATATAAAGAAGCTAATGATTTTTTAAAAAAAATAAACCAAAAAAAGATCAAAAATCAAAAAATAAAAAAC
GAAATCATTTCGCTAAAATTAAGAATAAATGAAGATAATATTAATGAAGAAGAAATCAAAAAAATTTTAAATAACG
AAAAAAATATAGATGTCAAAATAATTTATCAAATATTCAGTCTTATAAAATTTAAAAATAAAAAATTAGCAAATAA
AATTAAAAACATAATACTAACAAACTATCCCAAAAGCATTTATTCTTATAAAATAAAAAGAAATGAATAA

f290.aa

MNSIYVIGKLLLTLFLIFFPFCYNLFAVNLAEINKLSEYAKSIVLIDFDTKRILYSKKPNLVFPPASLTKIVTIYT
ALIEAEKRNIKLKSIVPISDSASYYNAPPNSSLMFLEKGQIVNFEEILKGLSVSSGNDSSIAIAEFVVGNLNSFVN
LMNINVLNLGLFNMHFVEPSGYSSENKITALDMAFFVKSYIEKFKFMLNIHSLKYFIYPKSRNLGTALSSKFLNLK
QRNANLLIYDYPYSDGIKTGYIKESGLNLVATAKKGERRLIAVVLGVEKGINGFGEKMRSSIAKNLFEYGFNKYSK
FPLIVKLKEKVYNGTVDTVALFSKEPFYYILTKDEFDKINISYTVDKLVAPLSGDMPVGRAMIFLENEKIGDVALF
SGKVKRLGFWQGLYKSFINLFSREY

t290.aa

VNLAEINKLSEYAKSIVLIDFDTKRILYSKKPNLVFPPASLTKIVTIYTALIEAEKRNIKLKSIVPISDSASYYNA
PPNSSLMFLEKGQIVNFEEILKGLSVSSGNDSSIAIAEFVVGNLNSFVNLMNINVLNLGLFNMHFVEPSGYSSENK
ITALDMAFFVKSYIEKFKFMLNIHSLKYFIYPKSRNLGTALSSKFLNLKQRNANLLIYDYPYSDGIKTGYIKESGL
NLVATAKKGERRLIAVVLGVEKGINGFGEKMRSSIAKNLFEYGFNKYSKFPLIVKLKEKVYNGTVDTVALFSKEPF
YYILTKDEFDKINISYTVDKLVAPLSGDMPVGRAMIFLENEKIGDVALFSGKVKRLGFWQGLYKSFINLFSREY

f290.nt

ATGAATAGTATCTATGTTATTGGGAAATTGTTATTAACTTTATTTTTAATTTTTTTCCCGTTTTGTTATAATCTTT
TTGCAGTTAATTTAGCTGAGATTAATAAATTATCAGAGTATGCAAAGTCAATAGTTTTAATAGATTTTGATACTAA
GCGAATACTTTATTCTAAGAAGCCCAATTTGGTTTTTCCTCCAGCATCTCTTACAAAGATTGTTACAATTTATACA
GCTTTAATTGAAGCTGAAAAGCGAAATATAAAATTAAAAAGCATAGTTCCTATTAGCGATTCTGCTTCATATTATA
ATGCACCCCCCAATTCTTCTTTGATGTTTTTAGAAAAAGGTCAAATTGTTAATTTTGAAGAGATTTTAAAAGGACT

TABLE 1. Nucleotide and Amino Acid Sequences

TTCAGTTTCTTCGGGTAATGATTCTTCTATTGCAATTGCTGAGTTTGTAGTAGGCAATTTAAATAGCTTTGTTAAT
TTAATGAATATTAATGTTTTAAATTTAGGGCTTTTTAATATGCATTTTGTTGAACCTTCTGGATATAGCAGCGAGA
ATAAGATTACAGCACTAGATATGGCTTTTTTTGTGAAATCTTATATAGAAAAGTTTAAATTTATGCTTAATATTCA
TTCTTTAAAGTATTTTATTTATCCAAAGAGTAGAAATTTAGGAACTGCTTTGTCATCAAAATTTTTAAACTTAAAA
CAAAGAAATGCTAATTTATTAATATATGATTACCCTTATTCAGATGGCATTAAAACGGGATATATTAAGGAATCAG
GCTTAAATCTTGTTGCTACTGCTAAAAAGGGTGAGAGAAGATTAATAGCAGTTGTATTGGGGGTTGAAAAAGGAAT
TAATGGATTTGGAGAGAAAATGAGATCTTCGATTGCAAAAAATTTATTTGAATATGGATTTAATAAATATTCTAAA
TTTCCTTTAATAGTAAAATTAAAAGAAAAAGTCTATAATGGTACAGTGGATACAGTTGCTCTTTTTTCTAAAGAGC
CTTTTTATTATATTTTAACTAAAGATGAATTTGATAAAATTAATATAAGTTATACTGTTGATAAATTGGTTGCTCC
ACTTAGTGGGGATATGCCTGTTGGGAGGGCTATGATTTTTTTAGAAAATGAAAAAATAGGGGATGTTGCTTTGTTT
AGTGGCAAGGTAAAAAGATTAGGGTTTTGGCAAGGTCTTTATAAGAGTTTTATAAATCTTTTTTCAAGAGAGTATT
AA

t290.nt

GTTAATTTAGCTGAGATTAATAAATTATCAGAGTATGCAAAGTCAATAGTTTTAATAGATTTTGATACTAAGCGAA
TACTTTATTCTAAGAAGCCCAATTTGGTTTTTCCTCCAGCATCTCTTACAAAGATTGTTACAATTTATACAGCTTT
AATTGAAGCTGAAAAGCGAAATATAAAATTAAAAAGCATAGTTCCTATTAGCGATTCTGCTTCATATTATAATGCA
CCCCCCAATTCTTCTTTGATGTTTTTAGAAAAAGGTCAAATTGTTAATTTTGAAGAGATTTTAAAAGGACTTTCAG
TTTCTTCGGGTAATGATTCTTCTATTGCAATTGCTGAGTTTGTAGTAGGCAATTTAAATAGCTTTGTTAATTTAAT
GAATATTAATGTTTTAAATTTAGGGCTTTTTAATATGCATTTTGTTGAACCTTCTGGATATAGCAGCGAGAATAAG
ATTACAGCACTAGATATGGCTTTTTTTGTGAAATCTTATATAGAAAAGTTTAAATTTATGCTTAATATTCATTCTT
TAAAGTATTTTATTTATCCAAAGAGTAGAAATTTAGGAACTGCTTTGTCATCAAAATTTTTAAACTTAAAACAAAG
AAATGCTAATTTATTAATATATGATTACCCTTATTCAGATGGCATTAAAACGGGATATATTAAGGAATCAGGCTTA
AATCTTGTTGCTACTGCTAAAAAGGGTGAGAGAAGATTAATAGCAGTTGTATTGGGGGTTGAAAAAGGAATTAATG
GATTTGGAGAGAAAATGAGATCTTCGATTGCAAAAAATTTATTTGAATATGGATTTAATAAATATTCTAAATTTCC
TTTAATAGTAAAATTAAAAGAAAAAGTCTATAATGGTACAGTGGATACAGTTGCTCTTTTTTCTAAAGAGCCTTTT
TATTATATTTTAACTAAAGATGAATTTGATAAAATTAATATAAGTTATACTGTTGATAAATTGGTTGCTCCACTTA
GTGGGGATATGCCTGTTGGGAGGGCTATGATTTTTTTAGAAAATGAAAAAATAGGGGATGTTGCTTTGTTTAGTGG
CAAGGTAAAAAGATTAGGGTTTTGGCAAGGTCTTTATAAGAGTTTTATAAATCTTTTTTCAAGAGAGTATTAA

f291.aa

MNSYDFITALVPIILIIIGLGIIKKPAYYVIPISLIATVAIVIFYKNLGIVNTSLAMLEGALMGIWPIATVIIAAI
FTYKMSEDQKDIETIKNILSNVSSDRRIIVLLVAWGFGNFLEGVAGYGTAVAIPVSILIAMGFEPFFACLICLIMN
TSSTAYGSVGIPITSLAQATNLDVNIVSSEIAFQLILPTLTIPFVLVILTGGGIKGLKGVFLLTLLSGMSMAISQV
FISKTLGPELPAILGSILSMTITIVYARFFGNKETTERQSKNTISLSKGIIACSPYILIVTFIVLVSPLFNKIHEY
LKTFQSTISIYPEANPLHFKWIISPGFLIILATTISYSIRGVPMLKQLKIFTLTLKKMALSSFIIICIVAISRLMT
HSGMIRDLANGISIITGKFGPLFSPLIGAIGTFLTGSDTVSNVLFGPLQTQMAENIGANPYWLAAANTTGATGGKM
ISPQNITIATTTAGLIGQEGKLLSKTIIYALYYILATGLLVYLV

t291.aa

QKDIETIKNILSNVSSDRRIIVLLVAWGFGNFLEGVAGYGTAVAIPVSILIAMGFEPFFACLICLIMNTSSTAYGS
VGIPITSLAQATNLDVNIVSSEIAFQLILPTLTIPFVLVILTGGGIKGLKGVFLLTLLSGMSMAISQVFISKTLGP
ELPAILGSILSMTITIVYARFFGNKETTERQSKNTISLSKGIIACSPYILIVTFIVLVSPLFNKIHEYLKTFQSTI
SIYPEANPLHFKWIISPGFLIILATTISYSIRGVPMLKQLKIFTLTLKKMALSSFIIICIVAISRLMTHSGMIRDL
ANGISIITGKFGPLFSPLIGAIGTFLTGSDTVSNVLFGPLQTQMAENIGANPYWLAAANTTGATGGKMISPQNITI
ATTTAGLIGQEGKLLSKTIIYALYYILATGLLVYLV

f291.nt

ATGAATTCTTATGATTTTATAACAGCTTTGGTACCAATAATCCTAATAATTATTGGACTTGGCATAATAAAAAAGC
CAGCTTACTATGTAATACCCATATCATTAATAGCCACCGTTGCTATAGTTATATTTTATAAAAACTTGGGAATAGT
AAACACAAGTCTTGCAATGCTTGAGGGCGCCTTAATGGGGATATGGCCAATAGCAACTGTAATTATTGCTGCCATA

TABLE 1. Nucleotide and Amino Acid Sequences

TTTACATACAAAATGTCAGAAGATCAAAAAGATATAGAAACTATTAAAAATATTTTATCAAACGTATCTTCTGATA
GAAGAATTATAGTATTACTAGTTGCATGGGGATTTGGAAATTTTTTAGAAGGAGTTGCTGGATATGGAACTGCTGT
TGCAATTCCTGTATCAATATTAATAGCAATGGGATTTGAACCATTTTTTGCCTGCTTAATCTGTTTAATAATGAAC
ACCTCATCAACCGCCTACGGATCTGTGGGAATCCCTATAACATCTTTAGCTCAAGCAACTAACTTGGATGTTAACA
TTGTTTCATCTGAGATTGCATTCCAACTAATACTTCCAACCTTAACAATACCTTTTGTACTGGTAATTCTTACAGG
AGGGGGCATTAAAGGATTAAAAGGAGTATTCCTTCTTACCTTACTCTCAGGAATGTCAATGGCAATATCTCAAGTA
TTTATATCAAAAACTTTGGGTCCAGAACTTCCTGCAATCCTTGGAAGCATTCTTTCTATGACAATAACAATAGTTT
ATGCAAGGTTTTTTGGAAATAAAGAAACTACTGAGCGCCAAAGCAAAAACACAATATCCTTATCAAAAGGAATTAT
TGCCTGCTCACCCTACATTTTAATAGTAACTTTTATAGTGCTTGTATCTCCTCTTTTTAACAAAATTCATGAATAC
CTAAAAACTTTTCAAAGCACTATTAGCATTTATCCAGAAGCAAATCCCTTACACTTTAAATGGATTATCTCTCCGG
GCTTCTTGATTATACTTGCAACAACAATATCCTATTCAATACGGGGAGTTCCAATGTTAAAACAGCTAAAAATATT
TACATTAACCTTGAAAAAAATGGCATTATCTTCCTTTATAATCATATGCATTGTTGCAATATCAAGATTAATGACA
CATAGTGGAATGATAAGAGATCTTGCTAATGGAATCTCAATAATAACAGGTAAATTTGGACCATTATTTAGCCCAC
TAATTGGAGCTATTGGGACATTTTTAACAGGAAGTGATACGGTTTCAAATGTTCTTTTTGGACCTTTACAAACACA
AATGGCAGAAAATATTGGAGCAAATCCTTACTGGCTTGCAGCAGCAAATACAACAGGAGCAACTGGAGGGAAAATG
ATTTCTCCCCAAAACATCACAATAGCAACAACAACTGCTGGATTAATTGGACAAGAAGGCAAGCTTTTATCAAAAA
CAATAATTTATGCTTTATACTACATTTTAGCAACAGGATTGCTAGTTTATTTAGTATAA

t291.nt

CAAAAAGATATAGAAACTATTAAAAATATTTTATCAAACGTATCTTCTGATAGAAGAATTATAGTATTACTAGTTG
CATGGGGATTTGGAAATTTTTTAGAAGGAGTTGCTGGATATGGAACTGCTGTTGCAATTCCTGTATCAATATTAAT
AGCAATGGGATTTGAACCATTTTTTGCCTGCTTAATCTGTTTAATAATGAACACCTCATCAACCGCCTACGGATCT
GTGGGAATCCCTATAACATCTTTAGCTCAAGCAACTAACTTGGATGTTAACATTGTTTCATCTGAGATTGCATTCC
AACTAATACTTCCAACCTTAACAATACCTTTTGTACTGGTAATTCTTACAGGAGGGGGCATTAAAGGATTAAAAGG
AGTATTCCTTCTTACCTTACTCTCAGGAATGTCAATGGCAATATCTCAAGTATTTATATCAAAAACTTTGGGTCCA
GAACTTCCTGCAATCCTTGGAAGCATTCTTTCTATGACAATAACAATAGTTTATGCAAGGTTTTTTGGAAATAAAG
AAACTACTGAGCGCCAAAGCAAAAACACAATATCCTTATCAAAAGGAATTATTGCCTGCTCACCCTACATTTTAAT
AGTAACTTTTATAGTGCTTGTATCTCCTCTTTTTAACAAAATTCATGAATACCTAAAAACTTTTCAAAGCACTATT
AGCATTTATCCAGAAGCAAATCCCTTACACTTTAAATGGATTATCTCTCCGGGCTTCTTGATTATACTTGCAACAA
CAATATCCTATTCAATACGGGGAGTTCCAATGTTAAAACAGCTAAAAATATTTACATTAACCTTGAAAAAAATGGC
ATTATCTTCCTTTATAATCATATGCATTGTTGCAATATCAAGATTAATGACACATAGTGGAATGATAAGAGATCTT
GCTAATGGAATCTCAATAATAACAGGTAAATTTGGACCATTATTTAGCCCACTAATTGGAGCTATTGGGACATTTT
TAACAGGAAGTGATACGGTTTCAAATGTTCTTTTTGGACCTTTACAAACACAAATGGCAGAAAATATTGGAGCAAA
TCCTTACTGGCTTGCAGCAGCAAATACAACAGGAGCAACTGGAGGGAAAATGATTTCTCCCCAAAACATCACAATAG
CAACAACAACTGCTGGATTAATTGGACAAG

f296.aa

MPSPIRVFFLVLLFIFIFNPVLIAMLFILFPFILILFSFLGVFRIYFTRDYSYSRSREFEFYKLSFLLMAKLLSIL
GTVTGEQLNYVNFIINSLNLSERGKSELYTIFHSAITKNNNADKILYTLKLGYFQHKDLFIWLFATLKEINRLSRY
KNLEAEKFISYVGVFLELESDGYEAYKDINIKIVNPYSVLGLTYSASDDEVKKAYKSLVIKYHPDKFANDPVRQKD
ANDKFIKIQDAYEKICKERNIR

t296.aa

IYFTRDYSYSRSREFEFYKLSFLLMAKLLSILGTVTGEQLNYVNFIINSLNLSERGKSELYTIFHSAITKNNNADK
ILYTLKLGYFQHKDLFIWLFATLKEINRLSRYKNLEAEKFISYVGVFLELESDGYEAYKDINIKIVNPYSVLGLTY
SASDDEVKKAYKSLVIKYHPDKFANDPVRQKDANDKFIKIQDAYEKICKERNIR

f296.nt

ATGCCAAGCCCAATTAGAGTGTTTTTTTTAGTGTTGTTGTTTATTTTTATTTTTAATCCCGTTTTAATAGCAATGC
TTTTTATTTTATTTCCTTTTATTTTGATATTATTTAGTTTTTTAGGTGTTTTTAGAATATACTTTACAAGGGATTA
CTCATATTCTAGATCTAGAGAGTTTGAATTTTATAAACTTTCTTTTTTATTAATGGCTAAATTGCTATCTATTTTA

TABLE 1. Nucleotide and Amino Acid Sequences

GGAACTGTAACTGGGGAGCAGCTAAATTATGTCAATTTTATTATCAATTCTTTGAATTTGTCTGAACGTGGTAAAT
CAGAATTGTATACCATTTTTCATTCTGCTATTACTAAAAATAATAATGCTGATAAAATTTTATATACCCTTAAGCT
TGGTTATTTTCAGCACAAAGATCTTTTTATATGGCTTTTTGCCACTCTTAAAGAAATTAACAGGCTTTCTAGGTAT
AAAAATTTAGAAGCTGAAAAATTTATTTCTTATGTTGGTGTTTTTTTAGAACTTGAATCTGATGGTTATGAAGCTT
ATAAAGATATTAATATTAAAATTGTAAATCCTTATAGTGTTTTGGGGTTAACATATAGTGCTAGCGATGATGAGGT
TAAAAAGGCGTATAAAAGCCTTGTTATAAAATATCATCCTGATAAGTTTGCAAATGATCCTGTAAGACAAAAAGAT
GCAAATGATAAATTTATAAAAATTCAAGATGCTTATGAAAAAATTTGCAAGGAAAGAAATATAAGGTAA

t296.nt

ATATACTTTACAAGGGATTACTCATATTCTAGATCTAGAGAGTTTGAATTTTATAAACTTTCTTTTTTATTAATGG
CTAAATTGCTATCTATTTTAGGAACTGTAACTGGGGAGCAGCTAAATTATGTCAATTTTATTATCAATTCTTTGAA
TTTGTCTGAACGTGGTAAATCAGAATTGTATACCATTTTTCATTCTGCTATTACTAAAAATAATAATGCTGATAAA
ATTTTATATACCCTTAAGCTTGGTTATTTTCAGCACAAAGATCTTTTTATATGGCTTTTTGCCACTCTTAAAGAAA
TTAACAGGCTTTCTAGGTATAAAAATTTAGAAGCTGAAAAATTTATTTCTTATGTTGGTGTTTTTTTAGAACTTGA
ATCTGATGGTTATGAAGCTTATAAAGATATTAATATTAAAATTGTAAATCCTTATAGTGTTTTGGGGTTAACATAT
AGTGCTAGCGATGATGAGGTTAAAAAGGCGTATAAAAGCCTTGTTATAAAATATCATCCTGATAAGTTTGCAAATG
ATCCTGTAAGACAAAAAGATGCAAATGATAAATTTATAAAAATTCAAGATGCTTATGAAAAAATTTGCAAGGAAAG
AAATATAAGGTAA

f3.aa

MKKKNLSIYMIMLISLLSCNTSDPNELTRKKMQDKNVKILGFLEKIQADNKEIVEKHIEKKEKQMVQAASVAPINV
ESNFPYYLQEEIEIKEEELVPNTDEEKKAEKAISDGSLEFAKLVDDENKLKNESAQLESSFNNVYKEILELADLIQ
AEVHVAGRINSYIKKRKTTKEKEYKKREIKNKIEKQALIKLFNQLLEKRGDIENLHTQLNSGLSERASAKYFFEKA
KETLKAAITERLNNKRKNRPWWARRTHSNLAIQAKNEAEDALNQLSTSSFRILEAMKIKEDVKQLLEEVKSFLDSS
KSKIFSSGDRLYDFLETSK

t3.aa

NELTRKKMQDKNVKILGFLEKIQADNKEIVEKHIEKKEKQMVQAASVAPINVESNFPYYLQEEIEIKEEELVPNTD
EEKKAEKAISDGSLEFAKLVDDENKLKNESAQLESSFNNVYKEILELADLIQAEVHVAGRINSYIKKRKTTKEKEY
KKREIKNKIEKQALIKLFNQLLEKRGDIENLHTQLNSGLSERASAKYFFEKAKETLKAAITERLNNKRKNRPWWAR
RTHSNLAIQAKNEAEDALNQLSTSSFRILEAMKIKEDVKQLLEEVKSFLDSSKSKIFSSGDRLYDFLETSK

f3.nt

ATGAAAAAAAAAAATTTATCAATTTACATGATAATGCTAATAAGTTTATTATCATGTAATACAAGTGACCCCAATG
AATTAACTCGTAAAAAAATGCAAGACAAGAACGTGAAAATTTTAGGATTTTTAGAGAAAATTCAAGCAGATAATAA
AGAAATTGTTGAAAAACATATAGAAAAAAAAGAAAAACAAATGGTGCAGGCTGCTTCTGTAGCACCTATTAATGTA
GAGAGTAATTTCCCATATTATCTTCAAGAAGAAATAGAGATAAAAGAAGAAGAGTTGGTTCCAAATACTGATGAAG
AAAAGAAGGCAGAGAAGGCAATTAGCGATGGGAGTCTTGAATTTGCTAAATTAGTTGATGATGAAAATAAACTTAA
AAATGAATCTGCGCAATTAGAATCTAGTTTTAATAATGTTTATAAAGAAATCTTAGAACTTGCAGATTTAATACAA
GCAGAGGTGCATGTTGCAGGAAGGATAAATAGCTATATAAAAAAAAGAAAGACCACTAAAGAAAAAGAATATAAGA
AGAGAGAAATTAAGAATAAGATAGAAAAACAGGCTCTAATTAAGTTGTTCAATCAGTTATTAGAAAAAAGAGGCGA
TATTGAAAATCTTCATACTCAATTAAATAGTGGACTTAGCGAGAGAGCATCTGCAAAATACTTTTTTGAGAAAGCC
AAAGAAACTTTAAAAGCTGCTATTACTGAAAGATTAAATAACAAACGTAAAAATCGGCCATGGTGGGCAAGAAGAA
CACATAGTAATTTAGCAATACAGGCAAAAAATGAGGCAGAGGATGCTTTAAACCAATTAAGTACTTCTTCTTTTAG
GATACTTGAAGCAATGAAAATAAAGGAAGATGTAAAACAGCTTCTTGAAGAAGTAAAATCTTTTTCTAGATTCTTCA
AAGAGCAAAATCTTTTTCTAGTGGCGATAGATTATATGATTTTTTAGAGACGAGTAAATAA

t3.nt

AATGAATTAACTCGTAAAAAAATGCAAGACAAGAACGTGAAAATTTTAGGATTTTTAGAGAAAATTCAAGCAGATA
ATAAAGAAATTGTTGAAAAACATATAGAAAAAAAAGAAAAACAAATGGTGCAGGCTGCTTCTGTAGCACCTATTAA
TGTAGAGAGTAATTTCCCATATTATCTTCAAGAAGAAATAGAGATAAAAGAAGAAGAGTTGGTTCCAAATACTGAT

TABLE 1. Nucleotide and Amino Acid Sequences

GAAGAAAAGAAGGCAGAGAAGGCAATTAGCGATGGGAGTCTTGAATTTGCTAAATTAGTTGATGATGAAAATAAAC
TTAAAAATGAATCTGCGCAATTAGAATCTAGTTTTAATAATGTTTATAAAGAAATCTTAGAACTTGCAGATTTAAT
ACAAGCAGAGGTGCATGTTGCAGGAAGGATAAATAGCTATATAAAAAAAAGAAAGACCACTAAAGAAAAAGAATAT
AAGAAGAGAGAAATTAAGAATAAGATAGAAAAACAGGCTCTAATTAAGTTGTTCAATCAGTTATTAGAAAAAAGAG
GCGATATTGAAAATCTTCATACTCAATTAAATAGTGGACTTAGCGAGAGAGCATCTGCAAAATACTTTTTTGAGAA
AGCCAAAGAAACTTTAAAAGCTGCTATTACTGAAAGATTAAATAACAAACGTAAAAATCGGCCATGGTGGGCAAGA
AGAACACATAGTAATTTAGCAATACAGGCAAAAAATGAGGCAGAGGATGCTTTAAACCAATTAAGTACTTCTTCTT
TTAGGATACTTGAAGCAATGAAAATAAAGGAAGATGTAAAACAGCTTCTTGAAGAAGTAAAATCTTTTCTAGATTC
TTCAAAGAGCAAAATCTTTTCTAGTGGCGATAGATTATATGATTTTTTAGAGACGAGTAAATAA

f30.aa

MNKKILTLLVLILSISSVLMLSKSITKKSKYKIIRDYFINSNYVLVKIENKDLKFTISKPIYDKKLNNYFFKGQTT
SHFLISNNVDIAINTSPYEVKQNMFFPKGLYIYNKKMISKQINNYGEIVIKHNKIILNPKEDEIENCDYGFSGFFV
LIKNGKYKKNFKETRHPRTIIGTDKNNKHLFLVTIEGRGVNNSKGASLNEAIDFALSYGMTNAINLDGGGSSTLVV
KSNNAPYKLNFTANIFGQERPVPFHLGIKLPN

t30.aa

LSKSITKKSKYKIIRDYFINSNYVLVKIENKDLKFTISKPIYDKKLNNYFFKGQTTSHFLISNNVDIAINTSPYEV
KQNMFFPKGLYIYNKKMISKQINNYGEIVIKHNKIILNPKEDEIENCDYGFSGFFVLIKNGKYKKNFKETRHPRTI
IGTDKNNKHLFLVTIEGRGVNNSKGASLNEAIDFALSYGMTNAINLDGGGSSTLVVKSNNAPYKLNFTANIFGQER
PVPFHLGIKLPN

f30.nt

ATGAATAAAAAAATATTAACACTGCTAGTATTGATTTTAAGTATTTCATCAGTACTAATGCTGTCCAAATCAATCA
CCAAAAAATCCAAATACAAAATTATTAGGGATTATTTCATAAACAGCAATTATGTTCTGGTGAAAATTGAAAATAA
AGATCTAAAATTTACCATATCAAAACCTATTTACGACAAAAAGCTAAATAATTACTTCTTTAAAGGCCAAACAACA
AGCCATTTCTTAATTTCTAACAATGTTGACATTGCAATTAACACAAGTCCATACGAAGTTAAACAAAACATGTTTT
TCCCAAAAGGACTATACATATATAATAAAAAAATGATTTCAAAACAAATAAATAACTACGGAGAGATTGTAATAAA
GCACAACAAAATTATATTAAATCCCAAGGAAGACGAAATAGAAAACTGCGATTATGGATTTAGCGGATTTTTTGTT
TTAATCAAAAACGGAAAGTATAAAAAAAATTTTAAAGAAACAAGGCACCCAAGAACAATAATAGGAACTGATAAAA
ATAACAAGCATTTATTTCTTGTTACAATAGAAGGAAGGGGTGTCAATAATAGCAAAGGGGCCTCTCTTAATGAAGC
TATTGATTTTGCATTAAGCTACGGCATGACTAACGCTATTAATCTAGACGGGGGGGGCTCAAGCACTCTTGTTGTA
AAATCAAATAACGCTCCTTACAAATTAAACTTCACAGCAAACATCTTTGGACAGGAAAGACCTGTCCCATTTCATT
TAGGAATAAAACTTCCTAATTGA

t30.nt

CTGTCCAAATCAATCACCAAAAAATCCAAATACAAAATTATTAGGGATTATTTCATAAACAGCAATTATGTTCTGG
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TAAAGGCCAAACAACAAGCCATTTCTTAATTTCTAACAATGTTGACATTGCAATTAACACAAGTCCATACGAAGTT
AAACAAAACATGTTTTTCCCAAAAGGACTATACATATATAATAAAAAAATGATTTCAAAACAAATAAATAACTACG
GAGAGATTGTAATAAAGCACAACAAAATTATATTAAATCCCAAGGAAGACGAAATAGAAAACTGCGATTATGGATT
TAGCGGATTTTTTGTTTTAATCAAAAACGGAAAGTATAAAAAAAATTTTAAAGAAACAAGGCACCCAAGAACAATA
ATAGGAACTGATAAAAATAACAAGCATTTATTTCTTGTTACAATAGAAGGAAGGGGTGTCAATAATAGCAAAGGGG
CCTCTCTTAATGAAGCTATTGATTTTGCATTAAGCTACGGCATGACTAACGCTATTAATCTAGACGGGGGGGGCTC
AAGCACTCTTGTTGTAAAATCAAATAACGCTCCTTACAAATTAAACTTCACAGCAAACATCTTTGGACAGGAAAGA
CCTGTCCCATTTCATTTAGGAATAAAACTTCCTAATTGA

f308.aa

MQLLKNKYPFKRALLDLFLVYAIVYLASPFVNVNSEFWNVDENHFYFWISRSFLIIFIIYFFKLTSSYDDFRVEFF
IPKFKFIFLWDSVLIFIKTILIAMIVIFLIAFLLEYLLPESVLVYYFQNNAGFNWKISSKKAFFLMTFTSFFTGAF

TABLE 1. Nucleotide and Amino Acid Sequences

EELFYRAFVITKFTQMGFPVVATAILSSMFFAYGHLYYGILGFLVTFILGIFFAFTYLRYKNVYYVIFIHSFYNII
VSSLLLFLN

t308.aa

NSEFWNVDENHFYFWISRSFLIIFIIYFFKLTSSYDDFRVEFFIPKFKFIFLWDSVLIFIKTILIAMIVIFLIAFL
LEYLLPESVLVYYFQNNAGFNWKISSKKAFFLMTFTSFFTGAFEELFYRAFVITKFTQMGFPVVATAILSSMFFAY
GHLYYGILGFLVTFILGIFFAFTYLRYKNVYYVIFIHSFYNIIVSSLLLFLN

f308.nt

ATGCAATTGTTAAAAAATAAATATCCATTCAAGCGGGCTTTGCTTGATCTTTTTTTGGTCTATGCTATTGTTTATT
TGGCATCTCCTTTTGTAAATGTTAATTCAGAATTTTGGAATGTTGATGAAAATCATTTTTATTTTTGGATTTCAAG
ATCTTTTTTAATTATTTTTATAATTTATTTTTTTAAACTTACCAGTTCTTATGATGATTTTAGAGTAGAGTTTTTT
ATTCCTAAATTTAAATTTATTTTTCTTTGGGATTCTGTTTTAATTTTTATTAAAACAATATTGATTGCAATGATAG
TCATTTTTTTAATAGCTTTTTTGCTTGAATATTTGTTGCCAGAATCGGTACTTGTCTATTATTTTCAAAACAATGC
TGGATTTAATTGGAAGATTAGCAGTAAAAAAGCATTTTTTTTAATGACTTTTACCTCTTTTTTTACAGGAGCTTTT
GAAGAACTTTTTTACAGGGCTTTTGTTATTACTAAGTTTACACAAATGGGATTTCCTGTTGTAGCTACCGCCATTC
TTAGTAGTATGTTTTTTGCTTATGGGCATTTATATTATGGAATTTTAGGATTTTTGGTTACATTTATATTAGGGAT
ATTTTTTGCTTTTACTTATTTAAGGTATAAAAATGTATATTATGTGATTTTTATACATAGTTTTTATAATATTATT
GTTAGCAGCTTGTTGCTTTTTTTGAATTAA

t308.nt

AATTCAGAATTTTGGAATGTTGATGAAAATCATTTTTATTTTTGGATTTCAAGATCTTTTTTAATTATTTTTATAA
TTTATTTTTTTAAACTTACCAGTTCTTATGATGATTTTAGAGTAGAGTTTTTTATTCCTAAATTTAAATTTATTTT
TCTTTGGGATTCTGTTTTAATTTTTATTAAAACAATATTGATTGCAATGATAGTCATTTTTTTAATAGCTTTTTTG
CTTGAATATTTGTTGCCAGAATCGGTACTTGTCTATTATTTTCAAAACAATGCTGGATTTAATTGGAAGATTAGCA
GTAAAAAAGCATTTTTTTTAATGACTTTTACCTCTTTTTTTACAGGAGCTTTTGAAGAACTTTTTTACAGGGCTTT
TGTTATTACTAAGTTTACACAAATGGGATTTCCTGTTGTAGCTACCGCCATTCTTAGTAGTATGTTTTTTGCTTAT
GGGCATTTATATTATGGAATTTTAGGATTTTTGGTTACATTTATATTAGGGATATTTTTTGCTTTTACTTATTTAA
GGTATAAAAATGTATATTATGTGATTTTTATACATAGTTTTTATAATATTATTGTTAGCAGCTTGTTGCTTTTTTT
GAATTAA

f31.aa

MKKYLFFILFLISSNNLIVSYPLSFGGGFSYQFTNYTDKTGATKFAPNFTRADHGINLNLFFDANYVLFEMSYKEA
FVVTHNGRYFSLGLYGTYPMVFKEQVRMLFPLIGFKYAFDLSSNNFNLFFLSMGLAADLFIPDLDGLYIRPLFMLS
ISPFSNYKNFSGLTTEIMLGFNIGWRFFN

t31.aa

IVSYPLSFGGGFSYQFTNYTDKTGATKFAPNFTRADHGINLNLFFDANYVLFEMSYKEAFVVTHNGRYFSLGLYGT
YPMVFKEQVRMLFPLIGFKYAFDLSSNNFNLFFLSMGLAADLFIPDLDGLYIRPLFMLSISPFSNYKNFSGLTTEI
MLGFNIGWRFFN

f31.nt

ATGAAGAAATATCTTTTTTTTTATTTTATTTCTCATCTCTTCTAATAATTTAATTGTTTCTTATCCACTTTCTTTTG
GTGGAGGTTTTTCTTATCAATTTACTAATTATACTGATAAAACAGGCGCCACTAAATTTGCTCCAAATTTTACCAG
AGCAGATCATGGGATTAATTTGAATTTATTTTTTGATGCAAATTATGTACTTTTTGAAATGTCTTACAAAGAGGCT
TTTGTTGTTACTCACAATGGGAGATATTTCTCGCTTGGGCTTTATGGAACATATCCAATGGTTTTCAAAGAGCAGG
TTAGAATGCTTTTCCCATTAATTGGGTTTAAATATGCTTTTGATTTAAGCTCTAATAACTTCAATCTCTTTTTTTT
AAGCATGGGGCTTGCTGCTGATCTTTTTATTCCCGATCTTGATGGTTTATATATTAGGCCTTTGTTTATGCTTTCT
ATTTCTCCATTTTCTAATTATAAAAATTTTTCTGGGTTAACAACTGAGATTATGCTTGGATTTAATATCGGTTGGA
GATTTTTCAATTAG

TABLE 1. Nucleotide and Amino Acid Sequences

t31.nt

ATTGTTTCTTATCCACTTTCTTTTGGTGGAGGTTTTTCTTATCAATTTACTAATTATACTGATAAAACAGGCGCCA
CTAAATTTGCTCCAAATTTTACCAGAGCAGATCATGGGATTAATTTGAATTTATTTTTTGATGCAAATTATGTACT
TTTTGAAATGTCTTACAAAGAGGCTTTTGTTGTTACTCACAATGGGAGATATTTCTCGCTTGGGCTTTATGGAACA
TATCCAATGGTTTTCAAAGAGCAGGTTAGAATGCTTTTCCCATTAATTGGGTTTAAATATGCTTTTGATTTAAGCT
CTAATAACTTCAATCTCTTTTTTTTAAGCATGGGGCTTGCTGCTGATCTTTTTATTCCCGATCTTGATGGTTTATA
TATTAGGCCTTTGTTTATGCTTTCTATTTCTCCATTTTCTAATTATAAAAATTTTTCTGGGTTAACAACTGAGATT
ATGCTTGGATTTAATATCGGTTGGAGATTTTTCAATTAG

f939.aa

MKQKYENYFKKRLILNLLIFLLLACSSESIFSQLGNLQKIKHEYNILGSSSPRGISLVGETLYIAAMHLFKKENGK
IEKIDLSNSYEFINDIVNISGKTYLLAQNKEEELEVCELNGKDWTLKFKKPLKAYKFLKSVGRDGVKEAYILAIDK
NNREKIFDLQGSDKTPPQATENDKFYQISNEENLITGNSLKIWQMNNNTYTNIDYQQAKEIMPIIKTSIRGSSEVL
VMTGGYNNLDTKFKVYSNTNNYTTPIFIQDEVGEFSSYFAREFNDAILIGSNNGFAEFTKNKEGIFALRAPSKSVE
PGAYNGSQLSKTGLNDIIPVSNNTIYILTQGKGLWKLENRKLTKE

f939.aa

CSSESIFSQLGNLQKIKHEYNILGSSSPRGISLVGETLYIAAMHLFKKENGKIEKIDLSNSYEFINDIVNISGKTY
LLAQNKEEELEVCELNGKDWTLKFKKPLKAYKFLKSVGRDGVKEAYILAIDKNNREKIFDLQGSDKTPPQATENDK
FYQISNEENLITGNSLKIWQMNNNTYTNIDYQQAKEIMPIIKTSIRGSSEVLVMTGGYNNLDTKFKVYSNTNNYTT
PIFIQDEVGEFSSYFAREFNDAILIGSNNGFAEFTKNKEGIFALRAPSKSVEPGAYNGSQLSKTGLNDIIPVSNNT
IYILTQGKGLWKLENR
KLTKE

f939.nt

ATGAAACAAAAATACGAAAACTATTTTAAAAAAAGATTAATTTTAAACCTATTAATATTTTTACTACTAGCATGCT
CAAGCGAATCCATATTTTCACAATTAGGAAATCTGCAAAAAATAAAACATGAATACAATATTTTGGGCAGTTCAAG
TCCAAGAGGAATTTCTCTAGTAGGAGAAACTCTCTACATTGCAGCCATGCATTTATTTAAAAAAGAAAACGGCAAG
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TAGCGCAAAACAAAGAAGAAGAATTAGAAGTTTGCGAGCTAAATGGAAAAGATTGGACATTAAAATTTAAAAAACC
GCTAAAAGCATATAAATTCTTAAAATCCGTAGGAAGAGATGGCGTAAAAGAAGCATATATTTTAGCTATAGATAAA
AATAATCGTGAGAAAATTTTTGATCTACAAGGATCTGACAAAACACCACCACAAGCTACTGAAAATGACAAATTTT
ATCAAATATCAAATGAAGAAAACTTAATTACAGGAAATTCACTCAAAATATGGCAAATGAATAACAATACATACAC
AAACATAGACTATCAACAGGCCAAAGAAATAATGCCTATCATTAAAACAAGCATTAGGGGCTCTTCTGAAGTTTTA
GTAATGACTGGTGGTTACAATAATTTAGATACAAAATTTAAAGTTTACTCAAATACAAATAATTACACAACGCCAA
TATTTATTCAAGACGAAGTAGGCGAATTTAGCAGCTACTTTGCAAGAGAATTTAATGATGCGATATTAATCGGAAG
TAATAATGGATTTGCAGAATTTACAAAAAATAAAGAAGGAATTTTTGCCCTACGGGCACCCTCAAAATCTGTAGAA
CCTGGAGCTTATAACGGATCTCAGCTAAGCAAAACAGGCCTTAATGATATTATTCCTGTATCAAACAACACGATTT
ACATATTAACTCAGGGCAAGGGTTTGTGGAAATTGGAAAACAGAAAATTAACTAAAGAATAA

t939.nt

TGCTCAAGCGAATCCATATTTTCACAATTAGGAAATCTGCAAAAAATAAAACATGAATACAATATTTTGGGCAGTT
CAAGTCCAAGAGGAATTTCTCTAGTAGGAGAAACTCTCTACATTGCAGCCATGCATTTATTTAAAAAAGAAAACGG
CAAGATTGAAAAAATTGATTTGAGCAATTCTTATGAGTTTATAAACGACATTGTAAATATATCTGGAAAAACCTAT
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AACCGCTAAAAGCATATAAATTCTTAAAATCCGTAGGAAGAGATGGCGTAAAAGAAGCATATATTTTAGCTATAGA
TAAAAATAATCGTGAGAAAATTTTTGATCTACAAGGATCTGACAAAACACCACCACAAGCTACTGAAAATGACAAA
TTTTATCAAATATCAAATGAAGAAAACTTAATTACAGGAAATTCACTCAAAATATGGCAAATGAATAACAATACAT

TABLE 1. Nucleotide and Amino Acid Sequences

ACACAAACATAGACTATCAACAGGCCAAAGAAATAATGCCTATCATTAAAACAAGCATTAGGGGCTCTTCTGAAGT
TTTAGTAATGACTGGTGGTTACAATAATTTAGATACAAAATTTAAAGTTTACTCAAATACAAATAATTACACAACG
CCAATATTTATTCAAGACGAAGTAGGCGAATTTAGCAGCTACTTTGCAAGAGAATTTAATGATGCGATATTAATCG
GAAGTAATAATGGATTTGCAGAATTTACAAAAAATAAAGAAGGAATTTTTGCCCTACGGGCACCCTCAAAATCTGT
AGAACCTGGAGCTTATAACGGATCTCAGCTAAGCAAAACAGGCCTTAATGATATTATTCCTGTATCAAACAACACG
ATTTACATATTAACTCAGGGCAAGGGTTTGTGGAAATTGGAAAACAGAAAATTAACTAAAGAATAA

f739.aa

MQSGLKIKLILFFCCFACSCDINYPEIKELDYKINYYFTENRLDYSMSFDFAIKVINSKDVFKLSIENKNTNEFIQ
VINNNYSSFFIDSSLGKDILYCKDLRFNFFDKTFEDFTSCVRLFDKGMRVYNRELVISLGMSKYDLDDVHNYVYKS
KDMEMLNKLSNSKVFFVKTYKDKLHPVSSVVRIDSIDILEIDKAFDNYISFYYVEKNSNLFFKVG

t739.aa

CCFACSCDINYPEIKELDYKINYYFTENRLDYSMSFDFAIKVINSKDVFKLSIENKNTNEFIQVINNNYSSFFIDS
SLGKDILYCKDLRFNFFDKTFEDFTSCVRLFDKGMRVYNRELVISLGMSKYDLDDVHNYVYKSKDMEMLNKLSNSK
VFFVKTYKDKLHPVSSVVRIDSIDILEIDKAFDNYISFYYVEKNSNLFFKVG

f739.nt

ATGCAGAGCGGATTAAAAATTAAATTAATATTGTTTTTTTGTTGTTTTGCTTGTTCTTGCGACATAAATTATCCGG
AGATAAAAGAGCTTGATTATAAGATAAATTATTATTTTACTGAAAATCGCTTAGATTACTCTATGAGTTTTGATTT
TGCAATTAAAGTTATAAATTCAAAAGATGTTTTTAAATTATCAATAGAGAATAAGAACACTAATGAGTTTATTCAA
GTGATTAATAATAATTATAGCTCTTTTTTTATTGATTCTAGCCTTGGAAAGGATATTCTATATTGTAAGGATTTGA
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CAATAGAGAGCTTGTTATTTCTTTGGGTATGTCAAAATATGATTTAGATGATGTTCACAATTATGTATATAAGTCT
AAAGATATGGAAATGTTAAACAAGTTAAGCAATTCCAAAGTATTTTTTGTTAAAACTTATAAAGACAAACTACATC
CGGTCTCTTCAGTTGTTAGAATTGATTCAATAGATATTCTAGAGATTGATAAAGCATTTGATAATTACATAAGTTT
TTATTATGTCGAAAAAAATTCAAATCTTTTTTTTAAAGTTGGCTGA

t739.nt

TGTTGTTTTGCTTGTTCTTGCGACATAAATTATCCGGAGATAAAAGAGCTTGATTATAAGATAAATTATTATTTTA
CTGAAAATCGCTTAGATTACTCTATGAGTTTTGATTTTGCAATTAAAGTTATAAATTCAAAAGATGTTTTTAAATT
ATCAATAGAGAATAAGAACACTAATGAGTTTATTCAAGTGATTAATAATAATTATAGCTCTTTTTTTATTGATTCT
AGCCTTGGAAAGGATATTCTATATTGTAAGGATTTGAGGTTTAATTTTTTTGATAAAACTTTTGAAGATTTTACCT
CATGTGTTCGTCTTTTTGATAAGGGCATGAGAGTATACAATAGAGAGCTTGTTATTTCTTTGGGTATGTCAAAATA
TGATTTAGATGATGTTCACAATTATGTATATAAGTCTAAAGATATGGAAATGTTAAACAAGTTAAGCAATTCCAAA
GTATTTTTTGTTAAAACTTATAAAGACAAACTACATCCGGTCTCTTCAGTTGTTAGAATTGATTCAATAGATATTC
TAGAGATTGATAAAGCATTTGATAATTACATAAGTTTTTATTATGTCGAAAAAAATTCAAATCTTTTTTTTAAAGT
TGGCTGA

f742.aa

MNKKHTNFSVLLLLIFLLILSFGGFGYYIYQSKLNDKNREIMLNEVKNSVIDRNYKKAYSVAKLLQDKYPQNEDIA
MLTNTLAEIANSSPFESKDLQRDSANQILDKIKGQDNTKTNVNENFDIAFNNRYIKDSTITENYSDRNDDVGIEDE
DISEFKKSKIPEKIKPNTNPKEEDQIIQSPNPKLSVNDQKNLFNLEKLKKNLSGKSNSENILNDSQKIENDKQNTN
LSKEKNSENILKTPDNSKYSNNNNTTSLKKISSNSQKESELSPPSQTIIGKIYRPYSYLIKKELYEILDDINTGRV
TLGKNRLKELIKKGLSNKFQKVNELIENSKNKEASNLLLTLIKKDIEPNLINIPKDPYKKEIFQLDKEDKKPQYLE
DLKSKVHSIKPIDLENTKSRQQAIKDLNEFLKNNPNDAQASKTLAQANKIQHLEDLKSKVHSIKPIDLENTKSRQQ
AIKDLNEFLKNNPNDAQASKTLAQANKIQHLEDLKSKVHSIKPIDLENTKSRQQAIKDLNEFLKNNPNDAQASKTL
AQANKIQHLEDLKSKVHSIKPIDLENTKSRQQAIKDLNEFXKNNPNDAQASKTLAQANKIQHLEDLKSKVHSIKPI
DLENTKSRQQAIKDLNEFXKNNPNDAQASKTLAQANKIQHLEDLKSKVHSIKPIDLENTKSRQQAIKDLNEFLKNN
PNDAQASKTLAQANKIQHLEDLKSKVHSIKPIDLENTKSRQQAIKDLNEFXKNNPNDAQASKTLAQAYENNGDLLK
AENAYEKIIKLTNTQEDHYKLGIIRFKLKKYEHSIESFDQTIKLDPKHKKALHNKGIALMMLNKNKKAIESFEKAI

TABLE 1. Nucleotide and Amino Acid Sequences

QIDKNYGTAYYQKGIAEEKNGDMQQAFASFKNAYNLDKNPNYALKAGIVSNNLGNFKQSEEYLNFFNANAKKPNEI
AIYNLSIAKFENNKLEESLETINKAIDLNPEKSEYLYLKASINLKKENYQNAISLYSLVIEKNPENTSAYINLAKA
YEKSGNKSQAISTLEKIINKNNKLALNNLGILYKKEKNYQKAIEIFEKAIINSDIEAKYNLATTLIEINDNTRAKD
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t742.aa

KLNDKNREIMLNEVKNSVIDRNYKKAYSVAKLLQDKYPQNEDIAMLTNTLAEIANSSPFESKDLQRDSANQILDKI
KGQD
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KESELSPPSQTIIGKIYRPYSYLIKKELYEILDDINTGRVTLGKNRLKELIKKGLSNKFQKVNELIENSKNKEASN
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DAQASKTLAQANKIQHLEDLKSKVHSIKPIDLENTKSRQQAIKDLNEFLKNNPNDAQASKTLAQANKIQHLEDLKS
KVHSIKPIDLENTKSRQQAIKDLNEFLKNNPNDAQASKTLAQANKIQHLEDLKSKVHSIKPIDLENTKSRQQAIKD
LNEFXKNNPNDAQASKTLAQANKIQHLEDLKSKVHSIKPIDLENTKSRQQAIKDLNEFXKNNPNDAQASKTLAQAN
KIQHLEDLKSKVHSIKPIDLENTKSRQQAIKDLNEFLKNNPNDAQASKTLAQANKIQHLEDLKSKVHSIKPIDLEN
TKSRQQAIKDLNEFXKNNPNDAQASKTLAQAYENNGDLLKAENAYEKIIKLTNTQEDHYKLGIIRFKLKKYEHSIE
SFDQTIKLDPKHKKALHNKGIALMMLNKNKKAIESFEKAIQIDKNYGTAYYQKGIAEEKNGDMQQAFASFKNAYNL
DKNPNYALKAGIVSNNLGNFKQSEEYLNFFNANAKKPNEIAIYNLSIAKFENNKLEESLETINKAIDLNPEKSEYL
YLKASINLKKENYQNAISLYSLVIEKNPENTSAYINLAKAYEKSGNKSQAISTLEKIINKNNKLALNNLGILYKKE
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f742.nt

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CCATTGATCTTGAAAACACAAAAT
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AGCTCAAGCTAATAAAATACAACACCTGGAGGACCTTAAATCTAAGGTTCATTCAATAAAACCCATTGATCTTGAA
AACACAAAATCACGCCAACAAGCCATTAAGGATCTAAACGAATTCTTAAAAACAATCCCAATGACGCCCAGGCCTC

TABLE 1. Nucleotide and Amino Acid Sequences

TAAAACTTTAGCTCAAGCTTATGAAAACAATGGAGATTTGCTAAAAGCAGAAAATGCATACGAAAAAATTATCAAA
CTCACAAATACCCAAGAAGATCACTATAAACTTGGAATCATTAGATTCAAGCTTAAAAAGTATGAACACTCAATAG
AATCATTTGATCAAACAATAAAACTCGACCCAAAACATAAAAAAGCACTTCATAACAAAGGAATAGCTTTAATGAT
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TACCAAAAAGGAATAGCAGAAGAAAAAAATGGCGATATGCAACAAGCATTTGCAAGCTTTAAAAATGCCTACAATC
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AACAATCCAGAGGCCTTACATGCACTAGGAATAATAGAATATAATGAAAATAACAATGATCAAACACTAAGAGAAC
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t742.nt

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CATATTCTGTTGCAAAACTTCTGCAAGACAAATACCCCCAAAATGAAGACATTGCAATGCTTACAAATACACTAGC
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AATCTTAAAAAAGAAAATTACCAAAATGCTATATCACTTTACAGCTTAGTAATTGAAAAAAACCCTGAAAATACTT

TABLE 1. Nucleotide and Amino Acid Sequences

CAGCCTATATAAACCTGGCAAAAGCATATGAAAAATCAGGAAATAAAAGTCAAGCAATCTCAACTCTTGAAAAGAT
AATAAACAAAAATAATAAATTAGCCTTAAACAATCTTGGGATACTTTACAAAAAAGAAAAAAATTATCAAAAAGCA
ATTGAAATTTTTGAAAAAGCAATAATCAATTCAGATATTGAAGCAAAATATAATCTTGCAACCACTCTAATTGAAA
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TGCACTAGGAATAATAGAATATAATGAAAATAACAATGATCAAACACTAAGAGAACTATAAAAAAATTTCCAAATT
ACAAAAAAAATGAAAATATTAAAAAAATAATAGGAATATAA

f743.aa

MRIYLFLNKNYKIFILFLILILNSKLAYSQRLIRIGKEEMKNKNYIQAIETLSDAIKKYPKVQLGYYFLSIAYREN
NQLTEAEGALLDGIAVGGEIDYILYYELGNIMFNRGEGYYPLAIKYYSNSIKSRPNYDSALLNRANAYVQQGKITS
KEKEYQKAWDSYTMAIHDYSQFITLRSKTEKKDSILLIISYLRNEKINLEQLDKSLKGRTEHIVYAKEDKNQILKD
SFKDNLETNSLIELEKLNWQEELYIDE

t743.aa

YSQRLIRIGKEEMKNKNYIQAIETLSDAIKKYPKVQLGYYFLSIAYRENNQLTEAEGALLDGIAVGGEIDYILYYE
LGNIMFNRGEGYYPLAIKYYSNSIKSRPNYDSALLNRANAYVQQGKITSKEKEYQKAWDSYTMAIHDYSQFITLRS
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f743.nt

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TGGC
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TTAAAGACAACCTAGAAACAAATTCTTTAATTGAGCTAGAAAAACTTAATTGGCAAGAGGAGTTATACATAGATGA
ATAA

t743.nt

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TAA

f748.aa

MKFIINLLLSTIKIITFTVIVCLTILSIFQPIYILKENEISITTRLGKIQRTENLAGLKYKIPLIENVQIFPKIIL
RWDGEPQRIPTGGEEKQLIWIDTTARWKIADINKFYTTIKTMSRAYVRIDAAIEPAVRGVIAKYPLLEIIRSSNDP
IQRLSNGILTPQETKINGIYKITKGRKIIEKEIIRIANNNTKDIGIEIVDVLIRKVTYDPSLIESVNNRMISERQQ
IAEEQRSIGLAEKTEILGSIEKEKLKILSEAKATAAKIKAEGDREAAKIYSNAYGKNIEFYKFWQALESYKAVLKD
KRKIFSTDMDFFQYLHKRN

TABLE 1. Nucleotide and Amino Acid Sequences

t748.aa

IFQPIYILKENEISITTRLGKIQRTENLAGLKYKIPLIENVQIFPKIILRWDGEPQRIPTGGEEKQLIWIDTTARW
KIADINKFYTTIKTMSRAYVRIDAAIEPAVRGVIAKYPLLEIIRSSNDPIQRLSNGILTPQETKINGIYKITKGRK
IIEKEIIRIANNNTKDIGIEIVDVLIRKVTYDPSLIESVNNRMISERQQIAEEQRSIGLAEKTEILGSIEKEKLKI
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f748.nt

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t748.nt

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f764.aa

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IAKDVEKDFQYEFNIYKQ

f764.aa

EKQFNYAIIFSDATEYFFEIQTTPFIKNEILFINDKNLEIIKDKLKTTKKILLTHKSNNEILNNEILKEKIFYLSK
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f764.nt

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CATAAAAAACGAAATACTATTTATAAATGACAAAAAATTTAGAAATTATAAAAGACAAGCTTAAAACAACAAAAAAA

TABLE 1. Nucleotide and Amino Acid Sequences

ATACTATTAACTCATAAATCAAATAATGAAATTCTAAATAACGAAATTCTAAAAGAGAAAATTTTTTATCTATCAA
AAATAAAATTTTCTCTAAAAAAATCTATTGACTTTCTGCTTAACGAAAAATCAATAGATTTGCAAAAAACATTACT
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t764.nt

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f770.aa

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t770.aa

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f770.nt

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TTAA

t770.nt

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f790.aa

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RVEITILNN

t790.aa

TABLE 1. Nucleotide and Amino Acid Sequences

SEIFEFKYIKGSKFRLEGTDNQKIYFNGHYNSSSNTNIQISSEIKDIKENFASIKAFFRILKRENINEPYLLNEEF
EEIFSVNKQGEYTIGANQKRPSVRGIPRFPKTPIKINEKWSYLAEEYIEASKIDKSIKDFVVKFNVNYEYKGKEEH
NGKHYHIILSNYESQYNVKNISFYQKVDQKIYFDNEIGNTYKYSDKYIFEINQNNNQHFKMIGNSLGRIVSIELPN
DNLIETEVENYIREKKIKAIEVEKNNKGINLSFDIEFYPNSFQILQKEYKKIDLIAKLLEKFKKNNILIEGHTEQF
GLEEEMHELSEKRARAIGNYLIKMKVKDKDQILFKGWGSQKPKYPKSSPLKAKNRRVEITILNN

f790.nt

ATGAATACCAAGGCGACTACACCATTGTTGTTATTATTTTTAATTCAAAGCTTAGCTTTTTCTTCTGAAATCTTTG
AATTTAAATACATTAAAGGTTCAAAGTTTAGATTAGAAGGCACAGATAATCAAAAAATATATTTCAATGGCCATTA
TAATTCAAGCTCTAATACCAATATTCAAATTTCAAGTGAAATAAAAGACATAAAAGAAAACTTTGCAAGCATTAAA
GCTTTTTTTAGAATCTTAAAAAGAGAAAATATTAATGAACCTTACCTATTAAATGAAGAGTTTGAAGAAATCTTCA
GCGTAAATAAGCAAGGAGAATATACAATAGGAGCAAATCAAAAAAGACCTTCTGTTAGAGGTATTCCAAGATTCCC
AAAAACACCAATCAAAATAAATGAAAAATGGTCATATCTTGCAGAAGAATATATAGAAGCGTCAAAAATAGACAAA
AGTATAAAAGATTTCGTTGTAAAATTTAATGTTAACTACGAATATAAAGGCAAAGAAGAGCACAATGGCAAGCATT
ACCACATAATTCTTTCGAATTATGAATCACAATACAATGTAAAAAACATCTCTTTCTATCAAAAAGTAGACCAAAA
AATTTATTTTGATAATGAAATTGGCAATACATATAAATACAGCGATAAATATATATTTGAAATAAATCAGAACAAC
AACCAACATTTTAAAATGATTGGAAACTCTCTTGGCAGAATAGTTTCAATTGAGCTTCCAAATGATAATCTTATTG
AAACTGAGGTTGAAAATTACATCCGAGAAAAAAAAATAAAAGCTATTGAAGTTGAAAAAAACAATAAAGGTATTAA
TTTAAGCTTTGACATTGAATTTTATCCTAACTCATTTCAAATACTACAAAAAGAATATAAAAAAATTGACCTTATA
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AGATGCACGAGCTATCTGAAAAAAGAGCTCGTGCAATTGGAAATTATTTAATAAAAATGAAAGTAAAAGACAAAGA
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CGAGTAGAAATTACAATATTAAATAACTAA

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GGCTAAAAATAGGCGAGTAGAAATTACAATATTAAATAACTAA

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MKIFIYWVVIFFFSVFKVFSIYSLTDEEFFKKYSLFFVHKGFLSKNVNGKITKVQVNGINSRWVYPFYKLVPSRIT
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KNLNRLIPQIYLGAGYYDIISAIEFSKEETNNLYFSSGVYGDIFLISQKSGFIKKISFPFKKQIIRILDLSSKNVE
KILVRTYDNHFYSYINGQWVFIGKLSLQDQDFFEKSQRMQLAKNKGSIYLTAYTLRNKKAVDERFKFIKDSGMNAV
VIDFKDDNGNLTYSSKLSLPNKLRSVKNFIDVPYILKKAKELGIYVIARCVVFKDSKLYYYDNFKHALWNKKTNKP
WAHLIKKVDSSGLVKYVQVEHWVDIFSPATWEYNISIAKEIQSFGVDEIQFDYIRFPSDGPVSLAISRMNKYEMQP
VDALESFLIMAREQLYVPISVDIYGYNGWFPTNSIGQNISMLSDYVDVISPMFYPSHYTDDFLPSNFYYTKRAYRI
YKEGSDRALAFSLDGVVIRPYVQAFLLGKERLVDDEIYLEYLKFQLKGIKESFGSGFSLWNASNVYYMIKGSLKEY
LDSF

TABLE 1. Nucleotide and Amino Acid Sequences

t792.aa

IYSLTDEEFFKKYSLFFVHKGFLSKNVNGKITKVQVNGINSRWVYPFYKLVPSRITSIYEDVYSSSSFLTTSNNLY
VSYDYSKNFRKLVGIDKFNSGAYITSSAFSQGDYKRIAIGTAIHGIYLSVNGAISFKNLNRLIPQIYLGAGYYDII
SAIEFSKEETNNLYFSSGVYGDIFLISQKSGFIKKISFPFKKQIIRILDLSSKNVEKILVRTYDNHFYSYINGQWV
FIGKLSLQDQDFFEKSQRMQLAKNKGSIYLTAYTLRNKKAVDERFKFIKDSGMNAVVIDFKDDNGNLTYSSKLSLP
NKLRSVKNFIDVPYILKKAKELGIYVIARCVVFKDSKLYYYDNFKHALWNKKTNKPWAHLIKKVDSSGLVKYVQVE
HWVDIFSPATWEYNISIAKEIQSFGVDEIQFDYIRFPSDGPVSLAISRMNKYEMQPVDALESFLIMAREQLYVPIS
VDIYGYNGWFPTNSIGQNISMLSDYVDVISPMFYPSHYTDDFLPSNFYYTKRAYRIYKEGSDRALAFSLDGVVIRP
YVQAFLLGKERLVDDEIYLEYLKFQLKGIKESFGSGFSLWNASNVYYMIKGSLKEYLDSF

f792.nt

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ATGAAGAATTTTTTAAAAAATATAGTTTATTTTTTGTTCATAAAGGATTTTTAAGTAAAAATGTTAATGGGAAAAT
AACCAAAGTTCAAGTCAATGGGATAAATTCTAGGTGGGTTTACCCTTTTTATAAGCTTGTTCCTAGTCGAATTACT
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AAAATTTTAGTCAGAACATATGACAATCATTTTTATTCTTATATTAATGGGCAATGGGTATTTATTGGAAAATTAT
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TATTAGGAAAAGAAAGATTGGTGGATGACGAGATTTATTTGGAGTATTTAAAGTTTCAGCTTAAAGGAATTAAAGA
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TTAGATTCTTTTTA

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ATATATTCATTAACCGATGAAGAATTTTTTAAAAAATATAGTTTATTTTTTGTTCATAAAGGATTTTTAAGTAAAA
ATGTTAATGGGAAAATAACCAAAGTTCAAGTCAATGGGATAAATTCTAGGTGGGTTTACCCTTTTTATAAGCTTGT
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CTAGTGCCTTTTCTCAAGGAGATTACAAGCGTATTGCTATTGGAACTGCGATTCATGGTATTTATCTTAGTGTTAA
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TTAGTCAGAAAAGTGGATTTATTAAAAAAATATCTTTTCCTTTCAAAAAGCAAATAATACGTATTTTAGACTTATC
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TTTATTGGAAAATTATCTTTGCAGGATCAGGATTTTTTTGAAAAATCACAAAGGATGCAGCTTGCTAAAAATAAAG
GGTCTATTTATTTAACAGCATATACATTGCGTAATAAGAAGGCAGTTGATGAAAGATTTAAATTTATTAAAGATTC
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TTATTGCTAGATGTGTTGTATTTAAAGATTCAAAATTGTATTATTATGATAATTTTAAACACGCCCTTTGGAATAA
AAAAACCAATAAACCTTGGGCTCATTTGATTAAAAAAGTTGATTCTAGTGGTCTTGTGAAATATGTACAAGTAGAG

TABLE 1. Nucleotide and Amino Acid Sequences

CATTGGGTAGATATTTTTTCTCCTGCTACTTGGGAATATAATATTTCTATCGCAAAAGAAATTCAATCTTTTGGAG
TTGACGAGATACAATTTGATTATATTAGATTTCCATCAGATGGGCCTGTGTCTCTTGCAATCTCAAGAATGAATAA
GTATGAGATGCAACCCGTTGATGCACTTGAATCTTTTTTGATTATGGCAAGAGAACAGCTTTATGTTCCTATTTCT
GTTGATATTTATGGGTACAATGGCTGGTTTCCTACTAATAGTATTGGGCAAAATATTTCAATGTTATCAGATTATG
TTGACGTCATATCTCCTATGTTTATCCTTCGCATTATACTGATGATTTTTGCCAAGCAATTTTTATTACACAAA
AAGAGCTTATAGGATTTATAAAGAGGGGAGTGATAGAGCACTTGCTTTTTCTTTAGATGGGGTTGTTATTAGGCCT
TATGTTCAAGCTTTTTTATTAGGAAAAGAAAGATTGGTGGATGACGAGATTTATTTGGAGTATTTAAAGTTTCAGC
TTAAAGGAATTAAAGAGTCATTTGGTAGTGGCTTTAGCCTTTGGAATGCATCTAATGTTTATTATATGATTAAAGG
TAGTTTAAAAGAATATTTAGATTCTTTTTAA

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MSIKKFILTLIILSLAKNSFSENEINIFENENYIVKENIKTEIKKLKQSFLLASVDVAISQPYIELADLNGEPIKE
LEGISYSFINVFSKIGSSAIISFDLSNEASKKYKIIKLEFLSPDKGNFINQLSSLTSGKQQSKKELAKDAYSFGTL
RTESLSKTIAEYYKDNNWYYILAAITVENNINKETEKYEIRINPKIYNDFQKKLRLHFKSNQIKKFPIPIIE

t797.aa

KNSFSENEINIFENENYIVKENIKTEIKKLKQSFLLASVDVAISQPYIELADLNGEPIKELEGISYSFINVFSKIG
SSAIISFDLSNEASKKYKIIKLEFLSPDKGNFINQLSSLTSGKQQSKKELAKDAYSFGTLRTESLSKTIAEYYKDN
NWYYILAAITVENNINKETEKYEIRINPKIYNDFQKKLRLHFKSNQIKKFPIPIIE

f797.nt

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CTTGAAGGGATTAGTTATTCATTTATAAATGTATTTTCAAAAATTGGATCTTCTGCTATTATTTCATTTGACCTAT
CAAACGAAGCTTCCAAGAAATACAAAATCATAAAATTAGAATTTTTAAGTCCAGATAAAGGCAATTTTATTAACCA
GCTAAGCAGCCTTACTAGTGGAAAACAGCAATCAAAAAAAGAGCTTGCAAAAGACGCTTACTCATTTGGTACATTA
AGAACTGAATCTCTTTCAAAAACAATTGCAGAATATTACAAAGATAACAACTGGTATTATATTTTAGCAGCAATAA
CAGTAGAAAATAATATAAATAAAGAAACTGAAAAATACGAAATTAGAATTAACCCTAAAATATATAATGATTTTCA
AAAAAAATTGAGATTACATTTTAAAAGCAACCAAATAAAAAAATTTCCAATACCCATTATAGAATAA

t797.nt

AAAAATAGCTTTTCTGAAAACGAAATTAATATCTTCGAAAACGAAAATTATATTGTAAAAGAAAATATAAAAACAG
AAATTAAAAAACTAAAACAAAGTTTTTTACTTGCATCTGTTGATGTCGCCATTAGCCAACCCTACATAGAATTGGC
AGATTTAAATGGAGAACCGATAAAAGAACTTGAAGGGATTAGTTATTCATTTATAAATGTATTTTCAAAAATTGGA
TCTTCTGCTATTATTTCATTTGACCTATCAAACGAAGCTTCCAAGAAATACAAAATCATAAAATTAGAATTTTTAA
GTCCAGATAAAGGCAATTTTATTAACCAGCTAAGCAGCCTTACTAGTGGAAAACAGCAATCAAAAAAAGAGCTTGC
AAAAGACGCTTACTCATTTGGTACATTAAGAACTGAATCTCTTTCAAAAACAATTGCAGAATATTACAAAGATAAC
AACTGGTATTATATTTTAGCAGCAATAACAGTAGAAAATAATATAAATAAAGAAACTGAAAAATACGAAATTAGAA
TTAACCCTAAAATATATAATGATTTTCAAAAAAAATTGAGATTACATTTTAAAAGCAACCAAATAAAAAAATTTCC
AATACCCATTATAGAATAA

f799.aa

MKKHIIIGIIFVAILLFFKILLIPRIQNHENNKNNIKMIISYKQDKNRLSLKINIKTKKTTNLGKAKLDIYLDSKL
IESNLLYISSKNFTTYANIIYQNESLLSIILKSNGNNNVFYSKRIKPRGKI

t799.aa

HENNKNNIKMIISYKQDKNRLSLKINIKTKKTTNLGKAKLDIYLDSKLIESNLLYISSKNFTTYANIIYQNESLLS
IILKSNGNNNVFYSKRIKPRGKI

TABLE 1. Nucleotide and Amino Acid Sequences

f799.nt

ATGAAAAAACATATCATTATTGGGATAATCTTTGTTGCAATTCTTTTATTTTTTAAAATTTTATTAATTCCCAGAA
TTCAAAATCACGAAAATAATAAAAATAATATCAAAATGATAATAAGCTACAAGCAAGACAAAAACAGATTATCGCT
AAAGATAAACATAAAAACAAAAAAAACTACCAACCTGGGAAAAGCCAAACTAGATATTTATCTAGACAGTAAATTA
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TATTAAGTATAATATTAAAGAGTAATGGCAATAATAATGTCTTTTATAGTAAAAGAATAAAACCTAGAGGTAAAAT
ATGA

t799.nt

CACGAAAATAATAAAAATAATATCAAAATGATAATAAGCTACAAGCAAGACAAAAACAGATTATCGCTAAAGATAA
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CAATTTGCTTTATATAAGCAGCAAAAACTTTACAACATATGCTAATATAATCTATCAAAATGAAAGTTTATTAAGT
ATAATATTAAAGAGTAATGGCAATAATAATGTCTTTTATAGTAAAAGAATAAAACCTAGAGGTAAAATATGA

f800.aa

MKKHYKALILSLLFAIISCNTKTLNELGEEQFKIPFGTLPGAIMPLNNKFTNSKFDIKTYNGLVYIAEIKTNKLMI
FNSYGKLIQTYQNGIFKTNPDLKIKKIDFEGIQAIYPLKDFIIVADKLNNKKSKFNQKENIAYFMRILILNKNSSV
EILGQEGLNGMPFPQIYDVNVDENGNIAIISIYSEGYIIYSYNKEFSPLYKIYVNKNLLKTIDNQKKKYNISIDKV
FFEVNKKTLYVKTTYYENIGDNENINDLGIKIKDQYIYKMSLKKNKELEVINKIALPKNLLDDKQESFINIIKIQK
DKIIASTNMKNLSNNLIWKLDSKGSIKEQIALIEPPNLMFLSESLSKDGILSILYGGKTGVSVYWWNLNALLKL

t800.aa

KTLNELGEEQFKIPFGTLPGAIMPLNNKFTNSKFDIKTYNGLVYIAEIKTNKLMIFNSYGKLIQTYQNGIFKTNPD
LKIKKIDFEGIQAIYPLKDFIIVADKLNNKKSKFNQKENIAYFMRILILNKNSSVEILGQEGLNGMPFPQIYDVNV
DENGNIAIISIYSEGYIIYSYNKEFSPLYKIYVNKNLLKTIDNQKKKYNISIDKVFFEVNKKTLYVKTTYYENIGD
NENINDLGIKIKDQYIYKMSLKKNKELEVINKIALPKNLLDDKQESFINIIKIQKDKIIASTNMKNLSNNLIWKLD
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f800.nt

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TTAAAGAACAAATAGCTTTAATTGAGCCTCCAAATTTAATGTTTCTCTCTGAGAGTTTATCTAAAGATGGAATACT
TAGTATACTTTATGGCGGAAAAACTGGTGTTAGTGTTTACTGGTGGAATTTAAATGCATTATTAAAATTATAA

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TAAATTAATGATTTTCAACTCATACGGAAAACTAATACAAACATATCAAAATGGAATATTTAAAACAAACCCCGAT
TTAAAAATAAAAAAAATAGATTTTGAAGGAATTCAAGCAATATACCCACTAAAAGATTTTATTATTGTCGCAGACA

TABLE 1. Nucleotide and Amino Acid Sequences

AACTAAATAATAAAAAATCAAAATTCAACCAAAAAGAGAATATTGCCTACTTCATGAGAATACTAATACTAAACAA
AAACTCATCTGTAGAAATTTTGGGTCAAGAAGGTTTAAACGGAATGCCATTTCCACAAATTTATGATGTTAATGTT
GATGAAAATGGCAACATTGCAATAATATCAATATATAGCGAAGGATATATAATATATTCTTACAATAAAGAATTTT
CCCCGCTTTATAAAATTTACGTCAACAAAAACCTGTTAAAAACAATAGACAATCAAAAGAAAAAATACAACATTTC
AATAGATAAGGTTTTTTTTGAAGTCAACAAAAAAACTCTTTATGTAAAAACTACTTACTATGAAAACATTGGTGAC
AATGAAAATATAAACGATCTTGGAATTAAAATTAAAGATCAATATATCTATAAAATGAGTTTGAAAAAAAACAAAG
AATTAGAAGTGATAAATAAAATTGCTCTTCCTAAAAACTTACTAGATGATAAACAAGAAAGCTTTATAAACATTAT
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AGCAAGGGCTCAATTAAAGAACAAATAGCTTTAATTGAGCCTCCAAATTTAATGTTTCTCTCTGAGAGTTTATCTA
AAGATGGAATACTTAGTATACTTTATGGCGGAAAAACTGGTGTTAGTGTTTACTGGTGGAATTTAAATGCATTATT
AAAATTATAA

f810.aa

MYKLFLFFIIFMFLSCDEKKSSKNLKSVKIGYVNWGGETAATNVLKVVFEKMGYNAEIFSVTTSIMYQYLASGKID
GTVSSWVPTADKFYYEKLKTKFVDLGANYEGTIQGFVVPSYVPISSISELKGKGDKFKNKMIGIDAGAGTQIVTEQ
ALNYYGLSKEYELVPSSESVMLASLDSSIKRNEWILVPLWKPHWAFSRYDIKFLDDPDLIMGGIESVHTLVRLGLE
NDDFDAYYVFDHFYWSDDLILPLMDKNDKEPGKEYRNAVEFVEKNKEIVKTWVPEKYKTLFD

t810.aa

CDEKKSSKNLKSVKIGYVNWGGETAATNVLKVVFEKMGYNAEIFSVTTSIMYQYLASGKIDGTVSSWVPTADKFYY
EKLKTKFVDLGANYEGTIQGFVVPSYVPISSISELKGKGDKFKNKMIGIDAGAGTQIVTEQALNYYGLSKEYELVP
SSESVMLASLDSSIKRNEWILVPLWKPHWAFSRYDIKFLDDPDLIMGGIESVHTLVRLGLENDDFDAYYVFDHFYW
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f810.nt

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t810.nt

TGTGATGAAAAAAAGAGTTCAAAGAATTTAAAATCGGTAAAAATTGGATATGTGAATTGGGGTGGAGAAACGGCAG
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CGTGCATACTCTTGTTAGACTTGGTCTTGAAAATGATGATTTTGATGCATATTATGTTTTTGATCATTTTTATTGG
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TTGTTGAAAAGAATAAAGAGATTGTAAAGACGTGGGTTCCAGAAAAATATAAGACCTTATTTGATTAA

f814.aa

TABLE 1. Nucleotide and Amino Acid Sequences

MLVKRIVGKPITMLILFSLLLMISLYTFSRLKVDLLPGIDIPQISIHTVYPGASPREVEESVSRVLESGLSSVKNL
KNIYSVSSKESSTVSLEFYHGTDLDLVLNEIRDALELVKSSLPSKSQTPRIFRYNLKNIPVMEIVINSVRPVSELK
RYADEIIKPGLERLDGVAIVTVNGGSKKRVLIEVSQNRLESYGLSLSRISSIIASQNLELSAGNILENNLEYLVEV
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KGYKSIIATLRADRITFNVLFPLKEESRDNLTQSVDYDSIKYKIMNRIGNLYPEFNIEPSISGNALGGGDSIKIKI
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EKGLNYDIVLKLDRMDVKNLKDLEKIFITNSSGVKIPFSSIATFEKTNKAESIYRENQALTIYLNAGISPDDNLTQ
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PIEIKLKDIANIKTDFEDLSEYVEYNGLPSISLSVQKRSDSNSIAVSNVVMNEIEKLKLSMPKDMKLEIASDSTDF
IKASISTVVNSAYFGAMLAIFVIFFFLRSFRATIIIGISIPIAIVLTFCLMYFVNISLNIMSLAGLALGIGMVVDC
SIVVIDNIYKYRQKGAKLISSSILGAQEMMLPITSSTFTSICVFGPFLIFKSELGVYGDFFKDFTFTIVISLGVSL
LVAIFLVPVLSSHYVGLYTSFQKNIKNAFIRKIDAFFASIYYFLEFLYINLLNIVLNHKLIFGLIVFFSFIGSLLL
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NSSGVKIPFSSIATFEKTNKAESIYRENQALTIYLNAGISPDDNLTQVTAKVVDFINNKVPHKEGITLKVEGEYNE
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TABLE 1. Nucleotide and Amino Acid Sequences

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GCATTTTCTAGCGGAAGTGGAAATGAACTTCTAAAACCAATTGCATTTACTTTTATTGGCGGAATGACAGCTAGCA
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TABLE 1. Nucleotide and Amino Acid Sequences

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GTCGTTCAAGGCTTAGGCCAATTTTAATGTCTTCTTTGACCTCAATAATAGGGCTTATTCCAATGGCATTTTCTAG
CGGAAGTGGAAATGAACTTCTAAAACCAATTGCATTTACTTTTATTGGCGGAATGACAGCTAGCACATTTCTTACT
TTGTTTTTTATTCCCATGCTTTTTGAAATTTTTCCAACATGTTTCAAGTTTCAAATCTAG

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MLKNHSKLIIQLKVVMMIYLKKMGNDMTKFYNYRIEIVSNLSLELDVFECIEKIEQELGESIYYSKIGNVYGKGKK
GEKHGNGVWPEENFILIIYTSNQSIVERLKDIVDDLNRSYPTEGINLFVLRNS

t818.aa

KKMGNDMTKFYNYRIEIVSNLSLELDVFECIEKIEQELGESIYYSKIGNVYGKGKKGEKHGNGVWPEENFILIIYT
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f818.nt

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t818.nt

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f820.aa

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NITGFVGTDNLGLEGIEFSLNSILGKDKTKQQFLNEEPETNNIHLTIDMDIQQGVSKIAKKYFKENNPESLITLVM
NSQNGEILSMVQFPQYDANFYSKYPEEIRKNLSSSLTYEPGSINKIFTVAIILESGKLNLEEKFLDNGIYQKQFPS
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SKATIGFGQEIGVSAVQILQAASILSNNGIMLKPRIIKKISNDKGENIKEFDKEEIRKVISKNSAQKVLKMMREVV
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t820.aa

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TABLE 1. Nucleotide and Amino Acid Sequences

YSEEDYTSSILAIYPTEQPKYIIYIVYRYPKKIIYGTRIAAPMAKEIIEFIEHQQNTIAYKKIKMPSKIKIPKAET
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TABLE 1. Nucleotide and Amino Acid Sequences

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AGAAGATATAACAGAGCTTGAACTGTATTTAAAATAA

f831.aa

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KVRALLSKAILIEEKDKELAVKVYEEIVKFPYENNLYINMANNKILELKQN

t831.aa

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TTAA

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AAAATTAA

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FEYFGSFLYGFLNRLLLPLGLHSILSFPPFEFTSLGGVEIVNGDTVRGLKNIFYAQLLDPSLGKFSSGFAKISSGFY
LSIMFGLPGAALGVYKGIVHEDKNKVAALLFSGALTAFLTGITEPLEFLFIFTAPLLYFVHAAYSGFALLLANFFN
VTIGNSFSTGFLDFFMFGILQGNSKTNWISVLPLGAMFFALYYFTFSWLYRYFDFQIFVTDDPFFEGQEGKLESLG
IAHLLIQGLGGFDNITKLDVCSTRLHVDVVNTELVDNNLLKEAGVLKIGLVNGKVQLFYGSNVYYIKNAIDTYSPK
SLFEASVMVAVDNVKKGFKTYIEMKEDKKLEKQGKSGKTYKLSELEED

t843.aa

RMGQGTAALGGLIGYLTFNITENYFIEAFSGLVEAETMSSVGRINFFGVQTLNTGIAGSLAVGLLVGYLHNKFYNM
KLPKPFVFFSECHFVPIVIILPFCVFLAIFFCLIWSSFDDLIASLGLFVFRFEYFGSFLYGFLNRLLLPLGLHSIL
SFPPFEFTSLGGVEIVNGDTVRGLKNIFYAQLLDPSLGKFSSGFAKISSGFYLSIMFGLPGAALGVYKGIVHEDKNK
VAALLFSGALTAFLTGITEPLEFLFIFTAPLLYFVHAAYSGFALLLANFFNVTIGNSFSTGFLDFFMFGILQGNSK
TNWISVLPLGAMFFALYYFTFSWLYRYFDFQIFVTDDPFFEGQEGKLESLGIAHLLIQGLGGFDNITKLDVCSTRL

TABLE 1. Nucleotide and Amino Acid Sequences

HVDVVNTELVDNNLLKEAGVLKIGLVNGKVQLFYGSNVYYIKNAIDTYSPKSLFEASVMVAVDNVKKGFKTYIEMK
EDKKLEKQGKSGKTYKLSELEED

f843.nt

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t843.nt

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f850.aa

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TABLE 1. Nucleotide and Amino Acid Sequences

t850.aa

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SKNFFITNNLNIKNFSTKENFLSVGGFGIIITPEEYKKISESNNEFNVISNNFYFGFDIMIPLKIRNSLFYKINEN
INHYFSISTNYYTNYNETNSFTNQLSSGIMYEFLPQKTFNPYLISGLFFAYNQNNKDIKSISRPIRIKNILQVGIE
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f850.nt
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AAATGCTAAAATACCGCAACACTGAGTATATTTTCAAAATATATTCAAAAGTTAACTATATTCCTATAGCTTATAA
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t850.nt

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ACTATATTCCTATAGCTTATAACTTAGATGAAAAAAAATTAGAAAAACATTCTATTAACTTTAATTATTTAGGAAT
TGGAATAGTCGTTAAATAA

f853.aa

MKSFLFWVILGTVGISSFAQNTPVAIINLYKNEIITKTGFDSKVDIFKKTQGRDLTDAEKKQVLQVLIADVLFSQE
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EIVEYYEANKTKFVNPDISRVSHIFFSTKDKKRSDVLDQAKNILSQIRSKKITFEEAVRKYSNDESSKAKNGDLGF

TABLE 1. Nucleotide and Amino Acid Sequences

LSRGDQNAQNLLGADFVKEVFNFNKGDISSPIASKEGFHIVKVTEKYAQRFLGLNDKVSPTADLIVKDAIRNNMIN
VQQQQIVVQVQQDMYGKLNKSANIQILDSSLK

t853.aa

QNTPVAIINLYKNEIITKTGFDSKVDIFKKTQGRDLTDAEKKQVLQVLIADVLFSQEASKQGIKISDDEVMQTIRT
QFGLVNFTDEQIKQMIEKQGTNWGELLSSMKRSLSSQKLVLKQAQPKFSEIKTPSEKEIVEYYEANKTKFVNPDIS
RVSHIFFSTKDKKRSDVLDQAKNILSQIRSKKITFEEAVRKYSNDESSKAKNGDLGFLSRGDQNAQNLLGADFVKE
VFNFNKGDISSPIASKEGFHIVKVTEKYAQRFLGLNDKVSPTADLIVKDAIRNNMINVQQQQIVVQVQQDMYGKLN
KSANIQILDSSLK

f853.nt

ATGAAGAGTTTTTTATTTTGGGTAATATTGGGAACTGTAGGGATTAGCTCTTTTGCTCAAAATACTCCTGTTGCTA
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TTACTGATGAACAAATCAAGCAAATGATAGAAAAACAAGGTACAAATTGGGGCGAGCTTTTGTCTTCAATGAAAAG
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TCTTGGATTCTAGTCTAAAATAA

t853.nt

CAAAATACTCCTGTTGCTATTATTAATTTATATAAGAATGAAATTATTACTAAAACTGGTTTTGATTCTAAGGTTG
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CAATTTGGGCTTGTGAATTTTACTGATGAACAAATCAAGCAAATGATAGAAAAACAAGGTACAAATTGGGGCGAGC
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TAAAACTCCTAGTGAGAAAGAAATTGTTGAGTATTATGAGGCTAATAAAACTAAGTTTGTAAATCCCGATATTTCA
AGAGTTAGTCATATCTTTTTTTCTACTAAAGATAAAAAAAGATCAGATGTTTTAGATCAAGCAAAAAATATTTTAA
GCCAAATAAGATCAAAAAAAATTACTTTTGAAGAAGCTGTAAGAAAATATTCAAATGACGAATCTTCTAAGGCTAA
AAATGGTGATCTTGGGTTTTTATCAAGAGGTGATCAAAATGCTCAAAATCTTCTTGGAGCCGATTTTGTGAAAGAG
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AAAAATATGCTCAGAGATTTTTAGGTTTGAATGATAAAGTGTCTCCTACTGCAGATTTGATTGTCAAAGATGCAAT
AAGAAATAACATGATTAATGTTCAACAACAGCAAATTGTTGTTCAAGTACAGCAAGATATGTATGGTAAGCTTAAC
AAGTCTGCAAATATACAAATCTTGGATTCTAGTCTAAAATAA

f859.aa

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IYIQKSKKINYPNRNLGNNINQKTANDVNFTKTSYVKVYPNYKDDNFQEIKNANKFPAKTEKTHMLIGPILKDNLG
IIIKMLKTKGYTLIEYIEDNN

t859.aa

VKDEKSDNKLELFSNVETKIKKNSKNYDSNSNSKKIKKESILKRDTNSEKNINSNIYIQKSKKINYPNRNLGNNIN
QKTA

f859.nt

TABLE 1. Nucleotide and Amino Acid Sequences

ATGAAATTACCAAAACTTTACAAATTAATACTACTCTTTCTTTTTACAACAAGATTGTTTTCAGTAAAAGATGAAA
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t859.nt

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TAA

f861.aa

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FVDDEFYLTENKNLTFYQNFCKKYNLRFKGMIV

t861.aa

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RFKGMIV

f861.nt

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TTCGCTTTAAGGGAATGATAGTTTGA

t861.nt

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CAAAAAATATGCTCTTAGATGTTTAGAAGCTTTAAAATTTGAAGTTGTAAATACTGGTAGAGAAATTGTTTTTCTT
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TABLE 1. Nucleotide and Amino Acid Sequences

TAGTGGTAAAAAATCTTATTAGATCAATGAATTTTTCTGAACACAAAGGTAATTATTATAAGAATGATTTTGATTT
TGTAGATGATGAGTTTTATTTGACCGAAAATAAAAATTTGACTTTTTATCAAAATTTTTGCAAAAAATATAATCTT
CGCTTTAAGGGAATGATAGTTTGA

f363.aa

MIRLKVLILCLFGIFVLNGFADTNFEFNFGGGVAFPVSPFSSFYNEALEINAKLKQNLPSDLSPIEKEEIVQNFSD
LANIAKAGIRYGTYAQFGAKFDDFVSIGFELLFNINLLKAIKRSDGTANENFSFIMAITPRFYTKLDFFVLALAFF
TGPKINIATSSADSVLAELGTMGWDIGARLSFSFLILEGYYVWNIKNPKFSDFKFGIGFEFGIV

t363.aa

DTNFEFNFGGGVAFPVSPFSSFYNEALEINAKLKQNLPSDLSPIEKEEIVQNFSDLANIAKAGIRYGTYAQFGAKF
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MGWDIGARLSFSFLILEGYYVWNIKNPKFSDFKFGIGFEFGIV

f363.nt

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TGCAAAGCTTAAGCAAAATTTGCCTTCAGATTTATCCCCAATAGAAAAAGAAGAGATAGTCCAAAATTTTTCCGAT
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TTTCTCGTTTATTATGGCAATAACACCAAGATTTTATACAAAATTAGATTTTTTTGTTTTAGCTTTAGCGTTTTTC
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GAATTGTGTAG

t363.nt

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ACCCTAAATTTTCTGATTTCAAGTTTGGAATAGGTTTTGAATTTGGAATTGTGTAG

f368.aa

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LVNMFFRSSGLNFLISILGVVIFTGLTAYDVQNISKMDKMLQDDTEIKNRMAVVASLKLYLDFINLFLYLLRFLGQ
RRND

t368.aa

TSENQTIKAIIFSNSMSFMAMILIQFGLVYAISGALNKISSNTATALFLLYSALTGVTLSSIFMIYTQGSIVFTFG
ITAGTFLGMSVYGYTTTTDLTKMGSYLIMGLWGIIIASLVNMFFRSSGLNFLISILGVVIFTGLTAYDVQNISKMD
KMLQDDTEIKNRMAVVASLKLYLDFINLFLYLLRFLGQRRND

f368.nt

TABLE 1. Nucleotide and Amino Acid Sequences

ATGATCGATTTAACACAAGAAAAACAAGAAATACTAATAAAAAACAAGTTTTTAGCCAAAGTTTTCGGGCTTATGT
CAATTGGACTTTTAATCTCAGCAGTATTTGCATATGCAACCTCAGAAAATCAAACAATCAAAGCAATAATATTCTC
AAATTCAATGTCATTTATGGCTATGATACTTATACAATTTGGACTTGTATATGCAATAAGTGGTGCTCTTAATAAA
ATATCAAGCAATACTGCAACAGCTCTTTTCTTGCTCTACTCAGCACTAACAGGAGTAACATTATCTTCTATATTTA
TGATTTACACACAAGGATCAATAGTATTCACATTCGGAATTACTGCTGGAACATTTCTTGGAATGTCTGTTTATGG
ATACACTACAACAACAGATCTAACAAAAATGGGAAGCTATTTAATAATGGGCTTATGGGGAATCATTATTGCATCT
CTTGTTAATATGTTTTTAGAAGCTCAGGTCTTAATTTCCTTATATCTATTTTGGGCGTAGTTATATTTACAGGCT
TAACAGCTTATGATGTTCAAAATATTTCTAAAATGGACAAAATGCTACAAGACGACACTGAAATAAAAAACAGAAT
GGCGGTTGTAGCCTCACTTAAACTTTATTTAGATTTTATAAATTTATTCTTATATCTTCTAAGATTTTTGGGCCAA
AGAAGAAACGATTAA

t368.nt

ACCTCAGAAAATCAAACAATCAAAGCAATAATATTCTCAAATTCAATGTCATTTATGGCTATGATACTTATACAAT
TTGGACTTGTATATGCAATAAGTGGTGCTCTTAATAAAATATCAAGCAATACTGCAACAGCTCTTTTCTTGCTCTA
CTCAGCACTAACAGGAGTAACATTATCTTCTATATTTATGATTTACACACAAGGATCAATAGTATTCACATTCGGA
ATTACTGCTGGAACATTTCTTGGAATGTCTGTTTATGGATACACTACAACAACAGATCTAACAAAAATGGGAAGCT
ATTTAATAATGGGCTTATGGGGAATCATTATTGCATCTCTTGTTAATATGTTTTTAGAAGCTCAGGTCTTAATTT
CCTTATATCTATTTTGGGCGTAGTTATATTTACAGGCTTAACAGCTTATGATGTTCAAAATATTTCTAAAATGGAC
AAAATGCTACAAGACGACACTGAAATAAAAAACAGAATGGCGGTTGTAGCCTCACTTAAACTTTATTTAGATTTTA
TAAATTTATTCTTATATCTTCTAAGATTTTTGGGCCAAAGAAGAAACGATTAA

f371.aa

MKFFFLLQIALILLSNSSLLFGQSPPKEKEDSLLLYKEGKFKEAILNTLEEIRLNPSNLDARTILIWSLIAIGEYK
RAEKEAIIGLGIKKHDIRIIQALGEAYFFQKNYDNALKYFQEYISLDSKGARIIKVYNLIADSFYELKRYNEADFA
YEHALRFSPNNQNLLIKLARSRINAKNKILAEEALIKILTISPNNLEAKNLLEELKKSNNKP

t371.aa

EDSLLLYKEGKFKEAILNTLEEIRLNPSNLDARTILIWSLIAIGEYKRAEKEAIIGLGIKKHDIRIIQALGEAYFF
QKNYDNALKYFQEYISLDSKGARIIKVYNLIADSFYELKRYNEADFAYEHALRFSPNNQNLLIKLARSRINAKNKI
LAEEALIKILTISPNNLEAKNLLEELKKSNNKP

f371.nt

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CTAAAGAAAAAGAAGACTCTCTTCTTCTATATAAAGAAGGAAAATTTAAAGAAGCTATTTTAAACACGTTAGAAGA
AATTCGACTAAATCCTAGTAACTTAGATGCTAGGACAATATTGATATGGAGCTTAATAGCCATAGGAGAATACAAG
AGAGCTGAAAAAGAGGCGATTATAGGACTTGGCATTAAAAAACATGACATAAGAATTATTCAAGCACTAGGAGAAG
CTTATTTCTTTCAAAAAAATTATGACAATGCATTAAAATACTTTCAAGAATACATTAGCCTTGATTCTAAAGGAGC
AAGAATAATAAAAGTTTATAATTTAATTGCAGATTCTTTTTATGAGCTAAAAAGATATAATGAAGCCGATTTTGCA
TACGAACATGCATTACGTTTTTCTCCTAATAACCAAAATCTATTAATAAAATTAGCAAGATCAAGAATAAATGCAA
AAAATAAAATATTAGCAGAAGAAGCACTAATTAAAATTCTTACAATCTCTCCTAATAATCTAGAGGCAAAAAATTT
ACTAGAAGAATTAAAAAAAAGCAACAACAAACCTTGA

t371.nt

GAAGACTCTCTTCTTCTATATAAAGAAGGAAAATTTAAAGAAGCTATTTTAAACACGTTAGAAGAAATTCGACTAA
ATCCTAGTAACTTAGATGCTAGGACAATATTGATATGGAGCTTAATAGCCATAGGAGAATACAAGAGAGCTGAAAA
AGAGGCGATTATAGGACTTGGCATTAAAAAACATGACATAAGAATTATTCAAGCACTAGGAGAAGCTTATTTCTTT
CAAAAAAATTATGACAATGCATTAAAATACTTTCAAGAATACATTAGCCTTGATTCTAAAGGAGCAAGAATAATAA
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TTAGCAGAAGAAGCACTAATTAAAATTCTTACAATCTCTCCTAATAATCTAGAGGCAAAAAATTTACTAGAAGAAT
TAAAAAAAAGCAACAACAAACCTTGA

TABLE 1. Nucleotide and Amino Acid Sequences

f502.aa

MKKANFLSTNFLILLLVCFVNVNLFSKDIFKFKLVDQFFPFYYKNNKGEYEGLIFSILDKWAKDNNADIMVEHIDN
LNESEIEDEAIYLGLTYNVKLNDFFYFKSELARSISILFFKNSNKKYKNTHSTFLSNFNIGVIKNTIYEDILRLKN
VNTIFLADNSQELVLALKNDKVDYIYGDCKTLHYIANNFLSEDLVIFTGDVFYSIKNRVAISRNAPEIVKNLNLDL
FSYLMKMPEELVFSFLDSNAKGSFVDVGLYNDYPPLSFINSQGKLSGILVDLWNLLSRQHIFKPIFKGFSKEDIKK
SLDGKSVGIFGGIISNDSVLENVNYVVSKPIYPLNFKFYSKDLSNDAGPINSQFIDFNFNNIQLNKNKDIVNNFID
IVNNSYGFIENSITTKYLLKLNGYNGRLKSYDSIFNKNRFLVLAIDNRIYKVIKYILNSIFDDISFESLLQIDKNW
LDKEEINSSRINSYKIMNKVKFNIEEKIWLSKNNKLNLAVKNWYPIDYVEANNYKGINQFLLDKIRMFSGLRFNII
KVHSSLDLKKLIKSGKIDMLNTNATDSNLDNVFNIKLNSRIPLYIFSNKKRVLPSRSLEKFAILDFLYSKNLASNI
KSKLILVSSFNEALLLLYKGKVDGIISDEYTAAAVFEELNIDDVEKIPTFRDLAFDLSLAIYNQDYILKEIIQKVV
MRSNVDSQMYLNDWKFDIYYKSRSIRFKNFKFLVITFIIFYFTFLGFVIIFMFRLSFEQKRRYSFVMNEKKIAEAA
NAAKTIFIANVSHDIRTPINGIMAATELLDTTILTDVQKDYVRMINYSSDSLLSLIDDILYLSKIDVNELYVESQE
IDLESEMEMVLKAFQSQCAKKNIDLFSYSKSIFNNYIKGDIVKIKQVLINLIGNAFKFTDDGVIVLNYEEVCRTRT
DGNRVLVTVEFKVIDTGKGIEKENFSKIFEIFKQEDDSSSRVHEGAGLGLSISRELIRLMGGLGIAVDSKVGEGTT
FSFMLPFLLGSELKSKKLSINRFQSVNGDNKVLNVLLSQKSIKIFEHCSILLGCSSNVRYVASFEDAYKVFKKYPS
YNFVYINVNNDNIQEGIRLANNIERLNSDVQIIFLFYYLDNKALKNLKYGYVKKPLMGLGICSILYKKEFNPEMDF
EDLVPIDSALRIKEPINVLIAEDNQVNQKVLKDILVVIGINENFIDVVDDGVKALKSLKDKKYTISFIDIRMPRYD
GFSVAKEIRKFEKAKNLKPCVLVAVTAHALQEYKDKCLASGMNDYISKPIHISSIKTILKKYLQFEVDDIGENENL
NQLVKFPNLDVNRALKELNLSYVSYSELCRGLVDFISINIIDLEKAFDEEDLSLIKDISHSISGALSNMRSELYKD
FQKIETSKDSISELKKMYSFVKDDLFQLISDIKENILFESEIVSENKLYFKNNDQFLNLLNKLLIGIKTRKPREYK
EILESINKYVLDDNIQVLFSDLRRNLRLYRFAESSKILEEIIEMLNNKRY

t502.aa

CFVNVNLFSKDIFKFKLVDQFFPFYYKNNKGEYEGLIFSILDKWAKDNNADIMVEHIDNLNESEIEDEAIYLGLTY
NVKLNDFFYFKSELARSISILFFKNSNKKYKNTHSTFLSNFNIGVIKNTIYEDILRLKNVNTIFLADNSQELVLAL
KNDKVDYIYGDCKTLHYIANNFLSEDLVIFTGDVFYSIKNRVAISRNAPEIVKNLNLDLFSYLMKMPEELVFSFLD
SNAKGSFVDVGLYNDYPPLSFINSQGKLSGILVDLWNLLSRQHIFKPIFKGFSKEDIKKSLDGKSVGIFGGIISND
SVLENVNYVVSKPIYPLNFKFYSKDLSNDAGPINSQFIDFNFNNIQLNKNKDIVNNFIDIVNNSYGFIENSITTKY
LLKLNGYNGRLKSYDSIFNKNRFLVLAIDNRIYKVIKYILNSIFDDISFESLLQIDKNWLDKEEINSSRINSYKIM
NKVKFNIEEKIWLSKNNKLNLAVKNWYPIDYVEANNYKGINQFLLDKIRMFSGLRFNIIKVHSSLDLKKLIKSGKI
DMLNTNATDSNLDNVFNIKLNSRIPLYIFSNKKRVLPSRSLEKFAILDFLYSKNLASNIKSKLILVSSFNEALLLL
YKGKVDGIISDEYTAAAVFEELNIDDVEKIPTFRDLAFDLSLAIYNQDYILKEIIQKVVMRSNVDSQMYLNDWKFD
IYYKSRSIRFKNFKFLVITFIIFYFTFLGFVIIFMFRLSFEQKRRYSFVMNEKKIAEAANAAKTIFIANVSHDIRT
PINGIMAATELLDTTILTDVQKDYVRMINYSSDSLLSLIDDILYLSKIDVNELYVESQEIDLESEMEMVLKAFQSQ
CAKKNIDLFSYSKSIFNNYIKGDIVKIKQVLINLIGNAFKFTDDGVIVLNYEEVCRTRTDGNRVLVTVEFKVIDTG
KGIEKENFSKIFEIFKQEDDSSSRVHEGAGLGLSISRELIRLMGGLGIAVDSKVGEGTTFSFMLPFLLGSELKSKK
LSINRFQSVNGDNKVLNVLLSQKSIKIFEHCSILLGCSSNVRYVASFEDAYKVFKKYPSYNFVYINVNNDNIQEGI
RLANNIERLNSDVQIIFLFYYLDNKALKNLKYGYVKKPLMGLGICSILYKKEFNPEMDFEDLVPIDSALRIKEPIN
VLIAEDNQVNQKVLKDILVVIGINENFIDVVDDGVKALKSLKDKKYTISFIDIRMPRYDGFSVAKEIRKFEKAKNL
KPCVLVAVTAHALQEYKDKCLASGMNDYISKPIHISSIKTILKKYLQFEVDDIGENENLNQLVKFPNLDVNRALKE
LNLSYVSYSELCRGLVDFISINIIDLEKAFDEEDLSLIKDISHSISGALSNMRSELYKDFQKIETSKDSISELKKM
YSFVKDDLFQLISDIKENILFESEIVSENKLYFKNNDQFLNLLNKLLIGIKTRKPREYKEILESINKYVLDDNIQV
LFSDLRRNLRLYRFAESSKILEEIIEMLNNKRY

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CTAAGGATATTTTCAAGTTTAAGCTTGTAGATCAATTTTTTCCTTTTTACTACAAGAATAATAAAGGAGAATATGA
AGGACTTATTTTTTCTATTTTAGATAAATGGGCAAAAGATAATAATGCTGATATTATGGTTGAGCATATTGATAAT
TTAAATGAAAGTGAAATTGAAGACGAAGCAATATATTTAGGATTAACTTATAATGTAAAATTAAATGATTTTTTTT
ATTTTAAAAGTGAGCTTGCTAGGAGTATTTCAATTTTATTTTTTAAAAACTCTAATAAAAAATATAAAAATACCCA
TTCAACATTTTTATCCAATTTTAATATAGGAGTTATTAAAAATACAATATATGAAGATATCTTAAGGTTAAAAAAC
GTTAACACCATTTTTTTGGCTGATAATTCTCAAGAGTTAGTATTGGCCTTAAAAAACGATAAAGTTGATTATATAT

TABLE 1. Nucleotide and Amino Acid Sequences

ATGGTGATTGCAAGACTTTACATTATATTGCAAATAACTTTTTAAGTGAAGATCTTGTGATTTTTACCGGGGATGT
TTTTTATAGTATCAAAAATAGAGTGGCTATTAGTAGAAATGCTCCTGAGATAGTAAAGAATTTGAATTTAGATTTG
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TCATTAGATGGAAAATCAGTAGGTATTTTTGGAGGAATTATTAGCAATGATAGTGTGTTGGAAAATGTTAATTATG
TAGTAAGTAAGCCAATATATCCTCTTAATTTTAAATTTTATTCTAAAGACCTAAGCAATGATGCTGGTCCAATAAA
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GTAGATTAAAATCTTACGATTCGATTTTTAATAAAAATAGGTTTTTAGTATTAGCCATTGATAATAGGATTTATAA
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ATTCAAATTTAGATAATGTTTTCAACATAAAATTAAATTCTCGAATTCCACTTTATATTTTTTCAAATAAGAAAAG
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AAATCAAAGCTTATTCTGGTAAGCAGTTTTAATGAAGCGTTGCTTCTTCTTTATAAGGGAAAGGTAGATGGGATTA
TTAGCGATGAGTATACAGCTGCTGCTGTTTTTGAGGAATTAAATATTGATGATGTTGAAAAAATTCCTACTTTTAG
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ATGCGTTCAAATGTTGACAGTCAGATGTATTTAAATGATTGGAAATTTGATATTTATTATAAATCCAGAAGTATCA
GGTTTAAAAATTTCAAATTTTTAGTGATAACATTCATTATATTTTATTTTACTTTTTTAGGATTTGTAATTATATT
TATGTTCAGATTATCATTTGAGCAGAAAAGAAGATATTCTTTTGTGATGAATGAAAAAAAGATTGCGGAAGCCGCT
AATGCTGCTAAAACCATTTTTATAGCCAATGTCAGTCATGATATTCGTACCCCTATTAACGGAATAATGGCGGCTA
CTGAGCTTTTGGATACAACTATTCTTACAGATGTTCAAAAAGATTATGTTAGGATGATAAATTATTCATCTGATTC
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ATTGATTTAGAGAGTGAAATGGAAATGGTTTTAAAAGCTTTTCAATCTCAATGTGCAAAGAAAAATATTGATTTAT
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G

t502.nt

TABLE 1. Nucleotide and Amino Acid Sequences

TGCTTTGTCAACGTCAATTTATTTTCTAAGGATATTTTCAAGTTTAAGCTTGTAGATCAATTTTTTCCTTTTTACT
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AGTAAAGAATTTGAATTTAGATTTGTTTTCATATTTAATGAAAATGCCTGAGGAACTTGTTTTTTCTTTTTTAGAT
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TAAGCAATGATGCTGGTCCAATAAATTCTCAGTTTATTGATTTTAATTTTAATAATATTCAATTAAATAAGAATAA
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TTGTTAAAATTAAATGGATATAACGGTAGATTAAAATCTTACGATTCGATTTTTAATAAAAATAGGTTTTTAGTAT
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GAAAGAAATTATTCAAAAAGTTGTTATGCGTTCAAATGTTGACAGTCAGATGTATTTAAATGATTGGAAATTTGAT
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CCTATTAACGGAATAATGGCGGCTACTGAGCTTTTGGATACAACTATTCTTACAGATGTTCAAAAAGATTATGTTA
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TGAAGAAGTATGTAGAACAAGAACTGATGGTAATAGGGTTTTGGTTACAGTTGAATTTAAGGTAATAGATACAGGC
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TAAAGTCTTCAAGAAATACCCTTCTTATAATTTTGTTTATATAAATGTAAATAACGATAATATTCAAGAGGGTATT
CGACTTGCCAATAATATTGAAAGACTAAATTCTGATGTACAAATTATTTTTTTATTTTATTATTTAGATAATAAAG
CTCTAAAAAATTTAAAATATGGTTATGTTAAAAAGCCTTTAATGGGGCTTGGTATATGCTCTATTCTTTATAAAAA
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TTAGTGAGAACAAGCTATATTTTAAAAATAATGATCAATTTTTAAACCTTCTCAACAAACTTTTAATTGGTATTAA

TABLE 1. Nucleotide and Amino Acid Sequences

GACTAGAAAGCCAAGAGAATACAAAGAAATTCTTGAGAGCATTAATAAATATGTTTTAGACGATAATATTCAGGTA
TTATTTAGTGATCTTCGCAGAAATTTAAGATTATATAGATTTGCTGAGAGCTCTAAGATTCTTGAAGAGATTATTG
AAATGCTTAATAATAAGAGATATTAG

f527.aa

MNLLVKIAKFILILFLFTSCNQKQSEIQNLTHLLKSSNKNRLDKFLIIDRVVNIYIANKNYEDALEIVNNGIIDDE
SREYYPLYLYLMGNIYDSMGEDFVAFNIYKRVVDNFDDYVYENHSMKTRVAKKIVNLNIDSIDKINYYKFILNMGI
DNLNNEEKGNYFYNLALSLEDVQDYDESYFYYKKFLSIPRAHLKIDSRDYFNVVTKINYFNNPEFVVYRNLGDLIQ
DVKNFVLSGNTSKLLNIRDKNNFFIQSWDQKGGKSNSINTNSFLTTMIRLGGRRKNGIQFAKHLEADSSDDISYLE
SRGWDHIHEWYFVFKRIVYPKDPEINNGWTWIGVYLGKK

t527.m

CNQKQSEIQNLTHLLKSSNKNRLDKFLIIDRVVNIYIANKNYEDALEIVNNGIIDDESREYYPLYLYLMGNIYDSM
GEDFVAFNIYKRVVDNFDDYVYENHSMKTRVAKKIVNLNIDSIDKINYYKFILNMGIDNLNNEEKGNYFYNLALSL
EDVQDYDESYFYYKKFLSIPRAHLKIDSRDYFNVVTKINYFNNPEFVVYRNLGDLIQDVKNFVLSGNTSKLLNIRD
KNNFFIQSWDQKGGKSNSINTNSFLTTMIRLGGRRKNGIQFAKHLEADSSDDISYLESRGWDHIHEWYFVFKRIVY
PKDPEINNGWTWIGVYLGKK

f527.nt

ATGAATCTATTGGTCAAAATTGCTAAATTTATTTTGATTTTGTTTTTATTTACTTCTTGCAACCAAAAGCAAAGCG
AGATTCAAAATCTTACACATCTTTTAAAATCTTCTAATAAAAATAGATTAGATAAATTTCTTATTATTGATAGAGT
TGTTAACATATATATTGCAAATAAAAATTATGAAGATGCTTTAGAAATTGTAAATAATGGAATTATTGATGATGAA
TCTAGAGAATATTATCCTTTGTATCTTTATTTAATGGGCAATATTTATGATTCCATGGGAGAAGATTTTGTAGCTT
TTAATATTTACAAGCGTGTTGTTGATAATTTTGATGATTATGTTTATGAAAACCATTCAATGAAAACAAGGGTTGC
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TCAAGGGGCTGGGACCATATTCATGAATGGTATTTTGTTTTTAAAAGAATTGTTTATCCTAAAGATCCAGAAATTA
ATAATGGCTGGACTTGGATAGGCGTGTATTTAGGTAAAAAATAA

t527.nt

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TGGAATTATTGATGATGAATCTAGAGAATATTATCCTTTGTATCTTTATTTAATGGGCAATATTTATGATTCCATG
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CAATGAAAACAAGGGTTGCTAAAAAGATTGTCAATTTAAATATTGATTCAATCGATAAAATCAATTATTACAAATT
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AAGAATAATTTTTTTATTCAAAGCTGGGATCAAAAGGGTGGAAAGAGTAATTCCATTAATACTAATAGCTTTTTAA
CCACTATGATTAGGCTTGGGGGGAGAAGAAAAAACGGAATACAATTTGCAAAGCATCTTGAGGCAGATTCTAGTGA
CGATATATCTTATCTTGAGTCAAGGGGCTGGGACCATATTCATGAATGGTATTTTGTTTTTAAAAGAATTGTTTAT
CCTAAAGATCCAGAAATTAATAATGGCTGGACTTGGATAGGCGTGTATTTAGGTAAAAAATAA

f541.aa

MNKILLLILLESIVFLSCSGKGSLGSEIPKVSLIIDGTFDDKSFNESALNGVKKVKEEFKIELVLKESSSNSYLSD
LEGLKDAGSDLIWLIGYRFSDVAKVAALQNPDMKYAIIDPIYSNDPIPANLVGMTFRAQEGAFLTGYIAAKLSKTG

TABLE 1. Nucleotide and Amino Acid Sequences

KIGFLGGIEGEIVDAFRYGYEAGAKYANKDIKISTQYIGSFADLEAGRSVATRMYSDEIDIIHHAAGLGGIGAIEV
AKELGSGHYIIGVDEDQAYLAPDNVITSTTKDVGRALNIFTSNHLKTNTFEGGKLINYGLKEGVVGFVRNPKMISF
ELEKEIDNLSSKIINKEIIVPSNKESYEKFLKEFI

t541.aa

CSGKGSLGSEIPKVSLIIDGTFDDKSFNESALNGVKKVKEEFKIELVLKESSSNSYLSDLEGLKDAGSDLIWLIGY
RFSDVAKVAALQNPDMKYAIIDPIYSNDPIPANLVGMTFRAQEGAFLTGYIAAKLSKTGKIGFLGGIEGEIVDAFR
YGYEAGAKYANKDIKISTQYIGSFADLEAGRSVATRMYSDEIDIIHHAAGLGGIGAIEVAKELGSGHYIIGVDEDQ
AYLAPDNVITSTTKDVGRALNIFTSNHLKTNTFEGGKLINYGLKEGVVGFVRNPKMISFELEKEIDNLSSKIINKE
IIVPSNKESYEKFLKE
FI

f541.nt

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CGTAAAAAAAGTTAAAGAAGAATTTAAAATTGAGCTTGTTTTAAAAGAATCCTCATCAAATTCTTATTTATCTGAT
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AAAATTGGATTTTTAGGGGGAATAGAAGGCGAGATAGTAGATGCTTTTAGGTATGGGTATGAAGCTGGTGCTAAGT
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GAACTTGAAAAAGAAATTGACAATCTTTCTAGCAAAATAATCAACAAAGAAATTATTGTTCCATCTAATAAAGAAA
GTTATGAGAAGTTTCTTAAAGAATTTATTTAA

t541.nt

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CTCATCAAATTCTTATTTATCTGATCTTGAAGGGCTTAAGGATGCGGGCTCAGATTTAATTTGGCTTATTGGGTAT
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CTAACGATCCTATTCCTGCAAATTTGGTGGGCATGACCTTTAGAGCTCAAGAGGGTGCATTTTTAACGGGTTATAT
TGCTGCAAAACTTTCTAAAACAGGTAAAATTGGATTTTTAGGGGGAATAGAAGGCGAGATAGTAGATGCTTTTAGG
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ACCATTTAAAAACTAATACTTTCGAAGGTGGCAAATTAATAAATTATGGCCTTAAAGAAGGAGTTGTGGGGTTTGT
AAGAAATCCTAAAATGATTTCCTTTGAACTTGAAAAAGAAATTGACAATCTTTCTAGCAAAATAATCAACAAAGAA
ATTATTGTTCCATCTAATAAAGAAAGTTATGAGAAGTTTCTTAAAGAATTTATTTAA

f561.aa

MYKNGFFKNYLSLFLIFLVIACTSKDSSNEYVEEQEAENSSKPDDSKIDEHTIGHVFHAMGVVHSKKDRKSLGKNI
KVFYFSEEDGHFQTIPSKENAKLIVYFYDNVYAGEAPISISGKEAFIFVGITPDFKKIINSNLHGAKSDLIGTFKD
LNIKNSKLEITVDENNSDAKTFLESVNYIIDGVEKISPMLTN

t561.aa

TABLE 1. Nucleotide and Amino Acid Sequences

CTSKDSSNEYVEEQEAENSSKPDDSKIDEHTIGHVFHAMGVVHSKKDRKSLGKNIKVFYFSEEDGHFQTIPSKENA
KLIVYFYDNVYAGEAPISISGKEAFIFVGITPDFKKIINSNLHGAKSDLIGTFKDLNIKNSKLEITVDENNSDAKT
FLESVNYIIDGVEKISPMLTN

f561.nt

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CTTAATATTAAAAATTCAAAATTGGAAATTACAGTTGATGAGAATAATTCAGATGCCAAGACCTTCCTTGAATCTG
TTAATTACATTATCGACGGCGTTGAAAAAATTTCACCTATGTTAACGAATTAA

t561.nt

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GGGGAAAAAATATAAAGGTTTTTTATTTTTCTGAAGAAGATGGACATTTTCAAACAATACCCTCAAAAGAGAATGCA
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TACTTTTAAAGATCTTAATATTAAAAATTCAAAATTGGAAATTACAGTTGATGAGAATAATTCAGATGCCAAGACC
TTCCTTGAATCTGTTAATTACATTATCGACGGCGTTGAAAAAATTTCACCTATGTTAACGAATTAA

f604.aa

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KVSDSELGIKAIDSKTLEITLTAPKPYFLELLLHYAFMPVPIHVIEKYKGNWTSPENMVTSGPFKLKKRLPNEKII
FEKNERYYNAKEVELDELVYITSDNDLTVYNMYKNNEIDAIFNSIPPDIVNEIKLQKDYYQHKSNAIYLYSFNTKI
KPLDDARVREALTLAIDRETLTYKVLNDGTVPTREITPDLKNYNYGKKLALFDPEKSKKLLADAGYPNGKGFPMLT
LKYNTNETHKKIAAFIQNQWKKILNINLMLTNENWPVLTNSRNTGNFEIIRVGRIGEYLDPHTYFTIFTRENSQLA
SYGYSNLEFDKLIRESDLEKDPIKRKQLLRKAESIIIEKDFPAAPIYIYSGHYLFRNDKWTGWNPNVSEVYYLSEL
KPIKNAKHN

t604.aa

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f604.nt

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AAAGTATCCGATTCTGAACTTGGAATCAAGGCAATTGATAGTAAAACGCTGGAAATAACACTTACGGCCCCAAAGC
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TABLE 1. Nucleotide and Amino Acid Sequences

TTGGACAAGCCCTGAAAACATGGTTACTAGCGGTCCTTTTAAATTAAAAAAAAGATTACCTAATGAAAAAATTATC
TTTGAAAAAAACGAACGTTATTATAATGCAAAAGAAGTAGAACTTGATGAGCTTGTCTACATTACGTCTGACAATG
ATCTTACTGTGTACAATATGTACAAAAACAACGAAATTGATGCTATTTTTAACAGCATCCCGCCGGACATTGTAAA
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ATTTGATCCTGAAAAATCTAAAAAGCTTTTGGCAGATGCAGGGTATCCTAATGGGAAAGGATTCCCAATGCTAACA
CTAAAATATAATACAAACGAAACTCATAAAAAAATTGCTGCATTTATTCAAAACCAATGGAAAAAAATTCTAAATA
TCAATCTTATGCTTACCAACGAAAATTGGCCTGTTCTTACCAACAGCAGAAATACTGGCAATTTTGAAATAATAAG
AGTTGGACGCATTGGGGAATATTTAGATCCACACACATACTTTACTATATTCACAAGAGAAAATTCACAACTTGCA
TCATACGGATATTCAAACCTAGAATTTGACAAACTCATCAGAGAATCAGATCTTGAAAAAGATCCTATAAAAAGAA
AACAATTACTCAGAAAAGCAGAATCAATAATAATTGAAAAAGATTTTCCTGCTGCACCAATATACATATATTCTGG
GCATTATCTTTTTAGAAACGATAAATGGACTGGATGGAATCCTAATGTATCAGAGGTTTATTATCTTTCTGAATTA
AAACCAATTAAAAATGCAAAACATAATTAA

t604.nt

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AGGAAAGCTAAAGCCCGGACTTGCTAAAAATTGGGAAGCCTCAAAAGATAAAAAAACATATCAATTTTATCTAAGG
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f736.aa

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IAISSRDLTKEEIEQGAKETVFAYDALIFITSPEIKITNITEENLAKILNGEIQNWKQVGGPDAKINFINRDSSSG
SYSSIKDLLLNKIFKTHEEAQFRQDGIVVKSNGEVIEKTSLTPHSIGYIGLGYAKNSIEKGLNILSVNSTYPTKET
INSNKYTIKRNLIIVTNNKYEDKSVTQFIDFMTSSTGQDIVEEQGFLGIKT

t736.aa

CKNQDNEKIVSIGGSTTVSPILDEMILRYNKINNNTKVTYDAQGSSVGINGLFNKIYKIAISSRDLTKEEIEQGAK
ETVFAYDALIFITSPEIKITNITEENLAKILNGEIQNWKQVGGPDAKINFINRDSSSGSYSSIKDLLLNKIFKTHE
EAQFRQDGIVVKSNGEVIEKTSLTPHSIGYIGLGYAKNSIEKGLNILSVNSTYPTKETINSNKYTIKRNLIIVTNN
KYEDKSVTQFIDFMTSSTGQDIVEEQGFLGIKT

f736.nt

TABLE 1. Nucleotide and Amino Acid Sequences

ATGAAAAAAGTTATTATCTTAATTTTTATGCTATCAACAAGTTTATTATACAACTGTAAAAATCAAGACAATGAAA
AAATTGTATCAATTGGAGGATCTACAACTGTAAGCCCAATACTAGACGAAATGATTTTAAGATATAATAAAATAAA
CAATAATACTAAAGTAACATACGATGCACAAGGAAGTAGTGTTGGCATAAACGGGCTATTTAACAAAATATATAAA
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CTCAATTTATTGATTTCATGACAAGCTCAACTGGACAAGATATTGTTGAAGAACAAGGCTTTTTAGGGATAAAAAC
ATAA

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f752.aa

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GSLIKNPYRQSTPESTEIHSFLSTMVKNEAQYAILESTSHGLDLETARLIDVNYFAVVFTNIGHEHLEFHGTIQNY
LNVKLGLFRSVSDDAGFGVINLDDLYSSDFKNAVKKSFTYSLKSSKADFFVSFIDEKTDSTRFEFYHKGVKYLANV
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TNRLISVFGSAGERDVEKRFLQGQIADIYSDLIILCDEDPRGENSMCIIKDIAKGIVNKVENKDLFFIADRKQAIE
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t752.aa

CVKGSLDLEISGVTYSSKLVLPRFVFFALPGIHFDGHDFIEIAIQKGSNVVVCSRDVDFYSPNVTYIKVDDFNIRK
FMSNFSNIFYDEPSKKLKVIGVTGTDGKSSVCYYIYLLFKKKGVKVGFISTVFFDDGSGSLIKNPYRQSTPESTEI
HSFLSTMVKNEAQYAILESTSHGLDLETARLIDVNYFAVVFTNIGHEHLEFHGTIQNYLNVKLGLFRSVSDDAGFG
VINLDDLYSSDFKNAVKKSFTYSLKSSKADFFVSFIDEKTDSTRFEFYHKGVKYLANVSLLGSFNVENVMAALILV
SQILNIDIQDIVDKLNCIKSLDGRMDSINLGQNFSVIIDYAHTPGAFSKLFPIFKRFATNRLISVFGSAGERDVEK
RFLQGQIADIYSDLIILCDEDPRGENSMCIIKDIAKGIVNKVENKDLFFIADRKQAIEKAISLAKAGDLVVALGKG
HESSIIYKNREVFWNEQEVVKNAILSLEKSEKEK

f752.nt

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TABLE 1. Nucleotide and Amino Acid Sequences

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TGTTAATTATTTTGCAGTTGTTTTTACCAATATTGGACATGAGCATCTTGAATTTCATGGCACAATTCAAAATTAT
TTGAATGTCAAGCTGGGTCTTTTTCGGTCTGTTAGTGATGATGCTGGTTTTGGGGTTATTAATCTTGATGACCTTT
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GAAGTGA

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TGTGTGTTCACGAGATGTGGATTTTTACAGTCCTAATGTTACTTATATTAAGGTAGATGACTTTAACATAAGAAAA
TTTATGTCTAATTTTTCAAATATTTTTTATGATGAGCCTTCAAAAAAATTAAAAGTTATTGGAGTCACTGGCACTG
ACGGGAAAAGTTCTGTTTGTTATTATATATATCTTCTTTTTAAAAAAAAGGGTGTTAAAGTAGGTTTTATATCGAC
AGTATTTTTTGATGATGGGAGTGGAAGCTTGATTAAAAATCCTTACAGACAATCAACTCCCGAGTCTACGGAAATA
CATTCATTTTTAAGCACCATGGTTAAAAATGAAGCTCAATATGCAATTCTTGAATCTACTTCTCATGGGCTTGACC
TTGAAACAGCAAGGCTTATTGATGTTAATTATTTTGCAGTTGTTTTTACCAATATTGGACATGAGCATCTTGAATT
TCATGGCACAATTCAAAATTATTTGAATGTCAAGCTGGGTCTTTTTCGGTCTGTTAGTGATGATGCTGGTTTTGGG
GTTATTAATCTTGATGACCTTTATTCTTCTGATTTTAAGAATGCTGTTAAGAAATCTTTTACTTATAGCTTAAAAA
GCAGTAAAGCGGATTTTTTTGTTAGTTTTATTGATGAGAAAACCGATTCTACTAGATTTGAATTTTATCACAAGGG
GGTTAAATATCTTGCTAATGTTAGCCTACTGGGGAGTTTTAATGTTGAGAATGTAATGGCTGCTCTTATTTTAGTT
TCTCAAATTTTAAATATCGATATTCAAGATATTGTTGATAAACTTAACTGCATTAAAAGTCTTGATGGGCGTATGG
ATAGTATTAATTTGGGGCAAAATTTTTCTGTAATAATTGATTATGCTCATACTCCTGGTGCTTTTTCCAAGCTTTT
TCCTATTTTTAAAAGATTTGCTACCAATAGATTGATTTCTGTTTTTGGCTCTGCAGGAGAAAGAGATGTTGAAAAA
AGATTTTTGCAAGGGCAAATCGCAGATATTTATTCTGATTTAATAATACTTTGCGATGAAGATCCAAGAGGCGAGA
ATAGTATGTGTATAATTAAAGACATTGCAAAAGGAATTGTAAATAAAGTTGAAAATAAGGATTTATTTTTTATTGC
TGATAGAAAGCAGGCTATTGAAAAAGCAATAAGTCTTGCAAAAGCAGGAGATTTGGTTGTTGCTTTGGGCAAAGGT
CATGAAAGTTCAATAATTTATAAAAATAGAGAAGTTTTTTGGAATGAACAAGAGGTAGTTAAAAATGCTATTTTAA
GTTTAGAAAAATCAGAAAAGGAGAAGTGA

f798.aa

MVFRTYKHLELIMLPMLMLSCAFFKKPQSVHQDSNTGKPISDEKLHLISGKISNKKLPIINSNHDVTWIKTKAMTI
LGEDGKEIPEFKNKFGYSYIISPVKMDGKYSYYASLLILFETTKNGDDEYEIEDVKFVTAGSTLELKNSLLAVENS
QEEGYVTAYPFGILMSDEIKNAFKLTYKNGHWNYMLADLTVKNKLTQETKIYKISLNSKLIIEFLKEVLKENSILK
DIAGDLFEDI

t798.aa

CAFFKKPQSVHQDSNTGKPISDEKLHLISGKISNKKLPIINSNHDVTWIKTKAMTILGEDGKEIPEFKNKFGYSYI
ISPVKMDGKYSYYASLLILFETTKNGDDEYEIEDVKFVTAGSTLELKNSLLAVENSQEEGYVTAYPFGILMSDEIK
NAFKLTYKNGHWNYMLADLTVKNKLTQETKIYKISLNSKLIIEFLKEVLKENSILKDIAGDLFEDI

f798.nt

ATGGTATTTAGAACATATAAACATTTGGAACTAATAATGCTGCCCATGTTAATGCTGAGTTGCGCTTTTTTTAAGA
AACCACAATCTGTACATCAAGACAGCAATACTGGCAAACCAATAAGCGATGAAAAATTACATTTAATATCAGGCAA
AATTTCAAATAAAAAATTGCCAATCATAAATAGTAATCATGACGTAACTTGGATAAAAACAAAGGCAATGACAATC

TABLE 1. Nucleotide and Amino Acid Sequences

TTAGGCGAAGATGGAAAAGAAATACCAGAATTTAAAAACAAATTTGGATATTCTTATATAATATCTCCTGTAAAAA
TGGATGGAAAATATAGTTATTACGCGTCATTATTAATACTTTTTGAAACAACTAAAAATGGAGATGATGAATATGA
AATTGAAGATGTTAAATTTGTAACAGCTGGTTCCACCCTAGAACTTAAAAATTCTCTTTTAGCTGTTGAAAATTCA
CAAGAAGAAGGATATGTTACTGCATACCCATTTGGAATATTGATGAGTGACGAGATTAAAAATGCTTTTAAATTAA
CATATAAAAATGGTCATTGGAATTATATGCTTGCAGATTTAACTGTCAAAAATAAACTTACTCAAGAAACTAAAAT
TTATAAAATTTCTCTTAATTCAAAATTAATTATTGAATTTTTAAAAGAAGTGCTAAAAGAAAATTCTATATTAAAA
GACATAGCTGGAGATTTATTTGAAGATATATAA

t798.nt

TGCGCTTTTTTTAAGAAACCACAATCTGTACATCAAGACAGCAATACTGGCAAACCAATAAGCGATGAAAAATTAC
ATTTAATATCAGGCAAAATTTCAAATAAAAAATTGCCAATCATAAATAGTAATCATGACGTAACTTGGATAAAAAC
AAAGGCAATGACAATCTTAGGCGAAGATGGAAAAGAAATACCAGAATTTAAAAACAAATTTGGATATTCTTATATA
ATATCTCCTGTAAAAATGGATGGAAAATATAGTTATTACGCGTCATTATTAATACTTTTTGAAACAACTAAAAATG
GAGATGATGAATATGAAATTGAAGATGTTAAATTTGTAACAGCTGGTTCCACCCTAGAACTTAAAAATTCTCTTTT
AGCTGTTGAAAATTCACAAGAAGAAGGATATGTTACTGCATACCCATTTGGAATATTGATGAGTGACGAGATTAAA
AATGCTTTTAAATTAACATATAAAAATGGTCATTGGAATTATATGCTTGCAGATTTAACTGTCAAAAATAAACTTA
CTCAAGAAACTAAAATTTATAAAATTTCTCTTAATTCAAAATTAATTATTGAATTTTTAAAAGAAGTGCTAAAAGA
AAATTCTATATTAAAAGACATAGCTGGAGATTTATTTGAAGATATATAA

f805.aa

MLRKLKDISKIVLVTDGLTPNCQTCGKLIANGDEVYIAEDGLFHSVKSNTIAGSTLTMIQGLKNLIEFGFSLSDAV
QASSYNPTRILNIDKKGLICHGYDANLNVLDKDFNLKLTMIESKIIFNNL

t805.aa

CQTCGKLIANGDEVYIAEDGLFHSVKSNTIAGSTLTMIQGLKNLIEFGFSLSDAVQASSYNPTRILNIDKKGLICH
GYDANLNVLDKDFNLKLTMIESKIIFNNL

f805.nt

ATGCTTAGAAAGCTTAAAGATATAAGTAAAATAGTCCTTGTAACTGACGGACTTACTCCGAATTGTCAAACTTGTG
GAAAACTAATTGCAAACGGAGACGAAGTTTATATTGCAGAAGATGGATTATTCCATAGCGTGAAAAGCAACACAAT
AGCTGGATCAACACTCACAATGATACAAGGTCTTAAAAATTTAATAGAATTTGGTTTCAGCTTAAGCGATGCTGTT
CAAGCAAGCTCTTACAATCCAACAAGAATTCTCAATATTGATAAAAAGGGCTTAATATGTCATGGATATGATGCAA
ACCTCAATGTCCTAGATAAAGATTTTAATCTAAAGTTAACAATGATAGAATCTAAAATAATTTTTAACAATCTCTA
A

t805.nt

TGTCAAACTTGTGGAAAACTAATTGCAAACGGAGACGAAGTTTATATTGCAGAAGATGGATTATTCCATAGCGTGA
AAAGCAACACAATAGCTGGATCAACACTCACAATGATACAAGGTCTTAAAAATTTAATAGAATTTGGTTTCAGCTT
AAGCGATGCTGTTCAAGCAAGCTCTTACAATCCAACAAGAATTCTCAATATTGATAAAAAGGGCTTAATATGTCAT
GGATATGATGCAAACCTCAATGTCCTAGATAAAGATTTTAATCTAAAGTTAACAATGATAGAATCTAAAATAATTT
TTAACAATCTCTAA

f635.aa

MKILWLIILVNLFLSCGNESKEKSNLGLRLRELEISGGGSESKIEVYKEFIEKEDKNILKIVNSIDKKARFFNLIG
LEFFKLGQYGPAIEYFAKNLEINPNNYLSHFYIGVASYNLAKNLRVKDEVEKYIILAENSFLKSLSIRDDFKDSLF
AISNMYVYDLDKQLEAKNYLNKLGDMGEDYFEFLMLRGANYYSLGDLGNAILFYDKASKKASTEEQKEGVSRIMSN
LK

t635.aa

TABLE 1. Nucleotide and Amino Acid Sequences

CGNESKEKSNLGLRLRELEISGGGSESKIEVYKEFIEKEDKNILKIVNSIDKKARFFNLIGLEFFKLGQYGPAIEY
FAKNLEINPNNYLSHFYIGVASYNLAKNLRVKDEVEKYIILAENSFLKSLSIRDDFKDSLFAISNMYVYDLDKQLE
AKNYLNKLGDMGEDYFEFLMLRGANYYSLGDLGNAILFYDKASKKASTEEQKEGVSRIMSNLK

f635.nt

ATGAAAATTTTGTGGTTAATAATTCTTGTTAATTTATTTTTATCTTGTGGCAATGAATCTAAAGAAAAATCAAATC
TTGGTCTTAGATTAAGAGAATTGGAAATTTCAGGTGGTGGATCTGAATCTAAGATTGAAGTTTATAAAGAATTTAT
TGAAAAAGAAGATAAGAATATTTTAAAGATAGTTAATTCCATTGATAAGAAAGCCAGATTTTTTAATTTAATTGGT
CTTGAATTTTTTAAGCTTGGTCAGTACGGACCTGCTATTGAATATTTTGCTAAAAATTTAGAAATCAATCCCAATA
ATTATTTATCTCATTTTTATATAGGTGTTGCTTCTTATAATTTAGCTAAAAATTTAAGAGTAAAAGATGAAGTTGA
AAAATACATAATTCTTGCTGAAAATTCTTTTTTAAAATCACTTTCAATTAGAGATGATTTTAAAGATTCTCTTTTT
GCCATTTCTAATATGTACGTATATGATCTTGATAAACAACTTGAAGCTAAAAATTATTTAAATAAACTTGGTGATA
TGGGTGAGGACTATTTTGAGTTTTTAATGTTAAGAGGTGCAAATTATTATTCGCTGGGCGATCTTGGTAATGCTAT
ATTGTTTTATGATAAAGCTAGTAAAAAGGCTTCAACTGAAGAGCAAAAAGAAGGTGTTTCTAGGATCATGAGTAAT
TTGAAGTAA

t635.nt

TGTGGCAATGAATCTAAAGAAAAATCAAATCTTGGTCTTAGATTAAGAGAATTGGAAATTTCAGGTGGTGGATCTG
AATCTAAGATTGAAGTTTATAAAGAATTTATTGAAAAAGAAGATAAGAATATTTTAAAGATAGTTAATTCCATTGA
TAAGAAAGCCAGATTTTTTAATTTAATTGGTCTTGAATTTTTTAAGCTTGGTCAGTACGGACCTGCTATTGAATAT
TTTGCTAAAAATTTAGAAATCAATCCCAATAATTATTTATCTCATTTTTATATAGGTGTTGCTTCTTATAATTTAG
CTAAAAATTTAAGAGTAAAAGATGAAGTTGAAAAATACATAATTCTTGCTGAAAATTCTTTTTTAAAATCACTTTC
AATTAGAGATGATTTTAAAGATTCTCTTTTTGCCATTTCTAATATGTACGTATATGATCTTGATAAACAACTTGAA
GCTAAAAATTATTTAAATAAACTTGGTGATATGGGTGAGGACTATTTTGAGTTTTTAATGTTAAGAGGTGCAAATT
ATTATTCGCTGGGCGATCTTGGTAATGCTATATTGTTTTATGATAAAGCTAGTAAAAAGGCTTCAACTGAAGAGCA
AAAAGAAGGTGTTTCTAGGATCATGAGTAATTTGAAGTAA

f314.aa

MNNCLIKFFIFLLVFSNSYVAFSKNVNVLIVTAMDSEFDQINKLMSNKEEIVLKEYGLNKKILKGKLSNRNVMVII
CGVGKVNAGVWTSYILSKYNISHVINSGVAGGVVSAKYKDIKVGDVVVSSEVAYHDVDLTKFGYKVGQLTGGLPQK
FNANKNLIKNAIEAIKSKVGGSNAYSGLIVSGDQFIDPTYINKIIGNFKDVIAVEMEGAAIGHVSHMFNIPFIVIR
SISDIVNKEGNEVEYSKFSKIAAFNSAKVVQEILRKLZ

t314.aa

KNVNVLIVTAMDSEFDQINKLMSNKEEIVLKEYGLNKKILKGKLSNRNVMVIICGVGKVNAGVWTSYILSKYNISH
VINSGVAGGVVSAKYKDIKVGDVVVSSEVAYHDVDLTKFGYKVGQLTGGLPQKFNANKNLIKNAIEAIKSKVGGSN
AYSGLIVSGDQFIDPTYINKIIGNFKDVIAVEMEGAAIGHVSHMFNIPFIVIRSISDIVNKEGNEVEYSKFSKIAA
FNSAKVVQEILRKLZ

f314.nt

ATGAATAATTGTTTAATAAAGTTTTTTATTTTTTTATTAGTTTTTTCAAACAGTTATGTTGCTTTTTCTAAAAATG
TCAATGTTTTAATAGTAACTGCTATGGACTCTGAGTTTGATCAGATAAATAAGCTTATGTCTAATAAGGAAGAAAT
AGTTCTTAAGGAGTATGGTCTTAATAAAAAGATTTTAAAGGGGAAGTTGTCTAATCGCAATGTTATGGTTATTATT
TGTGGGGTTGGTAAGGTTAATGCTGGTGTGTGGACTAGCTACATTTTGTCAAAATACAACATAAGTCATGTCATTA
ATTCTGGCGTTGCTGGTGGCGTTGTTAGTGCTAAATACAAAGATATTAAAGTGGGAGATGTGGTGGTGTCTTCAGA
GGTTGCATATCATGATGTTGATTTGACTAAATTTGGATACAAGGTAGGACAGCTTACAGGAGGATTGCCTCAAAAA
TTTAATGCCAATAAAAATTTAATTAAGAATGCCATAGAGGCCATTAAATCAAAGGTTGGAGGTTCTAATGCATATT
CAGGATTAATAGTTTCAGGAGATCAGTTTATTGATCCAACTTATATTAACAAAATTATAGGAAACTTTAAAGATGT
AATAGCTGTTGAGATGGAAGGTGCAGCAATAGGGCATGTTTCTCATATGTTTAATATACCTTTTATAGTTATTAGG
TCAATATCTGACATTGTAAATAAAGAAGGGAATGAGGTTGAATATAGTAAATTTTCTAAAATAGCTGCTTTCAATT
CAGCCAAAGTTGTACAAGAAATTTTAAGAAAACTTTAA

TABLE 1. Nucleotide and Amino Acid Sequences

t314.nt

AAAAATGTCAATGTTTTAATAGTAACTGCTATGGACTCTGAGTTTGATCAGATAAATAAGCTTATGTCTAATAAGG
AAGAAATAGTTCTTAAGGAGTATGGTCTTAATAAAAAGATTTTAAAGGGGAAGTTGTCTAATCGCAATGTTATGGT
TATTATTTGTGGGGTTGGTAAGGTTAATGCTGGTGTGTGGACTAGCTACATTTTGTCAAAATACAACATAAGTCAT
GTCATTAATTCTGGCGTTGCTGGTGGCGTTGTTAGTGCTAAATACAAAGATATTAAAGTGGGAGATGTGGTGGTGT
CTTCAGAGGTTGCATATCATGATGTTGATTTGACTAAATTTGGATACAAGGTAGGACAGCTTACAGGAGGATTGCC
TCAAAAATTTAATGCCAATAAAAATTTAATTAAGAATGCCATAGAGGCCATTAAATCAAAGGTTGGAGGTTCTAAT
GCATATTCAGGATTAATAGTTTCAGGAGATCAGTTTATTGATCCAACTTATATTAACAAAATTATAGGAAACTTTA
AAGATGTAATAGCTGTTGAGATGGAAGGTGCAGCAATAGGGCATGTTTCTCATATGTTTAATATACCTTTTATAGT
TATTAGGTCAATATCTGACATTGTAAATAAAGAAGGGAATGAGGTTGAATATAGTAAATTTTCTAAAATAGCTGCT
TTCAATTCAGCCAAAGTTGTACAAGAAATTTTAAGAAAACTTTAA

f32.aa

MNTKTLYLISLILLACNKNNKIPLIQKLDLPKSSILGFSNKMGIIIKDYAFLSKSTKKNSELDYDYAILLRKDEVV
KIEKTLEKTERYGIEGNWILVNYKGTKRYIFSKDINIVNNLIIDHSKZ

t32.aa

CNKNNKIPLIQKLDLPKSSILGFSNKMGIIIKDYAFLSKSTKKNSELDYDYAILLRKDEVVKIEKTLEKTERYGIE
GNWILVNYKGTKRYIFSKDINIVNNLIIDHSKZ

f32.nt

ATGAATACAAAAACATTATATTTAATATCCTTAATTCTTTTAGCTTGCAATAAAAATAACAAAATTCCTCTCATTC
AAAAATTAGATTTGCCCAAAAGCAGCATTCTTGGCTTTAGCAATAAAATGGGCATAATAATAAAAGATTATGCTTT
TCTTAGTAAAAGCACTAAGAAAAATAGCGAATTGGATTATGATTACGCAATTCTACTCAGAAAAGACGAAGTCGTA
AAAATTGAAAAAACACTAGAAAAAACAGAGCGCTATGGAATTGAAGGAAATTGGATCCTAGTCAATTACAAGGGAA
CTAAAAGATACATCTTTAGCAAAGACATCAATATAGTCAACAATTTAATAATTGATCATTCTAAATAG

t32.nt

TGCAATAAAAATAACAAAATTCCTCTCATTCAAAAATTAGATTTGCCCAAAAGCAGCATTCTTGGCTTTAGCAATA
AAATGGGCATAATAATAAAAGATTATGCTTTTCTTAGTAAAAGCACTAAGAAAAATAGCGAATTGGATTATGATTA
CGCAATTCTACTCAGAAAAGACGAAGTCGTAAAAATTGAAAAAACACTAGAAAAAACAGAGCGCTATGGAATTGAA
GGAAATTGGATCCTAGTCAATTACAAGGGAACTAAAAGATACATCTTTAGCAAAGACATCAATATAGTCAACAATT
TAATAATTGATCATTCTAAATAG

f320.aa

MKSIYALLFLFINLSLLANNISKKDLEVLLKIAQAMNKECKNFIEKNPIQFLKEIKPLVDAEKNNLLTLINKKIPI
PENYKIPDLVNIDDFEDLKNLGAKTIKVRKILIEDLIRLIKDAKKFGIEIKIKSAYRTQEYQKFLFDYNVKTYGRK
VAETQSAIPGHSQHHMGTAIDFINIDDNLLNTKEGKWLYENSLKYGFSVSYPKGYETDTGYKAEPWHYLYIGPKPC
FIQKKYFNNLQHKLLEFWNQNKTNLINLIEKYANZ

t320.aa

NNISKKDLEVLLKIAQAMNKECKNFIEKNPIQFLKEIKPLVDAEKNNLLTLINKKIPIPENYKIPDLVNIDDFEDL
KNLGAKTIKVRKILIEDLIRLIKDAKKFGIEIKIKSAYRTQEYQKFLFDYNVKTYGRKVAETQSAIPGHSQHHMGT
AIDFINIDDNLLNTKEGKWLYENSLKYGFSVSYPKGYETDTGYKAEPWHYLYIGPKPCFIQKKYFNNLQHKLLEFW
NQNKTNLINLIEKYANZ

f320.nt

TABLE 1. Nucleotide and Amino Acid Sequences

ATGAAATCAATTTATGCTTTATTATTTCTATTTATTAATTTATCTTTGTTGGCTAACAACATTTCAAAAAAAGATT
TAGAAGTACTGCTAAAGATTGCCCAAGCAATGAATAAGGAATGCAAAAATTTTATTGAAAAAAATCCTATTCAGTT
CTTAAAAGAAATAAAACCCTTAGTAGATGCAGAAAAAAAATAACCTCTTAACTCTAATAAATAAAAAAATACCAATT
CCTGAAAATTATAAAATACCTGATCTGGTAAATATTGATGATTTTGAAGATCTTAAAAATCTTGGAGCAAAGACTA
TTAAAGTAAGAAAAATATTAATCGAAGATTTAATTCGACTAATAAAAGATGCAAAAAAATTTGGGATTGAAATTAA
AATCAAATCTGCTTACAGAACGCAAGAATATCAAAAATTTTTATTTGATTACAATGTCAAAACTTATGGCAGAAAA
GTTGCAGAAACCCAATCAGCAATTCCAGGCCATTCTCAACATCATATGGGAACAGCAATAGATTTTATAAATATAG
ATGATAATTTACTAAACACAAAAGAAGGAAAATGGCTTTATGAAAACTCTCTAAAATACGGATTTTCCGTTTCATA
CCCAAAAGGATATGAAACGGACACTGGATATAAAGCAGAGCCTTGGCACTACTTATACATAGGACCTAAGCCATGC
TTTATTCAGAAAAAATATTTTAATAATTTACAACATAAGCTTCTTGAATTTTGGAACCAGAACAAAACAAATCTTA
TTAACCTAATTGAAAAATATGCAAACTAA

t320.nt

AACAACATTTCAAAAAAAGATTTAGAAGTACTGCTAAAGATTGCCCAAGCAATGAATAAGGAATGCAAAAATTTTA
TTGAAAAAAATCCTATTCAGTTCTTAAAAGAAATAAAACCCTTAGTAGATGCAGAAAAAAAATAACCTCTTAACTCT
AATAAATAAAAAAATACCAATTCCTGAAAATTATAAAATACCTGATCTGGTAAATATTGATGATTTTGAAGATCTT
AAAAATCTTGGAGCAAAGACTATTAAAGTAAGAAAAATATTAATCGAAGATTTAATTCGACTAATAAAAGATGCAA
AAAAATTTGGGATTGAAATTAAAATCAAATCTGCTTACAGAACGCAAGAATATCAAAAATTTTTATTTGATTACAA
TGTCAAAACTTATGGCAGAAAAGTTGCAGAAACCCAATCAGCAATTCCAGGCCATTCTCAACATCATATGGGAACA
GCAATAGATTTTATAAATATAGATGATAATTTACTAAACACAAAAGAAGGAAAATGGCTTTATGAAAACTCTCTAA
AATACGGATTTTCCGTTTCATACCCAAAAGGATATGAAACGGACACTGGATATAAAGCAGAGCCTTGGCACTACTT
ATACATAGGACCTAAGCCATGCTTTATTCAGAAAAAATATTTTAATAATTTACAACATAAGCTTCTTGAATTTTGG
AACCAGAACAAAACAAATCTTATTAACCTAATTGAAAAATATGCAAACTAA

f342.aa

MLYLGDNKAMRTKIIIMTIIIILLAPISGFSNSKESARGKFGAGIILPLPIALQINIGNFDLDIGLYSGVNNLFSDW
KTLFIALDYIFYIYTFPGAANILDFSVGAGGYGTIWFSRFGGSKSGSGPMSIGARLPLALNIAVFRKKFDIFLRIA
PGLGMNVWSNGVGFRWEVFAGLGLRFWFTZ

t342.aa

LAPISGFSNSKESARGKFGAGIILPLPIALQINIGNFDLDIGLYSGVNNLFSDWKTLFIALDYIFYIYTFPGAANI
LDFSVGAGGYGTIWFSRFGGSKSGSGPMSIGARLPLALNIAVFRKKFDIFLRIAPGLGMNVWSNGVGFRWEVFAGL
GLRFWFTZ

f342.nt

ATGCTATACTTAGGAGATAATAAAGCAATGAGAACAAAAATAATTATTATGACAATTATTATTTTATTAGCCCCAA
TCTCAGGATTTTCTAATTCAAAAGAATCTGCAAGGGGTAAATTTGGAGCAGGAATTATACTTCCATTACCAATTGC
TCTACAGATTAATATAGGAAACTTTGATCTTGACATTGGTCTTTACAGCGGAGTAAATAATTTGTTTTCAGACTGG
AAAACATTATTTATAGCATTAGACTATATTTTCTACATATACACATTCCCGGGAGCTGCTAATATTTTGGATTTTT
CAGTTGGCGCAGGGGGATATGGAACAATATGGTTTTCAAGATTTGGAGGCAGTAAGTCAGGCTCAGGACCAATGAG
CATTGGAGCAAGATTGCCTTTGGCCTTAAATATTGCAGTATTTAGGAAGAAATTCGACATATTTTTACGAATAGCA
CCCGGACTTGGAATGAATGTTTGGAGTAATGGCGTTGGATTTAGATGGGAAGTATTCGCAGGATTGGGACTAAGAT
TCTGGTTTACTTAA

t342.nt

TTAGCCCCAATCTCAGGATTTTCTAATTCAAAAGAATCTGCAAGGGGTAAATTTGGAGCAGGAATTATACTTCCAT
TACCAATTGCTCTACAGATTAATATAGGAAACTTTGATCTTGACATTGGTCTTTACAGCGGAGTAAATAATTTGTT
TTCAGACTGGAAAACATTATTTATAGCATTAGACTATATTTTCTACATATACACATTCCCGGGAGCTGCTAATATT
TTGGATTTTTCAGTTGGCGCAGGGGGATATGGAACAATATGGTTTTCAAGATTTGGAGGCAGTAAGTCAGGCTCAG
GACCAATGAGCATTGGAGCAAGATTGCCTTTGGCCTTAAATATTGCAGTATTTAGGAAGAAATTCGACATATTTTT

TABLE 1. Nucleotide and Amino Acid Sequences

ACGAATAGCACCCGGACTTGGAATGAATGTTTGGAGTAATGGCGTTGGATTTAGATGGGAAGTATTCGCAGGATTG
GGACTAAGATTCTGGTTTACTTAA

f352.aa

MNKTKNRSLTYFIILSCISLFGANNNTISYSSIEIPLEDLSEEFKSSGNKSDQINTSKHLNKNIVSYEDPKKGKDL
KLPENIRDKKLPQKRMDENDLKSVIENYENKIKNIEKLLKTKNQKTSENENKKIESIEKKAKKYEILTNKLKNEIV
EIKKLLNKKIKPKEDENYEKINIENIEEETDDDFEDNYEYNDEIEEQMRTITLLMKEZ

t352.aa

CISLFGANNNTISYSSIEIPLEDLSEEFKSSGNKSDQINTSKHLNKNIVSYEDPKKGKDLKLPENIRDKKLPQKRM
DENDLKSVIENYENKIKNIEKLLKTKNQKTSENENKKIESIEKKAKKYEILTNKLKNEIVEIKKLLNKKIKPKEDE
NYEKINIENIEEETDDDFEDNYEYNDEIEEQMRTITLLMKEZ

f352.nt

ATGAATAAAACAAAAAATCGAAGCCTTACGTATTTTATAATACTTTCATGTATATCATTATTTGGGGCTAATAATA
ATACAATAAGCTACTCTAGCATTGAAATTCCTCTAGAAGACTTAAGTGAAGAATTTAAAAGTTCTGGGAATAAAAG
CGATCAAATAAATACCTCAAAACATTTAAACAAAAACATAGTTTCTTATGAAGACCCAAAAAAGGGTAAAGATCTA
AAATTGCCAGAAAATATAAGAGACAAAAAACTACCCCAAAAAAGAATGGACGAAAATGATCTAAAATCTGTAATTG
AAAATTATGAAAATAAAATTAAAAACATAGAAAAGCTTTTAAAAACCAAAAATCAAAAAACATCGGAAAATGAAAA
TAAAAAAATAGAATCAATCGAAAAAAAAGCAAAAAAATATGAAATTTTAACCAATAAATTAAAAAACGAAATAGTA
GAAATAAAAAAGCTCCTTAACAAAAAAATCAAGCCTAAAGAAGATGAAAATTACGAAAAAATAAATATTGAAAACA
TTGAAGAAGAAACTGATGATGATTTTGAAGACAATTATGAATATAATGATGAAATTGAAGAACAAATGAGGACAAT
TACCCTTCTAATGAAGGAATAA

t352.nt

TGTATATCATTATTTGGGGCTAATAATAATACAATAAGCTACTCTAGCATTGAAATTCCTCTAGAAGACTTAAGTG
AAGAATTTAAAAGTTCTGGGAATAAAAGCGATCAAATAAATACCTCAAAACATTTAAACAAAAACATAGTTTCTTA
TGAAGACCCAAAAAAGGGTAAAGATCTAAAATTGCCAGAAAATATAAGAGACAAAAAACTACCCCAAAAAAGAATG
GACGAAAATGATCTAAAATCTGTAATTGAAAATTATGAAAATAAAATTAAAAACATAGAAAAGCTTTTAAAAACCA
AAAATCAAAAAACATCGGAAAATGAAAATAAAAAAATAGAATCAATCGAAAAAAAAGCAAAAAAATATGAAATTTT
AACCAATAAATTAAAAAACGAAATAGTAGAAATAAAAAAGCTCCTTAACAAAAAAATCAAGCCTAAAGAAGATGAA
AATTACGAAAAAATAAATATTGAAAACATTGAAGAAGAAACTGATGATGATTTTGAAGACAATTATGAATATAATG
ATGAAATTGAAGAACAAATGAGGACAATTACCCTTCTAATGAAGGAATAA

f301.aa

MQIDGKIYSIISFPVRDSVSTLGVIGILICFDESLDIIENQLYSSLKFGSKNYNFFMLDRNYMPIFSNLNNLQAKS
FSTAYSENFLSKVIAYAKKDSSSSQYTFNYERDFYSLNFVKTDDFLTQGLILNVNSIPIMFKSNWVIFVAFLLLSF
AIIFYLCNTFVFSLINDFNRIVDYQKSKSDPFSLESPLEVKYSSSIISYISSKLDNLSSKSNESFEKIKFYSEDLN
EYLEQIETAISNTESIDSSILVYEQLRDTFSRFEKSIVDILKGFESIADPINDHNKYISEISSNFEESVSFFYSID
KNLEIFNKVATINSTDIENIKSKVFDLNIVFENVNKNFADLLSQTNSLQSVNKLLVSISAQTNMLAMNAAIEAAKA
GDAGKSFAVVAEEIRKLAINSGKYSKTIKDELKTVDSIIAVINSEIDTIYKNFIDIQDNVDNNFSRHEKVDLTLAK
HFKEIGEFKERYLSHDTKIRDAKNMYKEIFNNHYFISGKFNNFSQDLKEFKVSKMNLDAVSSLQEYSSLVKSSKDK
ILKTKELIQKINDEIKDILFZ

t301.aa

CFDESLDIIENQLYSSLKFGSKNYNFFMLDRNYMPIFSNLNNLQAKSFSTAYSENFLSKVIAYAKKDSSSSQYTFN
YERDFYSLNFVKTDDFLTQGLILNVNSIPIMFKSNWVIFVAFLLLSFAIIFYLCNTFVFSLINDFNRIVDYQKSKS
DPFSLESPLEVKYSSSIISYISSKLDNLSSKSNESFEKIKFYSEDLNEYLEQIETAISNTESIDSSILVYEQLRDT
FSRFEKSIVDILKGFESIADPINDHNKYISEISSNFEESVSFFYSIDKNLEIFNKVATINSTDIENIKSKVFDLNI
VFENVNKNFADLLSQTNSLQSVNKLLVSISAQTNMLAMNAAIEAAKAGDAGKSFAVVAEEIRKLAINSGKYSKTIK

TABLE 1. Nucleotide and Amino Acid Sequences

DELKTVDSIIAVINSEIDTIYKNFIDIQDNVDNNFSRHEKVDLTLAKHFKEIGEFKERYLSHDTKIRDAKNMYKEI
FNNHYFISGKFNNFSQDLKEFKVSKMNLDAVSSLQEYSSLVKSSKDKILKTKELIQKINDEIKDILFZ

f301.nt

ATGCAAATAGATGGGAAAATTTATTCTATAATAAGTTTTCCAGTTAGAGATTCTGTTTCAACATTGGGTGTGATAG
GGATTTTAATATGCTTTGATGAGTCGTTAGATATTATTGAAAATCAGTTGTATTCTTCTCTTAAATTTGGTAGTAA
AAATTATAATTTTTTTATGCTTGACAGAAATTACATGCCCATTTTTTCAAACCTTAATAATCTTCAGGCCAAATCT
TTTTCTACAGCTTATAGTGAGAATTTTTTGAGTAAAGTTATAGCTTATGCTAAAAAAGATTCTTCTAGCTCTCAGT
ACACTTTTAATTATGAAAGAGATTTTTATTCTTTAAACTTTGTAAAAACCGATGATTTTTTGACTCAGGGGCTTAT
TTTAAATGTCAATTCCATTCCTATTATGTTTAAATCAAATTGGGTTATATTTGTTGCATTTTTATTATTGTCTTTT
GCAATTATTTTTTATTTATGCAATACTTTTGTTTTTTCATTAATTAATGATTTTAACAGAATTGTTGACTATCAAA
AATCAAAAAGCGATCCTTTTAGTCTTGAATCTCCCTTAGAGGTTAAGTATTCTTCATCTATTATTTCTTATATTAG
TTCAAAGCTAGATAATCTGTCTTCTAAGAGTAATGAATCTTTTGAGAAGATAAAATTTTATTCTGAAGATTTGAAT
GAATATTTGGAACAAATAGAAACTGCTATATCAAATACTGAGAGTATAGATTCTAGCATTTTAGTTTACGAACAAC
TAAGAGATACTTTTTCTAGATTTGAAAAAATCAATTGTTGATATTTTAAAAGGCTTTGAATCTATTGCTGATCCGAT
TAATGATCACAATAAATATATATCAGAAATCTCTTCAAATTTTGAAGAGAGTGTTAGTTTTTTCTATAGTATAGAT
AAAAATTTAGAAATTTTTAATAAGGTTGCTACTATAAATTCTACTGATATTGAAAATATTAAAAGTAAGGTTTTTG
ATTTAAATATTGTTTTTGAAAATGTGAATAAAAATTTTGCAGATCTTTTGTCTCAAACAAATAGTTTGCAAAGTGT
AAATAAACTTTTAGTTTCAATTTCAGCTCAGACCAATATGCTTGCTATGAATGCAGCAATTGAAGCAGCAAAAGCA
GGTGATGCAGGTAAAAGTTTTGCAGTTGTTGCTGAGGAGATTAGAAAGCTTGCTATTAATTCTGGAAAATATTCTA
AAACCATTAAAGATGAACTTAAAACGGTCGACAGCATTATTGCAGTAATTAATTCAGAGATTGATACAATTTATAA
AAATTTCATAGACATTCAAGATAATGTGGACAACAATTTTTCAAGACACGAGAAAGTAGATCTTACTCTTGCTAAG
CATTTTAAAGAAATTGGCGAGTTTAAAGAAAGGTATTTGTCTCACGATACTAAGATCAGAGATGCTAAGAATATGT
ATAAAGAAATATTTAATAATCATTATTTTATTAGTGGCAAGTTTAACAACTTTAGTCAAGATTTAAAAGAGTTTAA
AGTTTCTAAGATGAATTTAGATGCGGTAAGTTCTCTTCAAGAATATTCATCTTTAGTAAAGTCTTCTAAGGATAAG
ATATTAAAGACAAAGGAATTGATTCAAAAGATTAATGATGAGATTAAAGATATTCTTTTTTAG

t301.nt

TGCTTTGATGAGTCGTTAGATATTATTGAAAATCAGTTGTATTCTTCTCTTAAATTTGGTAGTAAAAATTATAATT
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TATGAAAGAGATTTTTATTCTTTAAACTTTGTAAAAACCGATGATTTTTTGACTCAGGGGCTTATTTTAAATGTCA
ATTCCATTCCTATTATGTTTAAATCAAATTGGGTTATATTTGTTGCATTTTTATTATTGTCTTTTGCAATTATTTT
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AATTGGCGAGTTTAAAGAAAGGTATTTGTCTCACGATACTAAGATCAGAGATGCTAAGAATATGTATAAAGAAATA
TTTAATAATCATTATTTTATTAGTGGCAAGTTTAACAACTTTAGTCAAGATTTAAAAGAGTTTAAAGTTTCTAAGA
TGAATTTAGATGCGGTAAGTTCTCTTCAAGAATATTCATCTTTAGTAAAGTCTTCTAAGGATAAGATATTAAAGAC
AAAGGAATTGATTCAAAAGATTAATGATGAGATTAAAGATATTCTTTTTTAG

f346.aa

TABLE 1. Nucleotide and Amino Acid Sequences

MSIDKVPDEAFAEKIVGDGIAILPTSNELLAPCDGKIGKIFKTNHAFSLETKEGVEIFVHFGINTLNLNGKGFTRV
AEEGINVKQGEVIIRLDLEYLKEHSESVITPVVIANSDEVSSIEYSFGRLENDSEYILSSSTVLTEEIRHKISQTK
PVIAGKDLVLRVKKZ

t346.aa

CDGKIGKIFKTNHAFSLETKEGVEIFVHFGINTLNLNGKGFTRVAEEGINVKQGEVIIRLDLEYLKEHSESVITPV
VIANSDEVSSIEYSFGRLENDSEYILSSSTVLTEEIRHKISQTKPVIAGKDLVLRVKKZ

f346.nt

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GCAATGAGTTGTTGGCGCCTTGTGATGGGAAAATAGGTAAAATTTTTAAAACCAATCATGCCTTTAGCCTTGAAAC
TAAAGAGGGCGTTGAAATTTTTGTCCATTTTGGAATTAATACTCTTAATTTAAATGGTAAGGGTTTTACAAGAGTT
GCTGAAGAGGGCATTAATGTTAAACAAGGTGAAGTTATTATTAGGCTTGATCTTGAATATTTAAAAGAGCATTCAG
AATCCGTTATTACTCCGGTTGTTATTGCAAATTCTGATGAAGTTTCAAGTATAGAATATTCTTTTGGAAGGCTTGA
AAATGATTCTGAATATATTTTATCATCTTCAACTGTCTTGACAGAAGAAATTAGGCATAAAATATCTCAAACAAAG
CCTGTTATAGCGGGCAAAGATTTGGTGTTGCGAGTTAAAAAGTAA

t346.nt

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TATCATCTTCAACTGTCTTGACAGAAGAAATTAGGCATAAAATATCTCAAACAAAGCCTGTTATAGCGGGCAAAGA
TTTGGTGTTGCGAGTTAAAAAGTAA

f373.aa

MNYQRIKNYCKFTSVFLFFLFSCVSNELKLDQSLVKGKLVNGLRYYIYKNQTPKNAVNMGIVFNVGSLNEEDNERG
IAHYLEHMAFNGTKDYPGNSIVDVLKKFGMQFGADINAATSFDFTYYRLDLSDGNNKDEIDESINILRNWASQISF
MKEEIDLERNIIIEEKKLGETYPGRIYEKMDKFLTSGSLYEFRSPIGLEEQILSFQPEDFKKFYRKWYRPELASVI
VVGDIDPIEIEEKIKKQFVSWKNPTDKIKEVKVSLDVELKDKFLLLEDLEVGEPSLMFFKKEIINFVKTKDDLLNA
IKKSLLAALFENRFSELKTAGVKQFKNVSNKDFFSFKSDNNTIVAKSISLNFNPDHLNEGIQDFFYELERIRKFGF
TQGELEKVRSQFYKSLELRKKNINKTNSWAIFQDLIEIAINGSNKFDMNEYCDLSFQYLEKIDLKTINNLVGREFD
VKNCAIFYSYHGRAHPVLTLEDIDNLQKIALKRELKPYENSLIEGKFFKKSLDDKDIIRENEFENEISSFVLENGV
EVYFKYNDQKKGVIDFSATSWGGLINEDLKLIPVLSFAPGVVSGSGYGDYSALQIEKYLSDKAVSLRVGVGAQESY
ISGSSDKKDLETLFQLIYFTFKEPKIDDVSLQNAINNIKALIKSNENSSDYHFHKAISKFLNNNDPRFEDTKDSDL
QYFTKENILSFYKKRFTYANNFKFVLLETQIFRQZ

t373.aa

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PGRIYEKMDKFLTSGSLYEFRSPIGLEEQILSFQPEDFKKFYRKWYRPELASVIVVGDIDPIEIEEKIKKQFVSWK
NPTDKIKEVKVSLDVELKDKFLLLEDLEVGEPSLMFFKKEIINFVKTKDDLLNAIKKSLLAALFENRFSELKTAGV
KQFKNVSNKDFFSFKSDNNTIVAKSISLNFNPDHLNEGIQDFFYELERIRKFGFTQGELEKVRSQFYKSLELRKKN
INKTNSWAIFQDLIEIAINGSNKFDMNEYCDLSFQYLEKIDLKTINNLVGREFDVKNCAIFYSYHGRAHPVLTLED
IDNLQKIALKRELKPYENSLIEGKFFKKSLDDKDIIRENEFENEISSFVLENGVEVYFKYNDQKKGVIDFSATSWG
GLINEDLKLIPVLSFAPGVVSGSGYGDYSALQIEKYLSDKAVSLRVGVGAQESYISGSSDKKDLETLFQLIYFTFK
EPKIDDVSLQNAINNIKALIKSNENSSDYHFHKAISKFLNNNDPRFEDTKDSDLQYFTKENILSFYKKRFTYANNF
KFVLLETQIFRQZ

f373.nt

TABLE 1. Nucleotide and Amino Acid Sequences

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ATGAGTTAAAGTTAGATCAAAGTTTGGTAAAAGGAAAACTTGTCAATGGGCTAAGGTATTATATTTATAAAAATCA
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ATAGCGCATTATCTTGAACATATGGCTTTTAATGGTACAAAAGATTATCCAGGGAATTCTATAGTTGATGTTCTTA
AAAAATTTGGAATGCAATTTGGTGCTGACATTAATGCTGCTACTAGTTTTGATTTCACTTATTATAGACTTGATTT
GTCAGATGGTAATAATAAAGATGAAATTGATGAATCTATAAATATTTTGAGAAACTGGGCTTCTCAAATCAGTTTC
ATGAAAGAAGAAATAGATCTAGAGCGAAATATTATTATTGAGGAAAAAAAGCTTGGTGAGACTTATCCTGGAAGAA
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CTTTAATCCAGATCATTTGAACGAAGGAATACAAGACTTTTTTTATGAGCTTGAGAGGATAAGAAAATTTGGATTT
ACCCAAGGTGAGCTTGAAAAAGTTAGATCTCAATTTTACAAATCTTTAGAATTAAGGAAAAAGAATATAAATAAAA
CAAATTCATGGGCTATTTTTCAGGATTTAATAGAAATTGCTATTAATGGTTCTAATAAATTTGATATGAATGAATA
TTGCGATCTTTCTTTTCAATATTTGGAAAAGATTGATTTAAAAACAATAAACAATCTTGTAGGAAGAGAGTTTGAT
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ATGAAGATTTAAAACTTATTCCTGTTTTATCTTTTGCTCCCGGAGTAGTATCTGGTTCGGGTTATGGTGATTATTC
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TCATTTTCATAAAGCCATTAGTAAATTTTTAAACAATAATGATCCTAGATTTGAAGATACAAAAGATAGTGATTTG
CAATATTTTACAAAAGAAAATATTTTGTCTTTTTTATAAGAAAAGGTTTACTTATGCAAATAATTTTAAGTTTGTCT
TGCTGGAGACTCAGATATTCAGACAATAA

t373.nt

TGTGTTTCTAATGAGTTAAAGTTAGATCAAAGTTTGGTAAAAGGAAAACTTGTCAATGGGCTAAGGTATTATATTT
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TGAGAGGGGAATAGCGCATTATCTTGAACATATGGCTTTTAATGGTACAAAAGATTATCCAGGGAATTCTATAGTT
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AATCAGTTTCATGAAAGAAGAAATAGATCTAGAGCGAAATATTATTATTGAGGAAAAAAAGCTTGGTGAGACTTAT
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AAGTGTTATTGTGGTAGGAGATATTGATCCTATAGAAATTGAAGAGAAGATAAAGAAGCAATTTGTTTCTTGGAAA
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TTTCTTTAAACTTTAATCCAGATCATTTGAACGAAGGAATACAAGACTTTTTTTATGAGCTTGAGAGGATAAGAAA
ATTTGGATTTACCCAAGGTGAGCTTGAAAAAGTTAGATCTCAATTTTACAAATCTTTAGAATTAAGGAAAAAGAAT
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ATTGACAATCTTCAAAAGATAGCTTTAAAAAGAGAGTTAAAGCCTTATGAGAATTCTTTAATTGAAGGTAAATTTT
TTAAGAAGTCTTTAGATGATAAAGATATTATTAGAGAAAATGAGTTTGAAAATGAAATTTCGTCATTTGTTCTTGA
AAATGGGGTTGAAGTTTATTTTAAATATAATGATCAAAAAAAAGGTGTAATTGATTTTAGTGCAACTTCTTGGGGA
GGTTTAATTAATGAAGATTTAAAACTTATTCCTGTTTTATCTTTTGCTCCCGGAGTAGTATCTGGTTCGGGTTATG
GTGATTATTCTGCATTACAGATTGAAAAATATTTATCAGATAAAGCTGTTTCTTTAAGAGTTGGGGTTGGAGCTCA
AGAATCATATATTTCTGGAAGTTCAGATAAAAAAGATCTTGAAACTCTTTTTCAGCTTATATATTTTACTTTTAAG

TABLE 1. Nucleotide and Amino Acid Sequences

GAACCCAAAATTGATGATGTTTCTTTGCAAAATGCTATTAATAATATAAAAGCATTAATAAAGAGCAATGAAAATA
GTTCTGATTATCATTTTCATAAAGCCATTAGTAAATTTTTAAACAATAATGATCCTAGATTTGAAGATACAAAAGA
TAGTGATTTGCAATATTTTACAAAAGAAAATATTTTGTCTTTTTATAAGAAAAGGTTTACTTATGCAAATAATTTT
AAGTTTGTCTTGCTGGAGACTCAGATATTCAGACAATAA

f384.aa

MDWDFEKIIFLLNESTRLALSGCAKLILDFKSDGSIVTQVDKQIEQFLFKEIKKPGNFVLGEETISTYKEEYIKDA
LISESTFIIDPIDGTSSFAAGLPSYGISLAYASGGKIIEGAISLPLSGEFFITSKDNVFYAKKNIGSYPLKKDFNK
FIFDNSKCYNIHSLLAVSRSIIRLFNLDISSHIHINGSCVYSFAKLFTGSYKAYFSFVGLWDIAACLAIGNKLGMV
GEFYCGNKMTLDILDSMYILEPNNHKRWSLKDFFIYSDNKSTIDIIRKDANKKINK

t384.aa

CAKLILDFKSDGSIVTQVDKQIEQFLFKEIKKPGNFVLGEETISTYKEEYIKDALISESTFIIDPIDGTSSFAAGL
PSYGISLAYASGGKIIEGAISLPLSGEFFITSKDNVFYAKKNIGSYPLKKDFNKFIFDNSKCYNIHSLLAVSRSII
RLFNLDISSHIHINGSCVYSFAKLFTGSYKAYFSFVGLWDIAACLAIGNKLGMVGEFYCGNKMTLDILDSMYILEP
NNHKRWSLKDFFIYSDNKSTIDIIRKDANKKINKZ

f384.nt

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GATCAAAAAGCCTGGAAATTTTGTTCTTGGAGAAGAGACAATATCTACTTATAAAGAAGAGTATATCAAAGATGCT
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TAAGGCCTACTTTTCTTTTGTAGGACTTTGGGATATTGCAGCGTGTTTAGCTATTGGTAATAAATTGGGCATGGTT
GGCGAATTTTATTGTGGTAATAAAATGACATTAGATATCTTAGATTCAATGTATATTTTAGAGCCTAATAATCATA
AAAGATGGTCCTTGAAAGATTTTTTTATTTATTCTGATAATAAATCAACAATAGACATTATAAGAAAAGATGCAAA
TAAAAAAATCAATAAGTAA

t384.nt

AGTGGTTGTGCTAAATTAATTTTAGATTTTAAATCTGATGGGTCTATTGTAACTCAGGTTGATAAGCAAATTGAGC
AATTCTTATTCAAAGAGATCAAAAAGCCTGGAAATTTTGTTCTTGGAGAAGAGACAATATCTACTTATAAAGAAGA
GTATATCAAAGATGCTTTAATATCAGAGAGTACTTTTATTATTGATCCTATTGATGGAACTTCTTCTTTTGCAGCA
GGCCTTCCTTCATATGGAATATCGCTAGCGTATGCTAGTGGCGGCAAAATTATTGAAGGAGCCATTTCTCTTCCTT
TAAGCGGAGAGTTTTTTATTACTTCTAAAGATAATGTATTTTATGCTAAAAAAAACATTGGTAGCTATCCTTTAAA
AAAGGATTTTAATAAATTTATTTTTGATAATTCTAAATGTTACAATATTCATAGTTTACTTGCAGTTTCAAGGTCT
ATTATAAGGTTATTTAATCTTGATATTTCTTCTCATATTCATATTAATGGTTCTTGTGTATATTCTTTTGCTAAAC
TTTTTACAGGTTCTTATAAGGCCTACTTTTCTTTTGTAGGACTTTGGGATATTGCAGCGTGTTTAGCTATTGGTAA
TAAATTGGGCATGGTTGGCGAATTTTATTGTGGTAATAAAATGACATTAGATATCTTAGATTCAATGTATATTTTA
GAGCCTAATAATCATAAAAGATGGTCCTTGAAAGATTTTTTTATTTATTCTGATAATAAATCAACAATAGACATTA
TAAGAAAAGATGCAAATAAAAAAATCAATAAGTAA

f860.aa

MAFYKLNDNIALAEDLLKYLLSSILNECSQDMDFLENYIEKGLIKKLENVINSNFEVITYTKAIEILENSKKNFEI
KPYWGIDLQTDHERYLTEETFKKPVVVIDYPKNFKAFYMKANKDNKTVKGMDILVPKIGEIIGGSEREDDLQKLEN
RIKELNLNIEHLNWYLDLRRFGSAPHSGFGLGLERLVQYSTGISNIRDSIPFPRTPKNLYFZ

t860.aa

TABLE 1. Nucleotide and Amino Acid Sequences

CSQDMDFLENYIEKGLIKKLENVINSNFEVITYTKAIEILENSKKNFEIKPYWGIDLQTDHERYLTEETFKKPVVV
IDYPKNFKAFYMKANKDNKTVKGMDILVPKIGEIIGGSEREDDLQKLENRIKELNLNIEHLNWYLDLRRFGSAPHS
GFGLGLERLVQYSTGISNIRDSIPFPRTPKNLYFZ

f860.nt

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ACGAATGCTCACAAGATATGGATTTTTTAGAAAATTACATTGAAAAAGGTTTAATTAAAAAACTAGAAAATGTAAT
AAATTCAAATTTTGAGGTTATTACCTATACTAAAGCAATTGAAATTCTTGAAAACTCAAAAAAAAATTTTGAAATA
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TGGTCATTGATTATCCAAAAAATTTCAAAGCATTTTACATGAAAGCAAATAAAGACAATAAAACTGTTAAAGGAAT
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ATTCCCAAGGACTCCTAAAAATCTTTATTTTTAA

t860.nt

TGCTCACAAGATATGGATTTTTTAGAAAATTACATTGAAAAAGGTTTAATTAAAAAACTAGAAAATGTAATAAATT
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GGCTTTGGACTTGGACTTGAAAGATTGGTGCAATACTCAACAGGAATATCTAATATAAGAGATTCAATACCATTCC
CAAGGACTCCTAAAAATCTTTATTTTTAA

f446.aa

MKILRLCLLFLFFACTFDYDEYSSRSDVAKKFPSIQILGIKYYDVVYNKEQTVLNSLSFSYFNDYKIYKAENGRFL
YHSLDNEISGKFNNLEGSYITKDLDMRDSVEFKIEDKNNYYLLNSNRLLWKNKDKKLQSPPNELVLIRFNDSKING
KGFSYFLKSNVFYFDSGVEGIMNZ

t446.aa

CTFDYDEYSSRSDVAKKFPSIQILGIKYYDVVYNKEQTVLNSLSFSYFNDYKIYKAENGRFLYHSLDNEISGKFNN
LEGSYITKDLDMRDSVEFKIEDKNNYYLLNSNRLLWKNKDKKLQSPPNELVLIRFNDSKINGKGFSYFLKSNVFYF
DSGVEGIMNZ

f446.nt

ATGAAAATACTTAGACTTTGTTTGTTGTTTTTGTTTTTTGCTTGTACTTTTGATTATGATGAGTATTCTAGTAGAT
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AACCGTTTTAAATTCTTTAAGCTTTAGTTATTTCAATGACTATAAAATTTATAAGGCAGAGAATGGAAGGTTTTTA
TATCATTCCCTAGATAATGAAATTTCAGGGAAGTTTAATAATTTGGAAGGTTCTTATATTACAAAGGATTTGGATA
TGAGAGATTCTGTAGAATTTAAAATAGAAGATAAAAATAATTATTATTTGCTTAATTCAAATAGGCTTTTATGGAA
GAATAAAGACAAGAAGTTGCAATCCCCCCCAAATGAGCTAGTATTAATTAGATTTAATGATAGCAAAATAAACGGA
AAAGGATTTTCTTATTTTTTAAAGAGCAATGTTTTTTATTTTGATTCTGGAGTTGAAGGAATCATGAATTGA

t446.nt

TGTACTTTTGATTATGATGAGTATTCTAGTAGATCTGATGTGGCCAAAAAGTTTCCTTCAATACAAATATTAGGAA
TCAAGTATTATGATGTTGTATACAATAAAGAGCAAACCGTTTTAAATTCTTTAAGCTTTAGTTATTTCAATGACTA
TAAAATTTATAAGGCAGAGAATGGAAGGTTTTTATATCATTCCCTAGATAATGAAATTTCAGGGAAGTTTAATAAT
TTGGAAGGTTCTTATATTACAAAGGATTTGGATATGAGAGATTCTGTAGAATTTAAAATAGAAGATAAAAATAATT
ATTATTTGCTTAATTCAAATAGGCTTTTATGGAAGAATAAAGACAAGAAGTTGCAATCCCCCCCAAATGAGCTAGT

TABLE 1. Nucleotide and Amino Acid Sequences

ATTAATTAGATTTAATGATAGCAAAATAAACGGAAAAGGATTTTCTTATTTTTTAAAGAGCAATGTTTTTTATTTT
GATTCTGGAGTTGAAGGAATCATGAATTGA

f457.aa

MKQKLSWILLFCFLSCRSESRLAENVLIEFFDSIKNFQSSPEIFFNYLNIPSDDDLKAKIRGLKSQAKDDFIFYPL
FFNNLRYEIIGRKNISKGFEFEVVIKNINFQNGIEKFLAKLNKIEGRSLNIKNLEKKERKKIFDNLINEVIGELDD
FDYTEVVHFFRVVKSSSESYKIELLGDVLNIQSRNKLINDLFLVLSPGIZ

t457.aa

CFLSCRSESRLAENVLIEFFDSIKNFQSSPEIFFNYLNIPSDDDLKAKIRGLKSQAKDDFIFYPLFFNNLRYEIIG
RKNISKGFEFEVVIKNINFQNGIEKFLAKLNKIEGRSLNIKNLEKKERKKIFDNLINEVIGELDDFDYTEVVHFFR
VVKSSSESYKIELLGDVLNIQSRNKLINDLFLVLSPGIZ

f457.nt

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TTTTTTAATAATCTAAGATATGAGATAATAGGTAGAAAAAATATTTCTAAGGGCTTTGAATTTGAAGTTGTTATTA
AAAATATTAACTTTCAAAACGGTATAGAAAAATTTTTGGCTAAATTAAATAAAATTGAAGGGAGATCTTTAAATAT
TAAAAATTTAGAAAAAAAAGAGCGTAAAAAAATATTTGACAATTTAATAAATGAAGTTATTGGAGAGTTGGATGAT
TTTGATTACACTGAAGTTGTTCATTTTTTTAGAGTAGTTAAGAGTTCTTCTGAAAGTTATAAAATAGAGCTTTTAG
GAGATGTTTTAAATATACAGTCTAGAAATAAGCTTATTAATGATCTTTTTTTGGTTTTATCGCCTGGAATTTAA

t457.nt

TGTTTTTTGTCTTGTAGATCTGAATCTAGATTGGCTGAAAATGTTTTAATAGAGTTTTTTGATTCTATTAAAAATT
TTCAAAGCAGTCCTGAAATATTTTTTAATTATTTAAATATTCCAAGTGATGATGATCTGAAGGCAAAAATTCGTGG
GTTGAAATCTCAGGCAAAGGATGATTTCATTTTTTATCCTTTGTTTTTTAATAATCTAAGATATGAGATAATAGGT
AGAAAAAATATTTCTAAGGGCTTTGAATTTGAAGTTGTTATTAAAAATATTAACTTTCAAAACGGTATAGAAAAAT
TTTTGGCTAAATTAAATAAAATTGAAGGGAGATCTTTAAATATTAAAAATTTAGAAAAAAAAGAGCGTAAAAAAAT
ATTTGACAATTTAATAAATGAAGTTATTGGAGAGTTGGATGATTTTGATTACACTGAAGTTGTTCATTTTTTTAGA
GTAGTTAAGAGTTCTTCTGAAAGTTATAAAATAGAGCTTTTAGGAGATGTTTTAAATATACAGTCTAGAAATAAGC
TTATTAATGATCTTTTTTTGGTTTTATCGCCTGGAATTTAA

f542.aa

MRIVIFIFGILLTSCFSRNGIESSSKKIKISMLVDGVLDDKSFNSSANEALLRLKKDFPENIEEVFSCAISGVYSS
YVSDLDNLKRNGSDLIWLVGYMLTDASLLVSSENPKISYGIIDPIYGDDVQIPENLIAVVFRVEPRCFFGWLYCSQ
KKLFWQNRFYRGNEGZ

t542.aa

CFSRNGIESSSKKIKISMLVDGVLDDKSFNSSANEALLRLKKDFPENIEEVFSCAISGVYSSYVSDLDNLKRNGSD
LIWLVGYMLTDASLLVSSENPKISYGIIDPIYGDDVQIPENLIAVVFRVEPRCFFGWLYCSQKKLFWQNRFYRGNE
GZ

f542.nt

ATGAGAATTGTAATTTTTATATTCGGTATTTTGTTGACTTCTTGCTTTAGTAGAAATGGAATAGAATCTAGTTCAA
AAAAAATTAAGATATCCATGTTGGTAGATGGTGTTCTTGACGACAAATCTTTTAATTCTAGTGCTAATGAGGCTTT
ATTACGCTTGAAAAAAGATTTTCCAGAAAATATTGAAGAAGTTTTTTCTTGTGCTATTTCTGGAGTTTATTCTAGT
TATGTTTCAGATCTTGATAATTTAAAAAGGAATGGCTCAGACTTGATTTGGCTTGTAGGGTACATGCTTACGGACG
CATCTTTATTGGTTTCATCGGAGAATCCAAAAATTAGCTATGGAATAATAGATCCCATTTATGGTGATGATGTTCA

TABLE 1. Nucleotide and Amino Acid Sequences

GATTCCTGAAAACTTGATTGCTGTTGTTTTCAGAGTAGAGCCAAGGTGCTTTTTTGGCTGGCTATATTGCAGCCAA
AAAAAGCTTTTCTGGCAAAATAGGTTTTATAGGGGGAATGAAGGGTAA

t542.nt

TGCTTTAGTAGAAATGGAATAGAATCTAGTTCAAAAAAAATTAAGATATCCATGTTGGTAGATGGTGTTCTTGACG
ACAAATCTTTTAATTCTAGTGCTAATGAGGCTTTATTACGCTTGAAAAAAGATTTTCCAGAAAATATTGAAGAAGT
TTTTTCTTGTGCTATTTCTGGAGTTTATTCTAGTTATGTTTCAGATCTTGATAATTTAAAAAGGAATGGCTCAGAC
TTGATTTGGCTTGTAGGGTACATGCTTACGGACGCATCTTTATTGGTTTCATCGGAGAATCCAAAAATTAGCTATG
GAATAATAGATCCCATTTATGGTGATGATGTTCAGATTCCTGAAAACTTGATTGCTGTTGTTTTCAGAGTAGAGCC
AAGGTGCTTTTTTGGCTGGCTATATTGCAGCCAAAAAAAGCTTTTCTGGCAAAATAGGTTTTATAGGGGGAATGAA
GGGTAA

f93.aa

MKRILAMHDISSMGRTSLTICIPVISSFNMQVCPFVTAVLSASTAYKKFEIVDLTDHLEKFINIWKEQNEHFDILY
TGFLGSEKQQITIEKIIKLIKFEKIVIDPVFADDGEIYPIFDNKIISGFRKIIKYANIITPNITELEMLSKSSKLN
NKDDIIKAILNLDTKATVVVTSVKRGNLLGNICYNPKNKEYSEFFLEGLEQNFSGTGDLFTSLLIGYLEKFETEQA
LEKTTKAIHLIIKESIKENVSKKEGVRIENFLKNTFZ

t93.aa

CIPVISSFNMQVCPFVTAVLSASTAYKKFEIVDLTDHLEKFINIWKEQNEHFDILYTGFLGSEKQQITIEKIIKLI
KFEKIVIDPVFADDGEIYPIFDNKIISGFRKIIKYANIITPNITELEMLSKSSKLNNKDDIIKAILNLDTKATVVV
TSVKRGNLLGNICYNPKNKEYSEFFLEGLEQNFSGTGDLFTSLLIGYLEKFETEQALEKTTKAIHLIIKESIKENV
SKKEGVRIENFLKNTFZ

f93.nt

ATGAAAAGAATTTTAGCAATGCATGATATTTCAAGCATGGGAAGAACATCTCTTACAATATGCATACCAGTAATAT
CTTCGTTTAATATGCAAGTTTGTCCTTTTGTGACAGCTGTCCTTTCTGCTTCCACAGCTTATAAAAAATTTGAAAT
AGTGGATTTAACCGATCATTTAGAAAAATTTATCAATATATGGAAAGAACAAAATGAGCACTTTGACATACTCTAT
ACCGGATTTCTGGGAAGCGAAAAACAACAAATAACAATAGAGAAAATAATTAAATTAATAAAATTTGAAAAAATTG
TAATTGATCCTGTGTTTGCTGACGATGGAGAAATTTACCCTATATTTGATAATAAAATAATTAGTGGATTTAGAAA
AATCATAAAGTACGCAAACATAATAACACCCAATATCACAGAACTTGAAATGCTAAGCAAAAGCTCAAAACTTAAC
AACAAAGATGATATCATAAAAGCAATATTAAATCTTGATACAAAAGCGACGGTAGTTGTTACAAGCGTTAAAAGGG
GAAATCTCTTGGGAAACATTTGCTACAATCCTAAAAACAAAGAATACTCGGAGTTTTTTTTAGAAGGATTAGAACA
AAATTTCAGTGGAACAGGAGATTTATTTACCAGCTTACTTATAGGATATTTGGAAAAATTTGAAACAGAGCAAGCC
TTAGAAAAAACAACAAAGGCTATTCACCTAATAATAAAAGAGTCAATTAAAGAAAATGTTTCAAAAAAAGAAGGGG
TCCGAATTGAAAATTTCTTAAAAAATACATTTTGA

t93.nt

TGCATACCAGTAATATCTTCGTTTAATATGCAAGTTTGTCCTTTTGTGACAGCTGTCCTTTCTGCTTCCACAGCTT
ATAAAAAATTTGAAATAGTGGATTTAACCGATCATTTAGAAAAATTTATCAATATATGGAAAGAACAAAATGAGCA
CTTTGACATACTCTATACCGGATTTCTGGGAAGCGAAAAACAACAAATAACAATAGAGAAAATAATTAAATTAATA
AAATTTGAAAAAATTGTAATTGATCCTGTGTTTGCTGACGATGGAGAAATTTACCCTATATTTGATAATAAAATAA
TTAGTGGATTTAGAAAAATCATAAAGTACGCAAACATAATAACACCCAATATCACAGAACTTGAAATGCTAAGCAA
AAGCTCAAAACTTAACAACAAAGATGATATCATAAAAGCAATATTAAATCTTGATACAAAAGCGACGGTAGTTGTT
ACAAGCGTTAAAAGGGGAAATCTCTTGGGAAACATTTGCTACAATCCTAAAAACAAAGAATACTCGGAGTTTTTTT
TAGAAGGATTAGAACAAAATTTCAGTGGAACAGGAGATTTATTTACCAGCTTACTTATAGGATATTTGGAAAAATT
TGAAACAGAGCAAGCCTTAGAAAAAACAACAAAGGCTATTCACCTAATAATAAAAGAGTCAATTAAAGAAAATGTT
TCAAAAAAAGAAGGGGTCCGAATTGAAAATTTCTTAAAAAATACATTTTGA

f105.aa

TABLE 1. Nucleotide and Amino Acid Sequences

MGLYLKLLRQSINLKSLFPLSVLFFSCNVVDTDFSVLEFKVANFNLNDDFSQGLLDSAYNILNRSFDLIIIKNLKN
KNVLDLINNRVLFRAFKNAYFIDQGSGLSVSILSKRKINIKVLSVMQDSCDLKLGLLVDFKFENNHYGIVIYNLSK
DFIKSIANLQISEQILYLKAQMDKLMFILDESEFVIFDLLIKNGFFSLINDSNYTSMLANKIDFRVFSNFFARVSL
YSFMFVIADYLHSNYVVENFPQKIVINZ

t105.aa

CNVVDTDFSVLEFKVANFNLNDDFSQGLLDSAYNILNRSFDLIIIKNLKNKNVLDLINNRVLFRAFKNAYFIDQGS
GLSVSILSKRKINIKVLSVMQDSCDLKLGLLVDFKFENNHYGIVIYNLSKDFIKSIANLQISEQILYLKAQMDKLM
FILDESEFVIFDLLIKNGFFSLINDSNYTSMLANKIDFRVFSNFFARVSLYSFMFVIADYLHSNYVVENFPQKIVI
NZ

f105.nt

ATGGGCTTGTATTTGAAGTTGTTGAGACAAAGTATCAACTTGAAGAGTTTATTTCCGCTTAGTGTTTTATTTTTTT
CCTGTAATGTTGTAGATACAGATTTTAGTGTTTTGGAGTTTAAGGTTGCAAATTTTAATTTAAATGATGATTTTTC
TCAAGGGTTACTTGATTCTGCTTATAATATTCTAAATCGAAGTTTTGATTTAATAATTATTAAGAATCTTAAGAAT
AAAAATGTTCTTGATTTAATTAATAATAGAGTTTTATTTAGAGCTTTTAAGAATGCTTATTTTATTGATCAAGGTA
GTGGCCTTTCTGTTAGCATTCTTTCTAAGCGCAAAATAAATATTAAAGTTTTAAGTGTAATGCAAGATTCTTGCGA
TTTAAAATTAGGATTGCTTGTGGATTTTAAATTTGAGAATAATCACTATGGTATTGTTATTTATAATTTAAGCAAG
GATTTTATTAAAAGTATTGCCAATTTGCAAATTAGTGAACAAATTTTATATTTAAAAGCCCAAATGGATAAATTGA
TGTTTATTTTAGATGAATCTGAATTTGTTATTTTTGATTTATTAATCAAAAATGGATTTTTTAGCTTAATAAATGA
TTCAAACTACACTTCAATGTTAGCAAATAAAATTGATTTTAGAGTTTTTTCTAATTTTTTTGCTAGGGTTTCTTTA
TATTCATTTATGTTTGTAATTGCAGATTATTTGCATAGCAATTATGTTGTTGAGAATTTTCCTCAAAAAATAGTTA
TCAATTGA

t105.nt

TGTAATGTTGTAGATACAGATTTTAGTGTTTTGGAGTTTAAGGTTGCAAATTTTAATTTAAATGATGATTTTTCTC
AAGGGTTACTTGATTCTGCTTATAATATTCTAAATCGAAGTTTTGATTTAATAATTATTAAGAATCTTAAGAATAA
AAATGTTCTTGATTTAATTAATAATAGAGTTTTATTTAGAGCTTTTAAGAATGCTTATTTTATTGATCAAGGTAGT
GGCCTTTCTGTTAGCATTCTTTCTAAGCGCAAAATAAATATTAAAGTTTTAAGTGTAATGCAAGATTCTTGCGATT
TAAAATTAGGATTGCTTGTGGATTTTAAATTTGAGAATAATCACTATGGTATTGTTATTTATAATTTAAGCAAGGA
TTTTATTAAAAGTATTGCCAATTTGCAAATTAGTGAACAAATTTTATATTTAAAAGCCCAAATGGATAAATTGATG
TTTATTTTAGATGAATCTGAATTTGTTATTTTTGATTTATTAATCAAAAATGGATTTTTTAGCTTAATAAATGATT
CAAACTACACTTCAATGTTAGCAAATAAAATTGATTTTAGAGTTTTTTCTAATTTTTTTGCTAGGGTTTCTTTATA
TTCATTTATGTTTGTAATTGCAGATTATTTGCATAGCAATTATGTTGTTGAGAATTTTCCTCAAAAAATAGTTATC
AATTGA

f150.aa

MKTFVIIGLSNLGIHLLEDLSRLDCQIIIIDTSKELIEEYDVISTESFVVEQFTKNALKRIIPVDTDAVVIDFDDD
LGKSALVTHYCNLLGLKEICVKTENRDDAEILKTLGATKIIFPSKDAARRLTPLLVSPNLSTYNIIGYDIIVAETV
IPKEYVGKTLFEADLRRECGITVIAVRNLSNSRYEFVDGDYFFLKDDKIVICGKPDSIENFTNNKDLIKDLISGSK
EDENLNKDAEKKSRFLGIFNFMKIFQKDRKDNZ

t150.aa

CQIIIIDTSKELIEEYDVISTESFVVEQFTKNALKRIIPVDTDAVVIDFDDDLGKSALVTHYCNLLGLKEICVKTE
NRDDAEILKTLGATKIIFPSKDAARRLTPLLVSPNLSTYNIIGYDIIVAETVIPKEYVGKTLFEADLRRECGITVI
AVRNLSNSRYEFVDGDYFFLKDDKIVICGKPDSIENFTNNKDLIKDLISGSKEDENLNKDAEKKSRFLGIFNFMKI
FQKDRKDNZ

f150.nt

TABLE 1. Nucleotide and Amino Acid Sequences

ATGAAAACATTTGTTATTATTGGACTTAGTAATTTAGGCATTCACTTACTTGAAGATTTAAGCAGGCTTGATTGTC
AAATTATTATTATAGATACATCTAAAGAGCTTATTGAAGAATATGATGTGATATCTACAGAAAGCTTTGTTGTTGA
GCAATTCACTAAAAATGCTTTGAAAAGAATAATTCCAGTAGATACAGACGCTGTTGTTATTGATTTTGATGATGAT
CTTGGCAAAAGTGCTCTTGTTACTCACTATTGTAATCTTTTAGGTTTGAAAGAAATATGCGTTAAGACAGAAAATA
GAGATGATGCTGAAATCTTAAAAACTCTTGGGGCAACAAAAATTATATTTCCAAGTAAAGATGCTGCAAGAAGATT
AACTCCATTATTAGTATCTCCAAATCTTTCAACTTATAATATTATTGGGTATGATATTATTGTTGCTGAAACTGTT
ATTCCCAAAGAATATGTTGGTAAAACTCTTTTTGAAGCCGATCTTAGAAGAGAATGTGGGATTACAGTTATTGCTG
TTAGAAATTTAAGTAATTCTAGGTATGAATTTGTTGATGGCGATTATTTTTTTTAAAAGATGATAAAATTGTAAT
TTGTGGTAAACCAGATAGCATTGAAAATTTTACAAATAATAAAGATTTAATTAAAGATTTAATTTCAGGCTCTAAA
GAGGATGAAAATTTAAATAAAGATGCTGAGAAAAAATCTAGATTTTTAGGGATTTTCAATTTTATGAAAATTTTTC
AAAAAGATCGTAAGGATAATTAG

t150.nt

TGTCAAATTATTATTATAGATACATCTAAAGAGCTTATTGAAGAATATGATGTGATATCTACAGAAAGCTTTGTTG
TTGAGCAATTCACTAAAAATGCTTTGAAAAGAATAATTCCAGTAGATACAGACGCTGTTGTTATTGATTTTGATGA
TGATCTTGGCAAAAGTGCTCTTGTTACTCACTATTGTAATCTTTTAGGTTTGAAAGAAATATGCGTTAAGACAGAA
AATAGAGATGATGCTGAAATCTTAAAAACTCTTGGGGCAACAAAAATTATATTTCCAAGTAAAGATGCTGCAAGAA
GATTAACTCCATTATTAGTATCTCCAAATCTTTCAACTTATAATATTATTGGGTATGATATTATTGTTGCTGAAAC
TGTTATTCCCAAAGAATATGTTGGTAAAACTCTTTTTGAAGCCGATCTTAGAAGAGAATGTGGGATTACAGTTATT
GCTGTTAGAAATTTAAGTAATTCTAGGTATGAATTTGTTGATGGCGATTATTTTTTTTAAAAGATGATAAAATTG
TAATTTGTGGTAAACCAGATAGCATTGAAAATTTTACAAATAATAAAGATTTAATTAAAGATTTAATTTCAGGCTC
TAAAGAGGATGAAAATTTAAATAAAGATGCTGAGAAAAAATCTAGATTTTTAGGGATTTTCAATTTTATGAAAATT
TTTCAAAAAGATCGTAAGGATAATTAG

f219.aa

MLIARIMNINTLFYGMIIIIFALISCNHKNIQYDKRIKKFLDKNKIEYKIDSENDFIAFKDINNNEKEEVIIRSRL
NSYKNSKIREIFGIVKVFDINTPKIKEISDSLMSDSYNNRVFGSWEIIHNAERGINSLVYIVKAEEFANDTFLLDA
IDEIASTISIFKKIITTNNENIDNNEENNNTNESNEQPTLKQEKTNSTKESNNELKEDQIEEELQEIKAQZ

t219.aa

CNHKNIQYDKRIKKFLDKNKIEYKIDSENDFIAFKDINNNEKEEVIIRSRLNSYKNSKIREIFGIVKVFDINTPKI
KEISDSLMSDSYNNRVFGSWEIIHNAERGINSLVYIVKAEEFANDTFLLDAIDEIASTISIFKKIITTNNENIDNN
EENNNTNESNEQPTLKQEKTNSTKESNNELKEDQIEEELQEIKAQZ

f219.nt

ATGCTAATTGCAAGAATAATGAATATTAATACATTATTCTACGGCATGATCATTATCATTTTTGCACTCATTTCTT
GCAATCATAAGAATATACAGTACGACAAGAGAATTAAAAAATTTTTAGATAAAAACAAAATTGAATATAAAATAGA
CTCAGAAAATGACTTTATAGCATTTAAAGATATAAACAATAACGAAAAAGAAGAAGTAATCATCAGATCAAGACTA
AACTCATATAAAAATTCAAAGATAAGAGAAATATTTGGAATTGTTAAAGTATTTGATATAAACACACCAAAAATAA
AAGAAATATCTGACTCGCTTATGAGCGATAGTTATAATAACAGAGTATTTGGATCGTGGGAGATTATTCATAATGC
AGAAAGAGGAATCAACTCTTTGGTATATATTGTAAAAGCAGAAGAATTTGCAAATGATACATTTTTGCTTGATGCA
ATTGATGAGATTGCCTCAACAATAAGTATTTTCAAAAAAATAATAACAACCAACAACGAAAACATTGATAATAATG
AAGAAAATAACAATACAAATGAATCAAATGAACAGCCCACCTTAAAGCAAGAAAAAACAAATTCAACAAAAGAATC
TAATAACGAACTTAAAGAAGATCAAATAGAAGAAGAACTTCAAGAAATCAAAGCCCAATAA

t219.nt

TGCAATCATAAGAATATACAGTACGACAAGAGAATTAAAAAATTTTTAGATAAAAACAAAATTGAATATAAAATAG
ACTCAGAAAATGACTTTATAGCATTTAAAGATATAAACAATAACGAAAAAGAAGAAGTAATCATCAGATCAAGACT
AAACTCATATAAAAATTCAAAGATAAGAGAAATATTTGGAATTGTTAAAGTATTTGATATAAACACACCAAAAATA
AAAGAAATATCTGACTCGCTTATGAGCGATAGTTATAATAACAGAGTATTTGGATCGTGGGAGATTATTCATAATG
CAGAAAGAGGAATCAACTCTTTGGTATATATTGTAAAAGCAGAAGAATTTGCAAATGATACATTTTTGCTTGATGC

TABLE 1. Nucleotide and Amino Acid Sequences

AATTGATGAGATTGCCTCAACAATAAGTATTTTCAAAAAAATAATAACAACCAACAACGAAAACATTGATAATAAT
GAAGAAAATAACAATACAAATGAATCAAATGAACAGCCCACCTTAAAGCAAGAAAAAACAAATTCAACAAAAGAAT
CTAATAACGAACTTAAAGAAGATCAAATAGAAGAAGAACTTCAAGAAATCAAAGCCCAATAA

f229.aa

MRVDLLPLVELSLYINLSFCCKDFSIFNRILEELKCHLILLGHPIIKTLYIKHVDFCLSRQDNLKFIFTSLSKYIN
LELLEEFTLEIIPGYVDFEKFKLLDEFCITRINLNVQSFSLEFRKIVGIPEISYKKLNILINNIRKFPFDLNIDMT
VNMPLQKKSHLKRDLQRIAFIYAZ

t229.aa

CKDFSIFNRILEELKCHLILLGHPIIKTLYIKHVDFCLSRQDNLKFIFTSLSKYINLELLEEFTLEIIPGYVDFEK
FKLLDEFCITRINLNVQSFSLEFRKIVGIPEISYKKLNILINNIRKFPFDLNIDMTVNMPLQKKSHLKRDLQRIAF
IYAZ

f229.nt

ATGAGAGTAGATCTTTTACCTCTTGTCGAGTTAAGTCTTTATATTAATTTGTCATTTTGTTGTAAAGATTTTAGCA
TTTTTAATAGAATTTTAGAGGAATTAAAATGTCATTTAATCTTGCTGGGTCATCCAATTATAAAAACACTTTACAT
TAAGCACGTAGATTTTTGTTTATCTAGGCAAGATAATTTAAAATTTATTTTCACTTCTTTGTCCAAGTATATTAAT
TTGGAGTTATTAGAAGAATTTACTTTAGAAATTATTCCGGGTTATGTTGATTTTGAAAAATTCAAACTTTTGGATG
AATTTTGTATTACTAGAATTAATCTTAATGTTCAAAGTTTTTCTTTAGAGTTTAGAAAGATTGTGGGGATACCCGA
AATTTCTTATAAAAAATTGAATATTTTGATTAACAATATTAGAAAGTTTCCTTTTGATTTGAATATTGACATGACT
GTCAATATGCCTTTGCAAAAAAAATCTCATCTCAAGCGAGATTTGCAAAGAATTGCTTTCATATATGCCTGA

t229.nt

TGTAAAGATTTTAGCATTTTTAATAGAATTTTAGAGGAATTAAAATGTCATTTAATCTTGCTGGGTCATCCAATTA
TAAAAACACTTTACATTAAGCACGTAGATTTTTGTTTATCTAGGCAAGATAATTTAAAATTTATTTTCACTTCTTT
GTCCAAGTATATTAATTTGGAGTTATTAGAAGAATTTACTTTAGAAATTATTCCGGGTTATGTTGATTTTGAAAAA
TTCAAACTTTTGGATGAATTTTGTATTACTAGAATTAATCTTAATGTTCAAAGTTTTTCTTTAGAGTTTAGAAAGA
TTGTGGGGATACCCGAAATTTCTTATAAAAAATTGAATATTTTGATTAACAATATTAGAAAGTTTCCTTTTGATTT
GAATATTGACATGACTGTCAATATGCCTTTGCAAAAAAAATCTCATCTCAAGCGAGATTTGCAAAGAATTGCTTTC
ATATATGCCTGA

f22.aa

MLKTLTKIITISCLIVGCASLPYTPPKQNLNYLMELLPGANLYAHVNLIKNRSIYNSLSPKYKSVLGLISNLYFSY
KKENNDFALLIMGNFPKDIFWGIHKNRNTESIGNIFTNPKWKLKNSNIYIIPNKARTSIAITQKDITAKDNNMLTT
KYIGEIEKNEMFFWIQDPTLLLPNQIVSSKNLIPFSSGTLSINSLNQEEYIFKSLIKTNNPPILKILSKKLIPTVL
TNMTNLTISSHIKTTIKDQNTVEIEFNIQKSSVESLIEKLASNIQT

t22.aa

CASLPYTPPKQNLNYLMELLPGANLYAHVNLIKNRSIYNSLSPKYKSVLGLISNLYFSYKKENNDFALLIMGNFPK
DIFWGIHKNRNTESIGNIFTNPKWKLKNSNIYIIPNKARTSIAITQKDITAKDNNMLTTKYIGEIEKNEMFFWIQD
PTLLLPNQIVSSKNLIPFSSGTLSINSLNQEEYIFKSLIKTNNPPILKILSKKLIPTVLTNMTNLTISSHIKTTIK
DQNTVEIEFNIQKSSVESLIEKLASNIQT

f22.nt

ATGTTAAAAACATTAACAAAAATAATTACCATTTCATGCCTCATAGTGGGATGCGCAAGCCTGCCTTACACTCCTC
CAAAACAAAATCTAAATTACTTAATGGAACTTTTACCTGGCGCAAATTTATACGCCCATGTAAATTTAATTAAAAA
CAGGTCTATTTATAACTCTTTAAGCCCTAAATATAAATCAGTTCTTGGGCTTATAAGCAATTTATACTTTAGCTAT
AAAAAAGAAAATAACGATTTTGCTCTACTAATAATGGGTAATTTCCCAAAAGATATTTTCTGGGGAATTCATAAAA

TABLE 1. Nucleotide and Amino Acid Sequences

ATAGAAATACAGAATCAATAGGCAATATATTTACAAATCCAAAATGGAAACTTAAAAATTCAAATATATACATTAT
TCCAAACAAAGCTAGAACTAGCATTGCAATAACCCAAAAAGATATAACCGCAAAAGACAATAATATGCTAACAACA
AAATATATTGGGGAAATAGAAAAAAAATGAAATGTTTTTTTGGATTCAAGATCCAACATTATTGCTCCCAAACCAAA
TAGTAAGCAGCAAAAATTTAATTCCCTTTAGCAGTGGAACTTTGTCTATAAACAGCTTAAATCAAGAAGAATATAT
TTTTAAATCCTTAATCAAAACAAATAATCCACCAATACTAAAAATATTGTCAAAAAAGTTAATTCCAACCGTCTTG
ACAAACATGACAAACCTCACAATATCAAGCCACATAAAGACCACAATAAAAGACCAAAATACGGTTGAAATAGAAT
TTAATATTCAAAAATCTAGTGTTGAAAGCCTTATAGAAAAACTAGCTTCAAATATTCAAACCTAA

t22.nt

TGCGCAAGCCTGCCTTACACTCCTCCAAAACAAAATCTAAATTACTTAATGGAACTTTTACCTGGCGCAAATTTAT
ACGCCCATGTAAATTTAATTAAAAACAGGTCTATTTATAACTCTTTAAGCCCTAAATATAAATCAGTTCTTGGGCT
TATAAGCAATTTATACTTTAGCTATAAAAAAGAAAATAACGATTTTGCTCTACTAATAATGGGTAATTTCCCAAAA
GATATTTTCTGGGGAATTCATAAAAATAGAAATACAGAATCAATAGGCAATATATTTACAAATCCAAAATGGAAAC
TTAAAAATTCAAATATATACATTATTCCAAACAAAGCTAGAACTAGCATTGCAATAACCCAAAAAGATATAACCGC
AAAAGACAATAATATGCTAACAACAAAATATATTGGGGAAATAGAAAAAAAATGAAATGTTTTTTTGGATTCAAGAT
CCAACATTATTGCTCCCAAACCAAATAGTAAGCAGCAAAAATTTAATTCCCTTTAGCAGTGGAACTTTGTCTATAA
ACAGCTTAAATCAAGAAGAATATATTTTTAAATCCTTAATCAAAACAAATAATCCACCAATACTAAAAATATTGTC
AAAAAAGTTAATTCCAACCGTCTTGACAAACATGACAAACCTCACAATATCAAGCCACATAAAGACCACAATAAAA
GACCAAAATACGGTTGAAATAGAATTTAATATTCAAAAATCTAGTGTTGAAAGCCTTATAGAAAAACTAGCTTCAA
ATATTCAAACCTAA

f32.aa

MNTKTLYLISLILLACNKNNKIPLIQKLDLPKSSILGFSNKMGIIIKDYAFLSKSTKKNSELDYDYAILLRKDEVV
KIEKTLEKTERYGIEGNWILVNYKGTKRYIFSKDINIVNNLIIDHSK

t32.aa

CNKNNKIPLIQKLDLPKSSILGFSNKMGIIIKDYAFLSKSTKKNSELDYDYAILLRKDEVVKIEKTLEKTERYGIE
GNWILVNYKGTKRYIFSKDINIVNNLIIDHSK

f32.nt

ATGAATACAAAAACATTATATTTAATATCCTTAATTCTTTTAGCTTGCAATAAAAATAACAAAATTCCTCTCATTC
AAAAATTAGATTTGCCCAAAAGCAGCATTCTTGGCTTTAGCAATAAAATGGGCATAATAATAAAAGATTATGCTTT
TCTTAGTAAAAGCACTAAGAAAAATAGCGAATTGGATTATGATTACGCAATTCTACTCAGAAAAGACGAAGTCGTA
AAAATTGAAAAAACACTAGAAAAAACAGAGCGCTATGGAATTGAAGGAAATTGGATCCTAGTCAATTACAAGGGAA
CTAAAAGATACATCTTTAGCAAAGACATCAATATAGTCAACAATTTAATAATTGATCATTCTAAATAG

t32.nt

TGCAATAAAAATAACAAAATTCCTCTCATTCAAAAATTAGATTTGCCCAAAAGCAGCATTCTTGGCTTTAGCAATA
AAATGGGCATAATAATAAAAGATTATGCTTTTCTTAGTAAAAGCACTAAGAAAAATAGCGAATTGGATTATGATTA
CGCAATTCTACTCAGAAAAGACGAAGTCGTAAAAATTGAAAAAACACTAGAAAAAACAGAGCGCTATGGAATTGAA
GGAAATTGGATCCTAGTCAATTACAAGGGAACTAAAAGATACATCTTTAGCAAAGACATCAATATAGTCAACAATT
TAATAATTGATCATTCTAAATAG

f186.aa

MKKLIIIFTLFLSQACNLSTMHKIDTKEDMKILYSEIAELRKKLNLNHLEIDDTLEKVAKEYAIKLGENRTITHTL
FGTTPMQRIHKYDQSFNLTREILASGIELNRVVNAWLNSPSHKEALINTDTDKIGGYRLKTTDNIDIFVVLFGKRK
YKN

t186.aa

TABLE 1. Nucleotide and Amino Acid Sequences

CNLSTMHKIDTKEDMKILYSEIAELRKKLNLNHLEIDDTLEKVAKEYAIKLGENRTITHTLFGTT
PMQRIHKYDQSFNLTREILASGIELNRVVNAWLNSPSHKEALINTDTDKIGGYRLKTTDNIDIFVVLFGKRKYKN

f186.nt

ATGAAAAAATTGATTATAATTTTTACACTGTTTTTATCTCAAGCATGCAATTTAAGTACAATGCATAAAATAGATA
CAAAAGAAGATATGAAAATTCTATATTCAGAAATTGCTGAATTGAGAAAAAAATTAAATCTAAACCATCTAGAAAT
AGATGATACCCTTGAAAAAGTTGCAAAAGAATATGCCATTAAACTGGGAGAAAATAGAACAATAACTCACACCCTT
TTTGGCACAACCCCAATGCAAAGAATACATAAATACGATCAATCCTTTAATTTAACAAGAGAAATACTGGCATCAG
GAATTGAACTTAACAGAGTAGTTAATGCATGGCTTAATAGTCCAAGCCACAAAGAAGCTCTTATTAATACAGATAC
CGATAAAATAGGTGGCTATAGATTAAAAACGACTGACAATATAGATATATTTGTAGTTCTTTTTGGAAAAAGAAAA
TATAAGAATTGA

t186.nt

TGCAATTTAAGTACAATGCATAAAATAGATACAAAAGAAGATATGAAAATTCTATATTCAGAAATTGCTGAATTGA
GAAAAAAATTAAATCTAAACCATCTAGAAATAGATGATACCCTTGAAAAAGTTGCAAAAGAATATGCCATTAAACT
GGGAGAAAATAGAACAATAACTCACACCCTTTTTGGCACAACCCCAATGCAAAGAATACATAAATACGATCAATCC
TTTAATTTAACAAGAGAAATACTGGCATCAGGAATTGAACTTAACAGAGTAGTTAATGCATGGCTTAATAGTCCAA
GCCACAAAGAAGCTCTTATTAATACAGATACCGATAAAATAGGTGGCTATAGATTAAAAACGACTGACAATATAGA
TATATTTGTAGTTCTTTTTGGAAAAAGAAAATATAAGAATTGA

f216.aa

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FLLSDSRFLYSFLKNGVYYVNLSREFYDSFNNGDYNESNESFDVKVNLFAMSLIKTMRFNYPGKIKKIVILVEGCI
LKEQS

t216.aa
CMVFLNYDNLFSKKVFYFHSSKGFVANLRYLRDEQNLKDNLDLLVKDFLLGSNEGFSFGFLLSDSRFLYSFLKNGV
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f216.nt

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t216.nt

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f328.aa

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IENPAKLFLGLIKACI

TABLE 1. Nucleotide and Amino Acid Sequences

t328.aa

CLGLQLAVIEFARNVCGILDADTEENLARDKPLKSPVIHLLPEQKGIKDKGATMRLGGYPVILKKNTIAFKLYGQD
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LGLIKACI

f328.nt

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t328.nt

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TGA

f352.aa

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EIKKLLNKKIKPKEDENYEKINIENIEEETDDDFEDNYEYNDEIEXTNEDNYPSNEGIINNLKENLNENEKYYAIN
EKKIDELEDRINENENTILDLQRELRNFKKKDNSDKNLEEIEENLSSIGRIINDLKRKISANEAINKENQKKIRTD
KHKLKELEDKIKENEETILKLQKELNNFKKKEIYQKPLNEETFTPSITSKNDDLEENKKLKKEYLKPIEKKESRDL
EENTKSTPKTTMIKTADFQIYPDIYLNNYKFKEKGDQFAFKKENTYYIEIDPTNNLNEALKNHEIISKYKFEKYFI
NPILKNKEEFFRNLIEVKNIHELGIMYKNLKPEFKQIKIIK

t352.aa

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NYEKINIENIEEETDDDFEDNYEYNDEIEXTNEDNYPSNEGIINNLKENLNENEKYYAINEKKIDELEDRINENEN
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TILKLQKELNNFKKKEIYQKPLNEETFTPSITSKNDDLEENKKLKKEYLKPIEKKESRDLEENTKSTPKTTMIKTA
DFQIYPDIYLNNYKFKEKGDQFAFKKENTYYIEIDPTNNLNEALKNHEIISKYKFEKYFINPILKNKEEFFRNLIE
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f352.nt

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TABLE 1. Nucleotide and Amino Acid Sequences

TTGAAGAAGAAACTGATGATGATTTTGAAGACAATTATGAATATAATGATGAAATTGAAGAACAAATGAGGACAAT
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t352.nt

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A

f867.aa

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NNGDIGSVTVGGSVSPAGGNFEEPVTQATLKVVGAFHGLTRERSDARKFPAISPLESWSKYKGVIDQKKTEYARSF
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QARDFINELRQNLLDMNLSSFKDHKFNKLEHALGELINFKKVI

t867.aa

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AACGERAGEVVETLKEFPELMDPKTGKSLMDRTCIICNTSSMPVAAREASVYTAITIGEYYRQMGLDILLLADSTS
RWAQAMREMSGRLEEIPGEEAFPAYLESVIASFYERAGIVVLNNGDIGSVTVGGSVSPAGGNFEEPVTQATLKVVG
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TABLE 1. Nucleotide and Amino Acid Sequences

SCYLQQNSFDSIDAAVSSERQNYMFDIVYNILKTNFEFSDKLQARDFINELRQNLLDMNLSSFKDHKFNKLEHALG
ELINFKKVI

f867.nt

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TABLE 1. Nucleotide and Amino Acid Sequences

f868.aa

MKRVYSKIESIAGNVITVTAQGIKYGELAIVKAKDTSSLAEVIKLDREKVSLQVYGGTRGVSTSDEIKFLGHSMQV
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t868.aa

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ISITMEQVPSNRGYPGDLYSQLAYRYEKAIDFEGAGSITILAVTTMPGDDVTHPVPDNTGYITEGQYYLKGGRIEP
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AGAGACTTATTGA

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TABLE 1. Nucleotide and Amino Acid Sequences

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f872.aa

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t872.aa

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f872.nt

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TGCATATTCTAATGGCAATTATAAATTTAGAGCAATAGATACTTGGAAATTAGTAGTAGATCTTGCGCCAAGGTTT
TCTCCTTATATTGCTAAATCAAGAAGTCAAATTAAAAATTCTGTATATTTAAAAAAAAAATTAA

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AGTAATAAAAATTTTCCGTATTGGATTTTACTTGAAAAAGGCAGGCAATTTCTTTATTCTAAATCTGAATTTAGTA
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TAA

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VVITAGLNQKPGETRLDLVDKNSKIFKDIITNVVSSGFDGIFVVASNPVDIMTYVTMKYSKFPIHKVIGTGTILDT
SRLRYFLSDHFNVNTQNIHSYIMGEHXDSSFATWDETKIAMKPLSEYLAEGKITELELDEIHKKVVNAAYEVIKLK

TABLE 1. Nucleotide and Amino Acid Sequences

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t874.aa

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IMGEHXDSSFATWDETKIAMKPLSEYLAEGKITELELDEIHKKVVNAAYEVIKLKGATYYAIGLGIKNIVNAIIGD
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f886.aa

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t886.aa

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IKVNDFQYNESDMIIFQNTKEKDKDQYTNTKIEYEYNKDNQLKSKKIYENDIIYLKTEYHNDNEYEEEIYYNKKPA
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TABLE 1. Nucleotide and Amino Acid Sequences

f886.nt

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ATCCAAAGAAAAAAACCAATATTTAGATGAAGAAAAAATAGTAAATACCTTTGAAGAAGAGAATACAAAAATCATA
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TGAATACGAATATAACAAAGACAATCAATTAAAAAGCAAAAAAATTTATGAGAACGATATAATTTATCTAAAAACT
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CTTAGGGTAAAACACAAGAACGGAAAAGTCACCGAAGAAAAACCAATAGGAACAAATTAA

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NQDIIKTELEISKLKKEMDKKKLQNIITAKEKHNTKTKIDELKKNIQNINNKQKKFAEYFNNLKKLKVKYKKIEEQ
TNISNLNKEFFIREELFFINYIDLKKIENYYLLEISNITPEKIETKKAVFKTSSSVNEIADHITKYSLKEILGREF
LKININVKNNSDAKIYINEKFVSKGIYHDNIFDISKLPNKEIEIQITSANFENYSIKRTVKNADSIILDIDLKRTI
SKKVSIKSNVQSKVFKKGIFMGETPIEIEKPENQDIILLKSKGYKDKFKLINKEEDQVEIEMIKTNKNRLIDTRDK
FYVNLAVFTLSTIGAIFAGTLLNNSEVLYKITGNHFINKRLTAEDVYMAKAEQMTATFLFGVGITLTIGSFISLIT
HLVEYIKEANMGE

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QNIITAKEKHNTKTKIDELKKNIQNINNKQKKFAEYFNNLKKLKVKYKKIEEQTNISNLNKEFFIREELFFINYID
LKKIENYYLLEISNITPEKIETKKAVFKTSSSVNEIADHITKYSLKEILGREFLKININVKNNSDAKIYINEKFVS
KGIYHDNIFDISKLPNKEIEIQITSANFENYSIKRTVKNADSIILDIDLKRTISKKVSIKSNVQSKVFKKGIFMGE
TPIEIEKPENQDIILLKSKGYKDKFKLINKEEDQVEIEMIKTNKNRLIDTRDKFYVNLAVFTLSTIGAIFAGTLLN
NSEVLYKITGNHFINKRLTAEDVYMAKAEQMTATFLFGVGITLTIGSFISLITHLVEYIKEANMGE

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TABLE 1. Nucleotide and Amino Acid Sequences

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TTGAATACAATTTTTCCTATATCATTAATACAAAAAAAGAAAATATTGACCTAAAAAAGGGTATTGAAAAACAATT
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CATTTAGTAGAATATATTAAAGAAGCAAATATGGGAGAATAG

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AGTAATATTGAATACAATTTTTCCTATATCATTAATACAAAAAAAGAAAATATTGACCTAAAAAAGGGTATTGAAA
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AATAACTCATTTAGTAGAATATATTAAAGAAGCAAATATGGGAGAATAG

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INKLNNLDLRKSIFLKKLSNLFNIEHKKLLYVENRFKSINFKNLKKELNINADIHSLDYKTKINFISSIIFLIIII
LLIFLDPTNSIFTLIFLLISSLAFMISKEIMYFYPFTVLSYLLFLIISNFNKNYNKIYLKEINFLTLMTKIKHLLF
LFTFTALYFITITTFFTTNIDPTFIAFVAIPTLCIFLIFSWIKTESNFKDTFLFPIEIKEKKIEGKKALKSKIAIH
LLLFTLSLIPFAYSSYMLNSYENINYLYSKKLNYFDYLNPNNIYIMLGYNKDMPNIIGYLSHILYQNELKYNITAK
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FSLPFFVLLFLFKAIRFTILLNIN
EKTYKKYIQG

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NLFNIEHKKLLYVENRFKSINFKNLKKELNINADIHSLDYKTKINFISSIIFLIIIILLIFLDPTNSIFTLIFLLI

TABLE 1. Nucleotide and Amino Acid Sequences

SSLAFMISKEIMYFYPFTVLSYLLFLIISNFNKNYNKIYLKEINFLTLMTKIKHLLFLFTFTALYFITITTFFTTN
IDPTFIAFVAIPTLCIFLIFSWIKTESNFKDTFLFPIEIKEKKIEGKKALKSKIAIHLLLFTLSLIPFAYSSYMLN
SYENINYLYSKKLNYFDYLNPNNIYIMLGYNKDMPNIIGYLSHILYQNELKYNITAKYGKIPKDIKENYFEIKNDK
IEIHPKTVYEVDKSFIDEILKKDLASLFLKNKNPILIYKENKNNINTDKKNYKILFFFSLPFFVLLFLFKAIRFTI
LLNINEKTYKKYIQG

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MIRALLTNDLFLSCLVSGISAQVIKYGIQTVKTRKLKLTPVHLLKKIFLETGGMPSSHSSTVTALSTSIALTEGID
TNFIIALAFALITIRDSFGVRYMSGVQAEYLNALSEKLKKEIKIDTTKIKVVKGHKKKEVLTGIIIGIVSAYIVCY
F

TABLE 1. Nucleotide and Amino Acid Sequences

t895.aa

AQVIKYGIQTVKTRKLKLTPVHLLKKIFLETGGMPSSHSSTVTALSTSIALTEGIDTNFIIALAFALITIRDSFGV
RYMSGVQAEYLNALSEKLKKEIKIDTTKIKVVKGHKKKEVLTGIIIGIVSAYIVCYF

f895.nt

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TTTTAG

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AACTGAAGGAATAGATACAAATTTTATAATAGCTCTTGCATTTGCCCTTATTACAATAAGAGATTCTTTCGGCGTA
AGATATATGTCTGGAGTTCAAGCAGAATATTTAAATGCATTATCAGAAAAATTAAAAAAAGAAATAAAAATTGACA
CAACAAAAATAAAAGTGGTCAAGGGGCACAAAAAGAAAGAGGTTCTAACGGGCATAATAATAGGAATAGTCTCTGC
GTATATTGTGTGCTATTTTTAG

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MYIGAAGKSFSIIIDSAFLSNCFLFIGSFSRSDSLMSLSNSRFEYPYDASCEFSLVNIVKYVCGSKYSPMRPTLII
SKLPVFLLLVRTGQFSLVSIRLIFRIFFHWFZ

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CFLFIGSFSRSDSLMSLSNSRFEYPYDASCEFSLVNIVKYVCGSKYSPMRPTLIISKLPVFLLLVRTGQFSLVSIR
LIFRIFFHWFZ

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t605.nt

TGTTTTCTTTTTATAGGATCTTTTTCAAGATCTGATTCTCTGATGAGTTTGTCAAATTCTAGGTTTGAATATCCGT
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AACTCTTATTATTTCAAAATTGCCAGTATTTCTGCTGTTGGTAAGAACAGGCCAATTTTCGTTGGTAAGCATAAGA
TTGATATTTAGAATTTTTTTCCATTGGTTTTGA

f606.aa

MKLQRSLFLIIFFLTFLCCNNKERKEGVSFKISLGAEPSSLDPQLAEDNVASKMIDTMFRGIVTGDPNTGGNKPGL
AKGWDISSDGTVYTFNLREKITWSDGVAITAEGIRKSYLRILNKETGSKYVEMVKSVIKNGQKYFDGQVTDSELGI
RAIDEKTLEITLESPKPYFIDMLVHQSFIPVPVHVTEKYGQNWTSPENMVTSGPFKLKERIPNEKYVFEKNNKYYD
SNEVELEEITFYTTNDSSTAYKMYENEELDAIFGSIPPDLIKNLKLRSDYYSSAVNAIYFYAFNTHIKPLDNVKIR
KALTLAIDRETLTYKVLDNGTTPTRRATPNFSSYSYAKSLELFNPEIAKTLLAEAGYPNGNGFPILKLKYNTNEAN

TABLE 1. Nucleotide and Amino Acid Sequences

KKICEFIQNQWKKNLNIDVELENEEWTTYLNTKANGNYEIARAGWIGDYADPLTFLSIFTQGYTQFSSHNYSNPEY
NELIKKSDLELDPIKRQDILRQAEEIIIEKDFPIAPIYIYGNSYLFRNDKWTGWNTNILERFDLSQLKLKNKZ

t606.aa

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STAYKMYENEELDAIFGSIPPDLIKNLKLRSDYYSSAVNAIYFYAFNTHIKPLDNVKIRKALTLAIDRETLTYKVL
DNGTTPTRRATPNFSSYSYAKSLELFNPEIAKTLLAEAGYPNGNGFPILKLKYNTNEANKKICEFIQNQWKKNLNI
DVELENEEWTTYLNTKANGNYEIARAGWIGDYADPLTFLSIFTQGYTQFSSHNYSNPEYNELIKKSDLELDPIKRQ
DILRQAEEIIIEKDFPIAPIYIYGNSYLFRNDKWTGWNTNILERFDLSQLKLKNKZ

f606.nt

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ATCAAAAATGATTGACACAATGTTTAGAGGGATTGTTACAGGAGATCCTAATACAGGGGGAAATAAACCGGGACTT
GCAAAAGGGTGGGATATTTCTTCTGATGGAACAGTTTACACATTTAACCTAAGAGAAAAAATCACTTGGAGTGACG
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t606.nt

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TABLE 1. Nucleotide and Amino Acid Sequences

TCATAATTACTCAAACCCAGAATACAACGAACTTATAAAGAAATCCGACCTTGAGCTTGATCCAATAAAAAGACAA
GACATTTTAAGACAAGCAGAAGAGATAATTATTGAAAAAGATTTTCCAATAGCACCAATATACATATATGGGAACA
GTTACCTTTTCAGAAATGACAAATGGACAGGGTGGAACACCAATATTTTAGAAAGATTTGATTTATCTCAGCTAAA
ATTAAAAAATAAATAA

f679.aa

MFNRSSCVLQNFLFLFLFLSLVSCFAKKEISGNNFIKAHSKEFDLNNLNWLWNFDYTKKNFDKHFNIDPSSYIYVA
YLFKKIGFEEKFVEYMKKAIANGDSIASQFAGIKLIEYFNSAKEYFASELIGEKLYKKYENNKFIILGYFKSLYWQ
KKNDKALSLLNKLDKMKFSDYQENENILLKAVLYLNLSNVSESKIYFNELFENLPANYLHVRAYDYFIIENKSRYF
GANFLNLVRFKYEVANGNFNGAINILNKNGLNDYYDNNIVLSDVYKAFISSGKVSNALTFFSKIKSKYKNYYLGIL
NLREKNNLGLLLLKEYLEGLDLNNEINRLDLLNTAFSNLIFTKSARDYFAESLPKFYTEGDKKNSTFIKILEEYIL
ESIQLEDYGNLYKLYSNAQKVISNSVLSKLAFINARLIYHKLIKPNVSGEYKSLLHSAVNYDKWSYSSFMSRYLLD
QNIDEFFTGGSDIKYEQSDYEIFLEGFLKFNLCNYVRGFISEDFRNGYKFSLDFYRKVYDELLKSENYYDATLVIN
YLVNQDESALMENDYKRLYPYLYGSLIEYWAKRRGLEASVVFSLIKAESSFEKNAVSKPGAVGLMQVMPSTANDIS
KELKYFNYDLKIPKDNIIIGTYYLKKRISTTGSLYKALASYNGGIGNVRKWEKSYGHLSKELFIEAIPFSQTRNYI
KKILVYSVFYDALYEKKGIDSVIVKIMGEFPKNZ

t679.aa

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NENILLKAVLYLNLSNVSESKIYFNELFENLPANYLHVRAYDYFIIENKSRYFGANFLNLVRFKYEVANGNFNGAI
NILNKNGLNDYYDNNIVLSDVYKAFISSGKVSNALTFFSKIKSKYKNYYLGILNLREKNNLGLLLLKEYLEGLDLN
NEINRLDLLNTAFSNLIFTKSARDYFAESLPKFYTEGDKKNSTFIKILEEYILESIQLEDYGNLYKLYSNAQKVIS
NSVLSKLAFINARLIYHKLIKPNVSGEYKSLLHSAVNYDKWSYSSFMSRYLLDQNIDEFFTGGSDIKYEQSDYEIF
LEGFLKFNLCNYVRGFISEDFRNGYKFSLDFYRKVYDELLKSENYYDATLVINYLVNQDESALMENDYKRLYPYLY
GSLIEYWAKRRGLEASVVFSLIKAESSFEKNAVSKPGAVGLMQVMPSTANDISKELKYFNYDLKIPKDNIIIGTYY
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VKIMGEFPKNZ

f679.nt

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TATCTTGTAAATCAAGATGAATCTGCTTTAATGGAGAATGACTATAAAAGACTTTATCCTTATTTGTATGGATCTT
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TABLE 1. Nucleotide and Amino Acid Sequences

TGAAAAAAATGCTGTCTCAAAACCGGGTGCTGTTGGCCTTATGCAGGTTATGCCATCAACAGCAAATGATATTTCT
AAAGAACTTAAGTATTTTAACTATGATTTAAAGATTCCAAAAGATAATATAATAATTGGAACATATTATTTAAAAA
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TTATGGGCGAATTCCCCAAAAATTAA

t679.nt

TGCTTTGCAAAAAAAGAAATCTCAGGCAATAATTTTATTAAGGCGCATTCAAAAGAGTTTGATTTAAATAATTTAA
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TTATATTAAAAAAATATTAGTTTATTCGGTATTTTATGATGCTTTGTATGAAAAGAAGGGAATAGATTCAGTAATA
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f11-12.nt

TAAAAGGAGA ATATTTTTAT GAGAAAAAGT TTGTTTTTAT ATGCATTATT AATGGGAGGA
TTGATGTCTT GTAATCTAGA TTCCAAATTA TCTAGTAACA AAGAACAAAA AAATAACAAT
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AATGAAGAAA AGGAAGCTGA TGCAGCAATT AAATATTTAG AAGAAAATAT TCTTAAAAAC
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AGCTCTGCGG CTTTCTTTTT TGACAACGCT CAGAAAAGGT TAAAAGAAAG CATTATTAAA
AGATTAGAGA GTAAAAATAA TAGATCTTAT GCATTAAAAT TGTCTAGACA GGCTTTAAGT
GACGCAAGAA GTGCTTTAAG TAATTTAGAA TCTTTTGCCT CTAAAAGAAT TGAACCAATG
GTGAGAAAGG AAGAAATAAA AGAGCTTATT AAACATGCAA AAACTGTTTT AGAAAGTCTC
AATAAAAAAT AA

TABLE 1. Nucleotide and Amino Acid Sequences

t11-12.nt

TTGTAATCTAGATTCCAAATTATCTAGTAACAAAGAACAAAAAAATAACAATAATGTAAAAGAAGTTTCGGATAGT
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AAATATTTCAATTGCGCATACTGAAAAAAAAGAGACAAAAAAGGAGAATTTAATCCCTTCTACTAATGAAGAAAAG
GAAGCTGATGCAGCAATTAAATATTTAGAAGAAAATATTCTTAAAAACTCTAAATTTTCTGAATTAATTAGAGAAG
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AACATCATTAATGGAGAATCCTAAGAACAATAGAGATAAGATAAATAAATTAACACAATTGTTGCAAAATAATTTA
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AAAAA

f11-12.aa

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PKNNRDKINK LTQLLQNNLK IDSELEQLIN MIDMAENEIS SAAFFFDNAQ KRLKESIIKR
LESKNNRSYA LKLSRQALSD ARSALSNLES FASKRIEPMV RKEEIKELIK HAKTVLESLN
KK

t11-12.aa

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NISIAHTEKKETKKENLIPSTNEEKEADAAIKYLEENILKNSKFSELIREVRVIKDEYALIKADLYDVIGKINNKK
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LKLSRQALSDARSALSNLESFASKRIEPMVRKEEIKELIKHAKTVLESLNKK

f11-4.nt

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ATCACAAAAT TAACTCCGGA AGAGCTAGAA AATTTAGCAA AGGAAGCTCA AGATGACTCT
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GCTGAAAATT CGGTAAGCGT TTCTTTTAAA GAACATTCAA ACAGTAAAAT TGAAACTAAA
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t11-4.nt

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TGAAATTACTGGATGAGTTGCTAAAAATATCGGTAAGTAGCAATGGTGATAAAAGTACCCAAAAATACAATGAACT
TAAAACCGTTGTAAATAAGTTTAATGCTGAAAATTCGGTAAGCGTTTCTTTTAAAGAACATTCAAACAGTAAAATT

TABLE 1. Nucleotide and Amino Acid Sequences

GAAACTAAAAAATGTATTCAAACTCTTATGAAAAATGTAGAAACATACTTTGAAGGTGTATGCAGCGAACTTAAAA
ACAAAAATGATGGTGAGTACGAAAAA

f11-4.aa

RSLQMSKLIL AISILLIISC KWYVDNTIDE ATVESKSALT SIDQVLDEIS EATGLSSEKI
TKLTPEELEN LAKEAQDDSE KSKKEIEDQK NTKESKNIEV KDTPRLIKLI KNSSEKIDSV
FQTLINIGYN ATYAAKSNLK NGLKMVKLLD ELLKISVSSN GDKSTQKYNE LKTVVNKFNA
ENSVSVSFKE HSNSKIETKK CIQTLMKNVE TYFEGVCSEL KNKNDGEYEK TLTTLS

t11-4.aa

CKWYVDNTIDEATVESKSALTSIDQVLDEISEATGLSSEKITKLTPEELENLAKEAQDDSEKSKKEIEDQKNTKES
KNIEVKDTPRLIKLIKNSSEKIDSVFQTLINIGYNATYAAKSNLKNGLKMVKLLDELLKISVSSNGDKSTQKYNEL
KTVVNKFNAENSVSVSFKEHSNSKIETKKCIQTLMKNVETYFEGVCSELKNKNDGEYEK

f112-1.nt

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ATGTTAATTT CAATAAGTTT ATTATCATGT GATGTTAGTA GATTAAATCA GAGAAATATT
AATGAGCTTA AAATTTTTGT TGAAAAGGCC AAGTATTATT CTATAAAATT AGACGCTATT
TATAACGAAT GTACAGGAGC ATATAATGAT ATTATGACTT ATTCGGAAGG TACATTTTCT
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t112-1.nt

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f112-1.aa

ISKDFSRGEN MKKSFLSIYM LISISLLSCD VSRLNQRNIN ELKIFVEKAK YYSIKLDAIY
NECTGAYNDI MTYSEGTFSD QSKVNQAISI FKKDNKIVNK FKELEKIIEE YKPMFLSKLI
DDFAGSV

t112-1.aa

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f14-8.nt

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TCTGATAAAG AGAAATCAAA ATCCAACATG GAAGCAAGCT CTAAAGAAGA AGATCCAAAT
AAAAAAATAA AAAATACACT GCTTAATGAT TTAATAAATT TGATAGAAAT AGCTAATGAG
CATAAAGAAA AATATGAAAA AAGAATGCAA GAAGAACCTT CAGATCAATA CGGAATATTG
GCTTTCCAGG AATTAGACTT GTCCGTTGGA AAAATATCTG AAGACACCCC GCAATCTAAA
AAATTTAGAA AAAACACCTA TTCTCCCTTA AGCGCTATTG ATGTCAATAA ATTAAAAGAT
CTTTCAGAGA TTATAAGAAA TTCGGGCCAA ATACAAGGTT TATTTAATAT TTTCAACAGA
TTCGGAGGCA TTTTTGACGA CTCACTTAAT CACGTATATT CTAAAAAAGA TATCCTAGGG
GGACTAGAAA TTTTGGATTT AGATAAACTA AAAAATTCGT TTGAAAAATT ACTATCTATA

TABLE 1. Nucleotide and Amino Acid Sequences

AAAGAAACTT TCTCAAAAAT GCTAAATCAA CTTTTATTAG ATTATAAAAA TGATAAAGAT
CATATACGAA CAGAGACAAA TAAACTTAAA TCTCATACAA CTGCACTTTT CGAACAACTT
GATAAAAAAG AAGACGAAGC ATATGAACCT AAAAATCAGA TATTTTCAAT AAGTAACCTT
TAA

t14-8.nt

TTGCAATTCAGATTTTAGCACTAATCAAGAAGATATTAAATATCCATCTGATAAAGAGAAATCAAAATCCAACATG
GAAGCAAGCTCTAAAGAAGAAGATCCAAATAAAAAAATAAAAAATACACTGCTTAATGATTTAATAAATTTGATAG
AAATAGCTAATGAGCATAAAGAAAAATATGAAAAAAGAATGCAAGAAGAACCTTCAGATCAATACGGAATATTGGC
TTTCCAGGAATTAGACTTGTCCGTTGGAAAAATATCTGAAGACACCCCGCAATCTAAAAAATTTAGAAAAAACACC
TATTCTCCCTTAAGCGCTATTGATGTCAATAAATTAAAAGATCTTTCAGAGATTATAAGAAATTCGGGCCAAATAC
AAGGTTTATTTAATATTTTCAACAGATTCGGAGGCATTTTTGACGACTCACTTAATCACGTATATTCTAAAAAAGA
TATCCTAGGGGGACTAGAAATTTTGGATTTAGATAAACTAAAAAATTCGTTTGAAAAATTACTATCTATAAAAGAA
ACTTTCTCAAAAATGCTAAATCAACTTTTATTAGATTATAAAAATGATAAAGATCATATACGAACAGAGACAAATA
AACTTAAATCTCATACAACTGCACTTTTCGAACAACTTGATAAAAAAGAAGACGAAGCATATGAACCTAAAAATCA
G

f14-8.aa

IQSHSRRVFM KYYICVCVFL LLNACNSDFS TNQEDIKYPS DKEKSKSNME ASSKEEDPNK
KIKNTLLNDL INLIEIANEH KEKYEKRMQE EPSDQYGILA FQELDLSVGK ISEDTPQSKK
FRKNTYSPLS AIDVNKLKDL SEIIRNSGQI QGLFNIFNRF GGIFDDSLNH VYSKKDILGG
LEILDLDKLK NSFEKLLSIK ETFSKMLNQL LLDYKNDKDH IRTETNKLKS HTTALFEQLD
KKEDEAYEPK NQIFSISNL

t14-8.aa

CNSDFSTNQEDIKYPSDKEKSKSNMEASSKEEDPNKKIKNTLLNDLINLIEIANEHKEKYEKRMQEEPSDQYGILA
FQELDLSVGKISEDTPQSKKFRKNTYSPLSAIDVNKLKDLSEIIRNSGQIQGLFNIFNRFGGIFDDSLNHVYSKKD
ILGGLEILDLDKLKNSFEKLLSIKETFSKMLNQLLLDYKNDKDHIRTETNKLKSHTTALFEQLDKKEDEAYEPKNQ

f17-6.nt

TAAAGGAGGG TATTTATGAA ATACCACATA ATTACAACTA TATTTGTTTT TCTGTTTTTA
GCTTGCAGGC CGGATTTTAA TATCGATCAA AAAGACATTA AATACCCGCC TACTGAAAAA
TCAAGGCCCA AAACTGAAAG CTCTAAGCAA AAAGAATCAA AGCCTAAAAC AGAAGAAGAG
CTTAAGAAAA AACAACAAGA AGAAGAGCTT AAGAAAAAAC AACAAGAAGA AGAGCTTAAG
AAAAAACAAC AAGAAGAAGA GCTTAAGAAA AAACAACAAG AAGAAGAGAA GGAAGAACTA
AGAAAAACAAC AACTAAAAAA TACGCTATCT AATGATTTAA AAAAGCAAAT AGAATCGGCC
TACAATTTTA AAGAAAAATA TGTAAAAAGT ATGGAAAAAG AACCTGAAGA CCATTACGGG
ATGACGTCTT TTAGGGGATT GAATTGGGGG CCAGGGACTG AAGATATATC TGACAATACC
GAAAGATCTA TAAGATATAG AAGACACACT TATACTGTTT TAAGCCCCCT GGATCCTCAT
GAATTAAAGG AATTCGCAAA TATTATTCAA GATATAAATA AACTAGCATC AGTAGCAAGT
ATATTTAATT CTTTTAGCGC TATTGGAGGA GCTCTTGACA TAGTAAGTGA TCACCTATAT
TTCAAAAAAG ACAATCTAGA CAAACTAGAT ATTGCAGATT TAGAAATACT TAAAAATTCA
TTTGAACAAA TATTATATAT AAAAGGAAGT GTTGCAGGAA AAGCAAAAAA ACTTTTATTA
GATTATAAAA ATCTAAAAAC AGATATTAAT AAGCTTAAAT CTTATTCAAA TGAACTGGTT
AATGGAATTA AGCAACAAGC TCTAGAAGCA GAAAATCTAG AAGAGCTTAT AGTGTCAAAA
TATAAACTTT AA

t17-6.nt

TTGCAGGCCGGATTTTAATATCGATCAAAAAGACATTAAATACCCGCCTACTGAAAAATCAAGGCCCAAAACTGAA
AGCTCTAAGCAAAAAGAATCAAAGCCTAAAACAGAAGAAGAGCTTAAGAAAAAACAACAAGAAGAAGAGCTTAAGA

TABLE 1. Nucleotide and Amino Acid Sequences

AAAAACAACAAGAAGAAGAGCTTAAGAAAAAACAACAAGAAGAAGAGCTTAAGAAAAAACAACAAGAAGAAGAGAA
GGAAGAACTAAGAAAACAACAACTAAAAAATACGCTATCTAATGATTTAAAAAAGCAAATAGAATCGGCCTACAAT
TTTAAAGAAAAATATGTAAAAAGTATGGAAAAAGAACCTGAAGACCATTACGGGATGACGTCTTTTAGGGGATTGA
ATTGGGGGCCAGGGACTGAAGATATATCTGACAATACCGAAAGATCTATAAGATATAGAAGACACACTTATACTGT
TTTAAGCCCCCTGGATCCTCATGAATTAAAGGAATTCGCAAATATTATTCAAGATATAAATAAACTAGCATCAGTA
GCAAGTATATTTAATTCTTTTAGCGCTATTGGAGGAGCTCTTGACATAGTAAGTGATCACCTATATTTCAAAAAAG
ACAATCTAGACAAACTAGATATTGCAGATTTAGAAATACTTAAAAATTCATTTGAACAAATATTATATATAAAAGG
AAGTGTTGCAGGAAAAGCAAAAAAACTTTTATTAGATTATAAAAATCTAAAAACAGATATTAATAAGCTTAAATCT
TATTCAAATGAACTGGTTAATGGAATTAAGCAACAAGCTCTAGAAGCAGAAAATCTAGAAGAGCTTATAGTGTCAA
AATATAAACTT

f17-6.aa

RRVFMKYHII TTIFVFLFLA CRPDFNIDQK DIKYPPTEKS RPKTESSKQK ESKPKTEEEL
KKKQQEEELK KKQQEEELKK KQQEEELKKK QQEEEKEELR KQQLKNTLSN DLKKQIESAY
NFKEKYVKSM EKEPEDHYGM TSFRGLNWGP GTEDISDNTE RSIRYRRHTY TVLSPLDPHE
LKEFANIIQD INKLASVASI FNSFSAIGGA LDIVSDHLYF KKDNLDKLDI ADLEILKNSF
EQILYIKGSV AGKAKKLLLD YKNLKTDINK LKSYSNELVN GIKQQALEAE NLEELIVSKY
KL

t17-6.aa

CRPDFNIDQKDIKYPPTEKSRPKTESSKQKESKPKTEEELKKKQQEEELKKKQQEEELKKKQQEEELKKKQQEEEK
EELRKQQLKNTLSNDLKKQIESAYNFKEKYVKSMEKEPEDHYGMTSFRGLNWGPGTEDISDNTERSIRYRRHTYTV
LSPLDPHELKEFANIIQDINKLASVASIFNSFSAIGGALDIVSDHLYFKKDNLDKLDIADLEILKNSFEQILYIKG
SVAGKAKKLLLDYKNLKTDINKLKSYSNELVNGIKQQALEAENLEELIVSKYKL

f19-2.nt

TAAAGAAAGA TTAAATCATA TTCAAGGAGA GTATTTATGA AACACTATAT AATTGTGCAT
ATATTTGTTT TTCTATTTTT AAATGCTTGT TATCCAGTTG CATCTAATAA AATAGAATTA
AAACCTAAAA CAGAAACAAG CTTAAATCAA GAAGAAGTCC CAAATCAAGA AGCAAACTAC
AAAGAAGAAA AAGAAGCAAA AGAAGAAGGC ATTAATAAAA AAACAGAAAA CACGCTGCTT
AATGATTTAA GAAATTTAAT AGAAACAGCT AAAAAAGATA ATGATAAATA TACACAAAAG
TTAAAAGAAG AATCCTCAAG CCAATACGGA ATACTGGCTT TCAAAGATTT GTTCTGGCTA
GATGGAACAA ATGAACAATT GTCCGCAAAT ACCGAAAGAT CTAAAGCCTA TAGAAAACGA
GCTTATAGCA TCTTAAATAC TATTAATGAC GCTTCCTTAA AGAATTTTTC AGAAATTGTA
ATGGCATCAG GACAAACACA GGGCATATTT AATACCCTTA ACTCACTTGG GGGTAATTTT
GAAAAGATAG TTAATTGTTT GTATCCCAAA AAAGACAATT TGGAAAAATT AGAGACTTCA
GTTTTAAAAA AGCTTAAAGA TTCTTTGGAA AATTTTTTAG AGATAAAAAA AATCGCCTCA
GAAATGATGC ACAAGCTCTT ATTAGACTAT CAAAATAATA CAAATCGTAT ACAAACAGAT
AAAAATGAAC TTAAGTCTTA TGCAGACACA CTTTTCAATC AAATGACAAA AAAACCCGAA
GAAGCACTAA AGCTAAAAAA TACCATATGC TCAATAGAGG ACCTTTAA

t19-2.nt

TTGTTATCCAGTTGCATCTAATAAAATAGAATTAAAACCTAAAACAGAAACAAGCTTAAATCAAGAAGAAGTCCCA
AATCAAGAAGCAAACTACAAAGAAGAAAAAGAAGCAAAAGAAGAAGGCATTAATAAAAAAACAGAAAACACGCTGC
TTAATGATTTAAGAAATTTAATAGAAACAGCTAAAAAAGATAATGATAAATATACACAAAAGTTAAAAGAAGAATC
CTCAAGCCAATACGGAATACTGGCTTTCAAAGATTTGTTCTGGCTAGATGGAACAAATGAACAATTGTCCGCAAAT
ACCGAAAGATCTAAAGCCTATAGAAAACGAGCTTATAGCATCTTAAATACTATTAATGACGCTTCCTTAAAGAATT
TTTCAGAAATTGTAATGGCATCAGGACAAACACAGGGCATATTTAATACCCTTAACTCACTTGGGGGTAATTTTGA
AAAGATAGTTAATTGTTTGTATCCCAAAAAAGACAATTTGGAAAAATTAGAGACTTCAGTTTTAAAAAAGCTTAAA
GATTCTTTGGAAAATTTTTTAGAGATAAAAAAAATCGCCTCAGAAATGATGCACAAGCTCTTATTAGACTATCAAA
ATAATACAAATCGTATACAAACAGATAAAAATGAACTTAAGTCTTATGCAGACACACTTTTCAATCAAATGACAAA
AAAACCCGAAGAAGCACTAAAG

TABLE 1. Nucleotide and Amino Acid Sequences

f19-2.aa

RKIKSYSRRV FMKHYIIVHI FVFLFLNACY PVASNKIELK PKTETSLNQE EVPNQEANYK
EEKEAKEEGI NKKTENTLLN DLRNLIETAK KDNDKYTQKL KEESSSQYGI LAFKDLFWLD
GTNEQLSANT ERSKAYRKRA YSILNTINDA SLKNFSEIVM ASGQTQGIFN TLNSLGGNFE
KIVNCLYPKK DNLEKLETSV LKKLKDSLEN FLEIKKIASE MMHKLLLDYQ NNTNRIQTDK
NELKSYADTL FNQMTKKPEE ALKLKNTICS IEDL

t19-2.aa

CYPVASNKIELKPKTETSLNQEEVPNQEANYKEEKEAKEEGINKKTENTLLNDLRNLIETAKKDNDKYTQKLKEES
SSQYGILAFKDLFWLDGTNEQLSANTERSKAYRKRAYSILNTINDASLKNFSEIVMASGQTQGIFNTLNSLGGNFE
KIVNCLYPKKDNLEKLETSVLKKLKDSLENFLEIKKIASEMMHKLLLDYQNNTNRIQTDKNELKSYADTLFNQMTK
KPEEALK

f19-4.nt

TAATCTATAC TAATTGAGGA GAATATTTTT ATGAAAAACA ACATAATTTT ATGCATGTGT
GTTTTTTTAC TTTTAAATAG CTGCACCGCT AACCATGAAG CTGAAGCGAA AATAAAAAAA
CATGTTGATA AAACAAAAAA CGAATATATT AATGAAATAA AAAATTTAAT AGCAACAACC
AAAGAAATCA TCGAAAAACG AAAATTGCTA CAAGCTAAAC CAGTAGATCA AAACCCCGTA
GATGATACAA ACAATAAGAA AGTTTTCGAG ATAGATAAAA GAGCTTTCGA TTTTATAAAT
AGTTTTTTAA CAGATGATGA ATTTAATAAA TTTGTAACAA TATTTCATAA ACCAACACTA
AAATCACCCG GAAAAGTATT AAATAGCATA GCAATTCTAG AGCTAAACAT AGAGCAGGTA
ATTAATCACC TAGACTCAAA AAATGAGACC TTAAATAAAG CAAGCTCTTT AGATTTGGAA
AAGATCAAAA ATTCCCTTGA ACAGCTGTTC TCTATAAGGA ATTTTTTTTC AACAATCATA
AAAAGGGTCT TATTAGATCA TCAAAACAAT GAAAATTCTA TAAAACCAGA TGATTCTAAA
TCAGGAACCT ATTTCGATAC GATATACGAT CAGTTTAATG AAAAAAATAA AGAGGTTAGA
AATCTGAAAA AAACCATATT ATCACTGCCG AATTAA

t19-4.nt

CTGCACCGCTAACCATGAAGCTGAAGCGAAAATAAAAAAACATGTTGATAAAACAAAAAACGAATATATTAATGAA
ATAAAAAATTTAATAGCAACAACCAAAGAAATCATCGAAAAACGAAAATTGCTACAAGCTAAACCAGTAGATCAAA
ACCCCGTAGATGATACAAACAATAAGAAAGTTTTCGAGATAGATAAAAGAGCTTTCGATTTTATAAATAGTTTTTT
AACAGATGATGAATTTAATAAATTTGTAACAATATTTCATAAACCAACACTAAAATCACCCGGAAAAGTATTAAAT
AGCATAGCAATTCTAGAGCTAAACATAGAGCAGGTAATTAATCACCTAGACTCAAAAAATGAGACCTTAAATAAAG
CAAGCTCTTTAGATTTGGAAAAGATCAAAAATTCCCTTGAACAGCTGTTCTCTATAAGGAATTTTTTTTCAACAAT
CATAAAAAGGGTCTTATTAGATCATCAAAACAATGAAAATTCTATAAAACCAGATGATTCTAAATCAGGAACCTAT
TTCGATACGATATACGATCAGTTTAATGAAAAAAATAAAGAGGTTAGAAATCTGAAAAAA

f19-4.aa

SILIEENIFM KNNIILCMCV FLLLNSCTAN HEAEAKIKKH VDKTKNEYIN EIKNLIATTK
EIIEKRKLLQ AKPVDQNPVD DTNNKKVFEI DKRAFDFINS FLTDDEFNKF VTIFHKPTLK
SPGKVLNSIA ILELNIEQVI NHLDSKNETL NKASSLDLEK IKNSLEQLFS IRNFFSTIIK
RVLLDHQNNE NSIKPDDSKS GTYFDTIYDQ FNEKNKEVRN LKKTILSLPN

t19-4.aa

CTANHEAEAKIKKHVDKTKNEYINEIKNLIATTKEIIEKRKLLQAKPVDQNPVDDTNNKKVFEIDKRAFDFINSFL
TDDEFNKFVTIFHKPTLKSPGKVLNSIAILELNIEQVINHLDSKNETLNKASSLDLEKIKNSLEQLFSIRNFFSTI
IKRVLLDHQNNENSIKPDDSKSGTYFDTIYDQFNEKNKEVRNLKK

f19-6.nt

TABLE 1. Nucleotide and Amino Acid Sequences

TAAAGGAGAG TATTAATGAA ATGCCATATA ATTGCAACTA TATTTGTTTT TCTATTTTTA
GCTTGCAGTA CAGATTTTAA TACTGATCAA AAAGGCATTA AATACCCGCC TACCGAAAAA
TCAAAGCCCA AAACTGAAGA CTCTAAGCAA AAAGAATTAA AGCCTAAAAC AGAAAAAGAA
CTAAAGAAAA AACAACAACT AAAAAATAAA CTACTTAATG ATTTAAAAAA TTCAATAGAA
ACAGCTAATA AGCATAAAGA AAAGTATAAA AAAAGAATGA AAGAAGAACC CGAAGATCAA
TACGGGGTAC AGGCTTTCAA AGGATCGAAT TGGGGGCCGG GGACTGAAGA TGTATCTGCC
AACACCGAAA GATCTATAAG ATTTAGAAGA CATACTTATA CTATTTTAAG CACGCTGAGT
CTTCATGAAT TAAAGGAATT CTCAAATATT GTTACAAATG AAAATAAACT GGTGCCAGTA
GTAGATATGT TTAATTTCTT TAGCTCTATT GGGACAGCTC TTGATATAAC AACCGATAGC
TTATATCCCA AAAAGACAAT CTGGACAAAC CAGATCTGTC GGATTTAG

t19-6.nt

TTGCAGTACAGATTTTAATACTGATCAAAAAGGCATTAAATACCCGCCTACCGAAAAATCAAAGCCCAAAACTGAA
GACTCTAAGCAAAAAGAATTAAAGCCTAAAACAGAAAAAGAACTAAAGAAAAAACAACAACTAAAAAATAAACTAC
TTAATGATTTAAAAAATTCAATAGAAACAGCTAATAAGCATAAAGAAAAGTATAAAAAAAGAATGAAAGAAGAACC
CGAAGATCAATACGGGGTACAGGCTTTCAAAGGATCGAATTGGGGGCCGGGGACTGAAGATGTATCTGCCAACACC
GAAAGATCTATAAGATTTAGAAGACATACTTATACTATTTTAAGCACGCTGAGTCTTCATGAATTAAAGGAATTCT
CAAATATTGTTACAAATGAAAATAAACTGGTGCCAGTAGTAGATATGTTTAATTTCTTTAGCTCTATTGGGACAGC
TCTTGATATAACAACCGATAGCTTATATCCCAAAAAGACAATCTGGACAAACCAGATCTGTCGG

f19-6.aa

RRVLMKCHII ATIFVFLFLA CSTDFNTDQK GIKYPPTEKS KPKTEDSKQK ELKPKTEKEL
KKKQQLKNKL LNDLKNSIET ANKHKEKYKK RMKEEPEDQY GVQAFKGSNW GPGTEDVSAN
TERSIRFRRH TYTILSTLSL HELKEFSNIV TNENKLVPVV DMFNFFSSIG TALDITTDSL
YPKKTIWTNQ ICRI

t19-6.aa

CSTDFNTDQKGIKYPPTEKSKPKTEDSKQKELKPKTEKELKKKQQLKNKLLNDLKNSIETANKHKEKYKKRMKEEP
EDQYGVQAFKGSNWGPGTEDVSANTERSIRFRRHTYTILSTLSLHELKEFSNIVTNENKLVPVVDMFNFFSSIGTA
LDITTDSLYPKKTIWTNQICR

f21-4.nt

TAGGAGACAA TCTTTATGAA TAAAAAAATA AAAATGTTTA TTATTTGTGC TATTTTTATG
CTGATAAGTT CTTGTAAGAA TGATGTAACT AGTAAAGATT TAGAAGGGGC GGTGAAAGAT
TTAGAAAGTT CAGAACAAAA TGTAAAAAAA ACAGAACAAG AGATAAAAAA ACAAGTTGAA
GGATTTTTAG AAATTTTAGA GACAAAAGAT TTAAACACAT TAGATACAAA AGAAATTGAA
AAACAAATTC AAGAATTAAA GAATAAGATA GAAAAATTAG ACTCTAAAAA AACTTCTATT
GAAACATATT CTGGGTATGA AGAAAAAATA AACAAAATAA AAGAAAAATT AAACGGAAAA
GGACTTGAAG ATAAATTAAA TGAACTTTCA GAGAGCTTAA AAAAGAAAAA AGAGGAGAGA
AAAAAAGCTT TACAAGAGGC TAAAAAGAAA TTTGAAGAGT ATAAAAAACCA AGCTGAATCT
GCAACTGGAG TAACGCATGG TTCTCAAGTC CAAAGACAAG GTGGTGTTGG ATTACAAGCT
TGGCAGTGTG CTAATAGTTT GGGGTTTAAA AATATGACTA GTGGTAATAA TACTAGCGAT
ATGACCAATG AAGTTATAAC TAATTCGCTT AAAAAGATTG AAGAAGAACT TAAAAATATT
GGAGAAACTG TAGAAGGTAA AAAAGAATAA

t21-4.nt

TTGTAAGAATGATGTAACTAGTAAAGATTTAGAAGGGGCGGTGAAAGATTTAGAAAGTTCAGAACAAAATGTAAAA
AAAACAGAACAAGAGATAAAAAAACAAGTTGAAGGATTTTTAGAAATTTTAGAGACAAAAGATTTAAACACATTAG
ATACAAAAGAAATTGAAAAACAAATTCAAGAATTAAAGAATAAGATAGAAAAATTAGACTCTAAAAAAACTTCTAT
TGAAACATATTCTGGGTATGAAGAAAAAATAAACAAAATAAAAGAAAAATTAAACGGAAAAGGACTTGAAGATAAA

TABLE 1. Nucleotide and Amino Acid Sequences

TTAAATGAACTTTCAGAGAGCTTAAAAAAGAAAAAAGAGGAGAGAAAAAAAGCTTTACAAGAGGCTAAAAAGAAAT
TTGAAGAGTATAAAAACCAAGCTGAATCTGCAACTGGAGTAACGCATGGTTCTCAAGTCCAAAGACAAGGTGGTGT
TGGATTACAAGCTTGGCAGTGTGCTAATAGTTTGGGGTTTAAAAATATGACTAGTGGTAATAATACTAGCGATATG
ACCAATGAAGTTATAACTAATTCGCTTAAAAAGATTGAAGAAGAACTTAAAAATATTGGAGAAACTGTAGAAGGTA
AAAAAGAA

f21-4.aa

ETIFMNKKIK MFIICAIFML ISSCKNDVTS KDLEGAVKDL ESSEQNVKKT EQEIKKQVEG
FLEILETKDL NTLDTKEIEK QIQELKNKIE KLDSKKTSIE TYSGYEEKIN KIKEKLNGKG
LEDKLNELSE SLKKKKEERK KALQEAKKKF EEYKNQAESA TGVTHGSQVQ RQGGVGLQAW
QCANSLGFKN MTSGNNTSDM TNEVITNSLK KIEEELKNIG ETVEGKKE

t21-4.aa

CKNDVTSKDLEGAVKDLESSEQNVKKTEQEIKKQVEGFLEILETKDLNTLDTKEIEKQIQELKNKIEKLDSKKTSI
ETYSGYEEKINKIKEKLNGKGLEDKLNELSESLKKKKEERKKALQEAKKKFEEYKNQAESATGVTHGSQVQRQGGV
GLQAWQCANSLGFKNMTSGNNTSDMTNEVITNSLKKIEEELKNIGETVEGKKE

f24-1.nt

TAAGCTGGTA ACACTGTAAA GACAGCTGAG GGGGCTTCAA GTGGTACTGA TGCAATTGGA
GAAGTTGTGG ATAATGATGC TAAGGTTGCT GATAAGGCGA GTGTGACGGG GATTGCTAAG
GGGATAAAGG AGATTGTTGA AGCTGCTAGG GGAGTGAAA AGCTGAAAGT TGCTGCTGCT
AAAGAGGGCA ATGAAAAGGC AGGGAAGTTG TTTGGGAAGG CTGGTGCTAA TGCTCATGGG
GACAGTGAGG CTGCTAGCAA GGCGGCTGGT GCTGTTAGTG CTGTTAGTGG GGAGCAGATA
TTAAGTGCGA TTGTTAAGGC TGCGGATGCG GCTGAGCAGG ATGGAAAGAA GCCTGCAGAT
GCTACAAATC CGATTGCTGC TGCTATTGGG AATAAAGATG AGGATGCGGA TTTTGGTGAT
GGGATGAAGA AGGATGATCA GATTGCTGCT GCTATTGCTT TGAGGGGGAT GGCTAAGGAT
GGAAAGTTTG CTGTGAAGAA TGATGAGAAA GGGAAGGCTG AGGGGGCTAT TAAGGGAGCT
GCTGCAATTG GAGAAGTTGT GGATAATGCT GGTGCTGCGA AGGCTGCTGA TAAGGATAGT
GTGAAGGGGA TTGCTAAGGG GATAAAGGAG ATTGTTGAAG CTGCTGGGGG GAGTGAAAAG
CTGAAAGCTG CTGCTGCTGA AGGGGAGAAT AATAAAAAGG CAGGGAAGTT GTTTGGGAAA
GTTGATGGTG CTGCTGGGGA CAGTGAGGCT GCTAGCAAGG CGGCTGGTGC TGTTAGTGCT
GTTAGTGGGG AGCAGATATT AAGTGCGATT GTTAAGGCTG CTGGTGAGGC TGAGCAGGAT
GGAGAGAAGC CTGAGGATGC TAAAAATCCG ATTGCTGCTG CTATTGGGAA GGGTAATGGG
GATGGTGCGG AGTTTGATCA GGATGAGATG AAGAAGGATG ATCAGATTGC TGCTGCTATT
GCTTTGAGGG GGATGGCTAA GGATGGAAAG TTTGCTGTGA AGGGTAATAA TGAGAAAGAG
AAGGCTGAGG GGGCTATTAA AGAAGTTAGC GAGTTGTTGG ATAAGCTGGT AACAGCTGTA
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GAAGCTGCTN GGGGGAGTGA AAAGCTGAAA GTTGCTGCTG CTANAGNGGN NAATAATAAA
GAGGCAGGGA AGTTGTTTGG GAAGGCTGGT GCTGATGCTA ATGGGGACAG TGAGGCTGCT
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CCGATTGCTG CTGCTATTGG GAAGGGTAAT GCGGATGATG GTGCGGATTT TGGTGATGGG
ATGAAGAAGG ATGATCAGAT TGCTGCTGCT ATTGCTTTGA GGGGGATGGC TAAGGATGGA
AAGTTTGCTG TGAAGAAGGA TGAGAAAGGG AAGGCTGAGG GGGCTATTAA GGGAGCTAGC
GAGTTGTTGG ATAAGCTGGT AAAAGCTGTA AAGACAGCTG AGGGGGCTTC AAGTGGTACT
GCTGCAATTG GAGAAGTTGT GGATAATGCT GCGAAGGCTG CTGATAAGGA TAGTGTGACG
GGGATTGCTA AGGGGATAAA GGAGATTGTT GAAGCTGCAG GGGGGAGTGA AAAGCTGAAA
GTTGCTGCTG CTAAAGGGGA GAATAATAAA GGGGCAGGGA AGTTGTTTGG GAAGGCTGGT
GCTAATGCTC ATGGGGACAG TGAGGCTGCT AGCAAGGCGG CTGGTGCTGT TAGTGCTGTT
AGTGGGGAAC AGATATTAAG TGCGATTGTT AAGGCTGCTG GTGAGGCTGC TGGTGATCAG
GAGGGAAAGA AGCCTGAGGA GGCTAAAAAT CCGATTGCTG CTGCTATTGG GGATAAAGAT
GGGGATGCGG AGTTTAATCA GGATGGGATG AAGAAGGATG ATCAGATTGC TGCTGCTATT

TABLE 1. Nucleotide and Amino Acid Sequences

GCTTTGAGGG GGATGGCTAA GGATGGAAAG TTTGCTGTGA AGGATGGTGG TGAGAAAGAG
AAGGCTGAGG GGGCTATTAA AGGAGTTAGC GAGTTGTTGG ATAAGCTGGT AAAAGCTGTA
AAGACAGCTG AGGGGGCTTC AAGTGGTACT GCTGCAATTG GAGAAGTTGT GGCTGATGCT
GCTAAGGTTG CTGATAAGGC GAGTGTGACG GGGATTGCTA AGGGGATAAA GGAGATTGTT
GAAGCTGCTG GGGACAGTGA GGCTGCTAGC AAGGCAGCTG GTGCTGTTAG TGCTGTTAGT
GGGGAGCAGA TATTAAGTGC GATTGTTAAG GCTGCGGCTG CTGGTGCGGC TGAGCAGGAT
GGAGAGAAGC CTGCAGAGGC TAAAAATCCG ATTGCTGCTG CTATTGGGAA GGGTGATGGG
GATGCGGATT TTGGTGAGGA TGGGATGAAG AAGGATGATC AGATTGCTGC TGCTATTGCT
TTGAGGGGGA TGGCTAAGGA TGGAAAGTTT GCTGTGAAGA ATGATGAGAA AGGGAAGGCT
GAGGGGGCTA TTAAGGGAGC TGCTGCAATT GGAGAAGTTG TGGATAATGC TGGTGCTGCG
AAGGCTGCTG ATAAGGATAG TGTGAAGGGG ATTGCTAAGG GGATAAAGGA GATTGTTGAA
GCTGCTGGGG GGAGTGAAAA GCTGAAAGCT GCTGCTGCTG AAGGGGAGAA TAATAAAAAG
GCAGGGAAGT TGTTTGGGAA AGTTGATGGT GCTGCTGGGG ACAGTGAGGC TGCTAGCAAG
GCGGCTGGTG CTGTTAGTGC TGTTAGTGGG GAGCAGATAT TAAGTGCGAT TGTTAAGGCT
GCGGATGCGG CTGAGCAGGA TGGAAAGAAG CCTGCAGATG CTACAAATCC GATTGCTGCT
GCTATTGGGA ATAAAGATGA GGATGCGGAT TTTGGTGATG GGATGAAGAA GGATGATCAG
ATTGCTGCTG CTATTGCTTT GAGGGGGATG GCTAAGGATG GAAAGTTTGC TGTGAAGGGT
AATAATGAGA AAGGGAAGGC TGAGGGGGCT TCAAGTGGTA CTGATGCAAT TGGAGAAGTT
GTGGATAATG ATGCGAAGGC TGCTGATAAG GCGAGTGTGA CGGGGATTGC TAAGGGGATA
AAGGAGATTG TTGAAGCTGC TGGGGGGAGT GAAAAGCTGA AAGCTGTTGC TGCTGCTACA
AGGGAGAATA ATAAAGAGGC AGGGAAGTTG TTTGGGAAAG TTGATGATGC TCATGCTGGG
GACAGTGAGG CTGCTAGCAA GGCGGCTGGT GCTGTTAGTG CTGTTAGTGG GGAGCAGATA
TTAAGTGCGA TTGTTACGGC TGCGGCTGCT GGTGAGCAGG ATGGAGAGAA GCCTGCAGAG
GCTACAAATC CGATTGCTGC TGCTATTGGG AAGGGTAATG AGGATGGTGC GGATTTTGGT
AAGGATGAGA TGAAGAAGGA TGATCAGATT GCTGCTGCTA TTGCTTTGAG GGGGATGGCT
AAGGATGGAA AGTTTGCTGT GAAGAGTAAT GATGGTGAGA AAGGGAAGGC TGAGGGGGCT
ATTAAGGAAG TTAGCGAGTT GTTGGATAAG CTGGTAAAAG CTGTAAAGAC AGCTGAGGGG
GCTTCAAGCG GTACTGATGC AATTGGAGAA GTTGTGGCTA ATGCTGGTGC TGCGAAGGCT
GCTGATAAGG CGAGTGTGAC GGGGATTGCT AAGGGGATAA AGGAGATTGT TGAAGCTGCT
GGGGGGAGTA AAAAGCTGAA AGCTGCTGCT GCTGAAGGGG AGAATAATAA AAAGGCAGGG
AAGTTGTTTG GGAAGGCTGG TGCTGGTGCT GGTGCTAATG GGGACAGTGA GGCTGCTAGC
AAGGCGGCTG GTGCTGTTAG TGCTGGTTAG

t24-1.nt

TGGTGAGGCTGAGCAGGATGGAGAGAAGCCTGAGGATGCTAAAAATCCGATTGCTGCTGCTATTGGGAAGGGTAAT
GGGGATGGTGCGGAGTTTGATCAGGATGAGATGAAGAAGGATGATCAGATTGCTGCTGCTATTGCTTTGAGGGGGA
TGGCTAAGGATGGAAAGTTTGCTGTGAAGGGTAATAATGAGAAAGAGAAGGCTGAGGGGGCTATTAAAGAAGTTAG
CGAGTTGTTGGATAAGCTGGTAACAGCTGTAAAGACAGCTGAGGGGGCTTCAAGTGGTACTGATGCAATTGGAGAA
GTTGTGGATAATGNTGCNAAGGNTGCTGATAAGGCGAGTGTGACGGGGATTGCTAAGGGGATAAAGGAGATTGTTG
AAGCTGCTNGGGGGAGTGAAAAGCTGAAAGTTGCTGCTGCTANAGNGGNNAATAATAAAGAGGCAGGGAAGTTGTT
TGGGAAGGCTGGTGCTGATGCTAATGGGGACAGTGAGGCTGCTAGCAAG

f24-1.aa

AGNTVKTAEG ASSGTDAIGE VVDNDAKVAD KASVTGIAKG IKEIVEAARG SEKLKVAAAK
EGNEKAGKLF GKAGANAHGD SEAASKAAGA VSAVSGEQIL SAIVKAADAA EQDGKKPADA
TNPIAAAIGN KDEDADFGDG MKKDDQIAAA IALRGMAKDG KFAVKNDEKG KAEGAIKGAA
AIGEVVDNAG AAKAADKDSV KGIAKGIKEI VEAAGGSEKL KAAAAEGENN KKAGKLFGKV
DGAAGDSEAA SKAAGAVSAV SGEQILSAIV KAAGEAEQDG EKPEDAKNPI AAAIGKGNGD
GAEFDQDEMK KDDQIAAAIA LRGMAKDGKF AVKGNNEKEK AEGAIKEVSE LLDKLVTAVK
TAEGASSGTD AIGEVVDNXA KXADKASVTG IAKGIKEIVE AAXGSEKLKV AAAXXXNNKE
AGKLFGKAGA DANGDSEAAS KAAGAVSAVS GEQILSAIVK AAAAGAADQD GEKPGDAKNP
IAAAIGKGNA DDGADFGDGM KKDDQIAAAI ALRGMAKDGK FAVKKDEKGK AEGAIKGASE
LLDKLVKAVK TAEGASSGTA AIGEVVDNAA KAADKDSVTG IAKGIKEIVE AAGGSEKLKV
AAAKGENNKG AGKLFGKAGA NAHGDSEAAS KAAGAVSAVS GEQILSAIVK AAGEAAGDQE

TABLE 1. Nucleotide and Amino Acid Sequences

GKKPEEAKNP IAAAIGDKDG DAEFNQDGMK KDDQIAAAIA LRGMAKDGKF AVKDGGEKEK
AEGAIKGVSE LLDKLVKAVK TAEGASSGTA AIGEVVADAA KVADKASVTG IAKGIKEIVE
AAGDSEAASK AAGAVSAVSG EQILSAIVKA AAAGAAEQDG EKPAEAKNPI AAAIGKGDGD
ADFGEDGMKK DDQIAAAIAL RGMAKDGKFA VKNDEKGKAE GAIKGAAAIG EVVDNAGAAK
AADKDSVKGI AKGIKEIVEA AGGSEKLKAA AAEGENNKKA GKLFGKVDGA AGDSEAASKA
AGAVSAVSGE QILSAIVKAA DAAEQDGKKP ADATNPIAAA IGNKDEDADF GDGMKKDDQI
AAAIALRGMA KDGKFAVKGN NEKGKAEGAS SGTDAIGEVV DNDAKAADKA SVTGIAKGIK
EIVEAAGGSE KLKAVAAATR ENNKEAGKLF GKVDDAHAGD SEAASKAAGA VSAVSGEQIL
SAIVTAAAAG EQDGEKPAEA TNPIAAAIGK GNEDGADFGK DEMKKDDQIA AAIALRGMAK
DGKFAVKSND GEKGKAEGAI KEVSELLDKL VKAVKTAEGA SSGTDAIGEV VANAGAAKAA
DKASVTGIAK GIKEIVEAAG GSKKLKAAAA EGENNKKAGK LFGKAGAGAG ANGDSEAASK
AAGAVSAG

t24-1.aa

GEAEQDGEKPEDAKNPIAAAIGKGNGDGAEFDQDEMKKDDQIAAAIALRGMAKDGKFAVKGNNEKEKAEGAIKEVS
ELLDKLVTAVKTAEGASSGTDAIGEVVDNXAKXADKASVTGIAKGIKEIVEAAXGSEKLKVAAAXXXNNKEAGKLF
GKAGADANGDSEAASK

f28-2.nt

TAAAAAGGAA ATATAAATAT TATGCGATTA TGTTTAATAA AAATTTTTAT TATACCTAAT
TTAGTATTTA GTTCTCTTTT TTTATTTGAA AGTTGTTCTG GTTTTCTATC TAAAAAATCT
ATAGAACAGT TTGCATTAGC ATTAAAAGAT CATCAAGAAA ATAAAAATAC TACTAATACT
TCAGTAGATA AAAATAGTAA GGAAATTGAA TCTCCTAAAG ACGTTACATC ATCAAATAAA
AAAACTTATG ATCCAATCTT ACAAGTAGGT TCTAATCAAC ATATGTCAGA TGATCCTGGT
GCTAATAATA AAGAATCCCT ACCAAATTCA AGTCCAGCAA TAATACAAAA TGACTCGCAT
GCTCAAAATA ATGTAAAGAT GGAAGAAAAT AAATCAGCTA CTCCACAACA TGATCCAATT
GAACAAAGTA ATTTTAAAAA TAGCCTTACT ACAACAAGTA AAACTCCTGC TATTCCTTCA
GAAGAAGAAA TTAAAGCTAA CTTAGATGAA TTTGCACAAG AAGAGTATGA GCAAACATCT
CTTTCAGAAA TTAAAAATGC CACGCAAATT GTTAATCATG CTAATCCTGA AAACAAATTA
AACAATACAC TCCTTGAGTT TGAAAAAGAT TATGAAACTT TATCAAACTT GTTATTCTCT
AATTTAGACG CATCTCCTTT GAATAGAAAA ATAAAGACTA TTATGCCTAA ATTACAAGAA
ATGCGTTCTT TTATGGAGCA AGCAACTAAT TCTTGGGTAT CTGCTAAAGG CATGCTAGAT
GAGGCTAAGG ATAAACTAGC AGAATCTATT TATAAAAGAC TATACAATGG CAATTCATAC
CGGTTCGGTG GCAGTTTTAA CGGACGTGAT ATGCAACATG CAAAAAATTT AGCATACAGA
GCTATAGACT TTGCTTCTGC ATGCATTGAA TATACACAAA AAGCTATTGA TTATCTTCAA
CAGGGAAATT CTTGCAAAAA AGAAATAGAA AATATATTCA AGCTTTAA

t28-2.nt

AAAAGATCATCAAGAAAATAAAAATACTACTAATACTTCAGTAGATAAAAATAGTAAGGAAATTGAATCTCCTAAA
GACGTTACATCATCAAATAAAAAAACTTATGATCCAATCTTACAAGTAGGTTCTAATCAACATATGTCAGATGATC
CTGGTGCTAATAATAAAGAATCCCTACCAAATTCAAGTCCAGCAATAATACAAAATGACTCGCATGCTCAAAATAA
TGTAAAGATGGAAGAAAATAAATCAGCTACTCCACAACATGATCCAATTGAACAAAGTAATTTTAAAAATAGCCTT
ACTACAACAAGTAAAACTCCTGCTATTCCTTCAGAAGAAGAAATTAAAGCTAACTTAGATGAATTTGCACAAGAAG
AGTATGAGCAAACATCTCTTTCAGAAATTAAAAATGCCACGCAAATTGTTAATCATGCTAATCCTGAAAACAAATT
AAACAATACACTCCTTGAGTTTGAAAAAGATTATGAAACTTTATCAAACTTGTTATTCTCTAATTTAGACGCATCT
CCTTTGAATAGAAAAATAAAGACTATTATGCCTAAATTACAAGAAATGCGTTCTTTTATGGAGCAAGCAACTAATT
CTTGGGTATCTGCTAAAGGCATGCTAGATGAGGCTAAGGATAAACTAGCAGAATCTATTTATAAAAGACTATACAA
TGGCAATTCATACCGGTTCGGTGGCAGTTTTAACGGACGTGATATGCAACATGCAAAAAATTTAGCATACAGAGCT
ATAGACTTTGCTTCTGCATGCATTGAATATACACAAAAAGCTATTGATTATCTTCAACAGGGAAATTCTTGCAAAA
AAGAAATAGAAAATATATTCAAG

f28-2.aa

TABLE 1. Nucleotide and Amino Acid Sequences

KGNINIMRLC LIKIFIIPNL VFSSLFLFES CSGFLSKKSI EQFALALKDH QENKNTTNTS
VDKNSKEIES PKDVTSSNKK TYDPILQVGS NQHMSDDPGA NNKESLPNSS PAIIQNDSHA
QNNVKMEENK SATPQHDPIE QSNFKNSLTT TSKTPAIPSE EEIKANLDEF AQEEYEQTSL
SEIKNATQIV NHANPENKLN NTLLEFEKDY ETLSNLLFSN LDASPLNRKI KTIMPKLQEM
RSFMEQATNS WVSAKGMLDE AKDKLAESIY KRLYNGNSYR FGGSFNGRDM QHAKNLAYRA
IDFASACIEY TQKAIDYLQQ GNSCKKEIEN IFKL

t28-2.aa

KDHQENKNTTNTSVDKNSKEIESPKDVTSSNKKTYDPILQVGSNQHMSDDPGANNKESLPNSSPAIIQNDSHAQNN
VKMEENKSATPQHDPIEQSNFKNSLTTTSKTPAIPSEEEIKANLDEFAQEEYEQTSLSEIKNATQIVNHANPENKL
NNTLLEFEKDYETLSNLLFSNLDASPLNRKIKTIMPKLQEMRSFMEQATNSWVSAKGMLDEAKDKLAESIYKRLYN
GNSYRFGGSFNGRDMQHAKNLAYRAIDFASACIEYTQKAIDYLQQGNSCKKEIENIFK

f28-3.nt

TAGATGAATT TAATTGCTAA ATTATTTATT TTATCCACTT TAGTTTCAAT TCCAAATATC
CTCTCTTGTA ACCTATATGA TAATCTTGCA GACAACGCTG AGCAGGTTAC AGACATACTA
GACAACAACA AGTCTTTTAA TACTTTAGGA AGCAGCAATG AGAGTAGAAG TCGCAGGCCT
AGAAGTACAA ATAATGCTTA TATGAAACAA AACATAGACA AAAATCATTT AGTTGTTGCA
GATATGCAAA ATGATAATAG TAGCAGCAGT CTTCCCCAAC AAGTTAATAG TGAATCCAGT
AAAGCTAATG AAGATAGTAA TATTATGAAG GAAATTGAAT CTTCTACAGA AGAGTGCGCT
AGACTAAGAA AAGATTTAGA AACTATAAAA CAAATACTTG ATAATATAGA AAGCTTGCTT
AATACAGCTA ATTCTTATTT AGAGAACGCT AGAAAAGCAC CTAAATCTAA TCAAGATAAT
CAAACCTTAT TGCTTAGCCT GCACCAAGCT ATTGCTAAGG TTAAGAGTAG TCATACTTCT
TTTATCATTT GTTATAATGA TGCATTTAAT TCCCTGGGAA TAGCTGATAC TGCCTTTAAA
GATGCAAAGA GAAAGGCAGT TGAGGCATAA

t28-3.nt

TTGTAACCTATATGATAATCTTGCAGACAACGCTGAGCAGGTTACAGACATACTAGACAACAACAAGTCTTTTAAT
ACTTTAGGAAGCAGCAATGAGAGTAGAAGTCGCAGGCCTAGAAGTACAAATAATGCTTATATGAAACAAAACATAG
ACAAAAATCATTTAGTTGTTGCAGATATGCAAAATGATAATAGTAGCAGCAGTCTTCCCCAACAAGTTAATAGTGA
ATCCAGTAAAGCTAATGAAGATAGTAATATTATGAAGGAAATTGAATCTTCTACAGAAGAGTGCGCTAGACTAAGA
AAAGATTTAGAAACTATAAAACAAATACTTGATAATATAGAAAGCTTGCTTAATACAGCTAATTCTTATTTAGAGA
ACGCTAGAAAAGCACCTAAATCTAATCAAGATAATCAAACCTTATTGCTTAGCCTGCACCAAGCTATTGCTAAGGT
TAAGAGTAGTCATACTTCTTTTATCATTTGTTATAATGATGCATTTAATTCCCTGGGAATAGCTGATACTGCCTTT
AAAGATGCAAAGAGAAAGGCAGTTGAGGCA

f28-3.aa

MNLIAKLFIL STLVSIPNIL SCNLYDNLAD NAEQVTDILD NNKSFNTLGS SNESRSRRPR
STNNAYMKQN IDKNHLVVAD MQNDNSSSSL PQQVNSESSK ANEDSNIMKE IESSTEECAR
LRKDLETIKQ ILDNIESLLN TANSYLENAR KAPKSNQDNQ TLLLSLHQAI AKVKSSHTSF
IICYNDAFNS LGIADTAFKD AKRKAVEA

t28-3.aa

CNLYDNLADNAEQVTDILDNNKSFNTLGSSNESRSRRPRSTNNAYMKQNIDKNHLVVADMQNDNSSSSLPQQVNSE
SSKANEDSNIMKEIESSTEECARLRKDLETIKQILDNIESLLNTANSYLENARKAPKSNQDNQTLLLSLHQAIAKV
KSSHTSFIICYNDAFNSLGIADTAFKDAKRKAVEA

f31-2.nt

TAAAAAAATA AGGAGGTATT AATGAAAAGG AAAAGCAATA TATGTATTTC ACTTCTAGTC
ACAATATTAT TTGTGTCTTG CAAGTTTTTT GGAAATAAAA GCGCAAGTAA AGAAAAAGAA

TABLE 1. Nucleotide and Amino Acid Sequences

GAAACTTCTT TTTCTGATAC TGCTAGCAAG ATTAGTAAGT CGGGAACAGC TGCTTCTTCA
GACAAACAAG AAAAAAATAC AAGTGATGTT ACAGGTGACG CCAAAAAGCA TACTAGTAGC
CCTTACATGC TTGCTGATGC CCTTATTGTT AGTGATACTA CTAATAGAGA TAGAGATAAG
CAAGAAAATA AAGATAAATT AAATGAAGAA GATAAAAAAA AGCTTAATGC TTTTTTTAGC
ACAACTAAAA CATATCAATC TAGCCTAGAT TCCATTTATA ACAAATATAC AGGCTATTAT
AATACCATTG ATACCTATGG CAGCTGTGAT ACGTATCGCA TTGAGTGTTT TAGTGTAGGA
CCTTCTGAAA AACGTAAACA AGCTCTTGCT GATCTAGAGA AGTTAAAACT AGACGAAAAG
TACACTCAGC TTAGCACAAT GTTAAAGAGT GCTGTGCCTA GTTATTACAA AAAAAATTTA
GATGATTCTA TTGCACAGTA TAAGGAAGCC ATAAAGCAGG CTATTGAAGC TGAAAGTAAA
ATAGAGACAG TAAAAGACTA TGCAACAGCT CAAAGTGCTG CCGATGACGA AAAGAAAAGA
AATATAGATA ATTTAAAAAT AGTTAGAGAT GTTCTTCTTA TTATTAAAAA AACTATTGAG
AAAGCCAGCC GATCTTATGC TGATGCTTTT GCTATTGCAA CATCTAGCTT ATCTTGTAGC
GAATTTAAGC AAGCTGTTAA AGAGTTTAAT GATGCTGCTA AACAATATGC TAATGGAAAT
AAAGGAGACA ATGCTGTCAA TGTTATTGTA GGCACTATTT CTAGTATGCC TTATGTCAAA
TTTAAAGATG AGTTTGCAAG AGCAAAAATG TTTGCTCGTA ATTATAGAGG AGACGAGGTA
GACAAGATGA TAAGAGCTAT CGACAAGCTG TGTGATGTTT ATAAAAAAGT TGCGCTTTAG

t31-2.nt

TTGCAAGTTTTTTGGAAATAAAAGCGCAAGTAAAGAAAAAGAAGAAACTTCTTTTTCTGATACTGCTAGCAAGATT
AGTAAGTCGGGAACAGCTGCTTCTTCAGACAAACAAGAAAAAAATACAAGTGATGTTACAGGTGACGCCAAAAAGC
ATACTAGTAGCCCTTACATGCTTGCTGATGCCCTTATTGTTAGTGATACTACTAATAGAGATAGAGATAAGCAAGA
AAATAAAGATAAATTAAATGAAGAAGATAAAAAAAAGCTTAATGCTTTTTTTAGCACAACTAAAACATATCAATCT
AGCCTAGATTCCATTTATAACAAATATACAGGCTATTATAATACCATTGATACCTATGGCAGCTGTGATACGTATC
GCATTGAGTGTTTTAGTGTAGGACCTTCTGAAAAACGTAAACAAGCTCTTGCTGATCTAGAGAAGTTAAAACTAGA
CGAAAAGTACACTCAGCTTAGCACAATGTTAAAGAGTGCTGTGCCTAGTTATTACAAAAAAAATTTAGATGATTCT
ATTGCACAGTATAAGGAAGCCATAAAGCAGGCTATTGAAGCTGAAAGTAAAATAGAGACAGTAAAAGACTATGCAA
CAGCTCAAAGTGCTGCCGATGACGAAAAGAAAAGAAATATAGATAATTTAAAAATAGTTAGAGATGTTCTTCTTAT
TATTAAAAAAACTATTGAGAAAGCCAGCCGATCTTATGCTGATGCTTTTGCTATTGCAACATCTAGCTTATCTTGT
AGCGAATTTAAGCAAGCTGTTAAAGAGTTTAATGATGCTGCTAAACAATATGCTAATGGAAATAAAGGAGACAATG
CTGTCAATGTTATTGTAGGCACTATTTCTAGTATGCCTTATGTCAAATTTAAAGATGAGTTTGCAAGAGCAAAAAT
GTTTGCTCGTAATTATAGAGGAGACGAGGTAGACAAGATGATAAGAGCTATCGACAAG

f31-2.aa

KNKEVLMKRK SNICISLLVT ILFVSCKFFG NKSASKEKEE TSFSDTASKI SKSGTAASSD
KQEKNTSDVT GDAKKHTSSP YMLADALIVS DTTNRDRDKQ ENKDKLNEED KKKLNAFFST
TKTYQSSLDS IYNKYTGYYN TIDTYGSCDT YRIECFSVGP SEKRKQALAD LEKLKLDEKY
TQLSTMLKSA VPSYYKKNLD DSIAQYKEAI KQAIEAESKI ETVKDYATAQ SAADDEKKRN
IDNLKIVRDV LLIIKKTIEK ASRSYADAFA IATSSLSCSE FKQAVKEFND AAKQYANGNK
GDNAVNVIVG TISSMPYVKF KDEFARAKMF ARNYRGDEVD KMIRAIDKLC DVYKKVAL

t31-2.aa

CKFFGNKSASKEKEETSFSDTASKISKSGTAASSDKQEKNTSDVTGDAKKHTSSPYMLADALIVSDTTNRDRDKQE
NKDKLNEEDKKKLNAFFSTTKTYQSSLDSIYNKYTGYYNTIDTYGSCDTYRIECFSVGPSEKRKQALADLEKLKLD
EKYTQLSTMLKSAVPSYYKKNLDDSIAQYKEAIKQAIEAESKIETVKDYATAQSAADDEKKRNIDNLKIVRDVLLI
IKKTIEKASRSYADAFAIATSSLSCSEFKQAVKEFNDAAKQYANGNKGDNAVNVIVGTISSMPYVKFKDEFARAKM
FARNYRGDEVDKMIRAIDK

f32-4.nt

TAAGGAAATA TGAGGAATAT TAGCAATTGT ATCAAATATA TTATATTAAC AATGCTTATT
GGATTATTAA TTTTTTGTTG TGCAACCTTT GTTTGGTTGA TTGGAATTTT TTATTCAAAT
AACTTTAAAG AAGAGCGGAA TTATTCAATA AGCCCAATAG ATAGTGTTAT TATGCGTAAA
TGTTATTTTA AAGAATTTAA GTCTGGACTT ATTAAAAGCG TATTCTTTAA GAAATTAGAT

TABLE 1. Nucleotide and Amino Acid Sequences

GTAAATGTTA ACTCTAAAAA TTTTAAGGAG CTAAATAAGG TAGATAAACA AAATCTGCTA
AATTCTTATC CATCTTATCA TATGGAGTTT GTCGTAGTTG ATAATGGATT TTTAATGAAT
TTTAAAAATG TTATTTTTAA TGGTATAGAT GATGCTAAAT TATACGATCA ACGTGATATG
GTTTACGGAG GATTTAGATA CTCAAAAGAG GCTTATTTCC AAATTATTGG CAATTATGAT
GTTAAATTAA ATAAAATGAA ACAATATACT CCAGCAATTG TAGTAAATGT TTTCAAAATT
AACATTAATG ATGCTTTATT TAACTCGTTA TTAAAGCAAA AAACTTTAAA AGTTACTTTG
ATTTCCCATA ATAATAAAGA GTATATTTTA CAAACTAATA ATTTCTTATC AAAGTATAAT
TTTCAAACAC CAGAAAAGGA GAATAGTTCT TACTAA

t32-4.nt

AAATAACTTTAAAGAAGAGCGGAATTATTCAATAAGCCCAATAGATAGTGTTATTATGCGTAAATGTTATTTTAAA
GAATTTAAGTCTGGACTTATTAAAAGCGTATTCTTTAAGAAATTAGATGTAAATGTTAACTCTAAAAATTTTAAGG
AGCTAAATAAGGTAGATAAACAAAATCTGCTAAATTCTTATCCATCTTATCATATGGAGTTTGTCGTAGTTGATAA
TGGATTTTTAATGAATTTTAAAAATGTTATTTTTAATGGTATAGATGATGCTAAATTATACGATCAACGTGATATG
GTTTACGGAGGATTTAGATACTCAAAAGAGGCTTATTTCCAAATTATTGGCAATTATGATGTTAAATTAAATAAAA
TGAAACAATATACTCCAGCAATTGTAGTAAATGTTTTCAAAATTAACATTAATGATGCTTTATTTAACTCGTTATT
AAAGCAAAAAACTTTAAAAGTTACTTTGATTTCCCATAATAATAAAGAGTATATTTTACAAACTAATAATTTCTTA
TCAAAGTATAATTTTCAAACACCAGAAAAGGAGAATAGTTCTTAC

f32-4.aa

GNMRNISNCI KYIILTMLIG LLIFCCATFV WLIGIFYSNN FKEERNYSIS PIDSVIMRKC
YFKEFKSGLI KSVFFKKLDV NVNSKNFKEL NKVDKQNLLN SYPSYHMEFV VVDNGFLMNF
KNVIFNGIDD AKLYDQRDMV YGGFRYSKEA YFQIIGNYDV KLNKMKQYTP AIVVNVFKIN
INDALFNSLL KQKTLKVTLI SHNNKEYILQ TNNFLSKYNF QTPEKENSSY

t32-4.aa

NNFKEERNYSISPIDSVIMRKCYFKEFKSGLIKSVFFKKLDVNVNSKNFKELNKVDKQNLLNSYPSYHMEFVVVDN
GFLMNFKNVIFNGIDDAKLYDQRDMVYGGFRYSKEAYFQIIGNYDVKLNKMKQYTPAIVVNVFKININDALFNSLL
KQKTLKVTLISHNNKEYILQTNNFLSKYNFQTPEKENSSY

f4-15.nt

TAAATGAGCA AAAAAGTAAT TTTAATATTA CTAGAAATTT TGATCTTGTC TTGTGATTTA
TCTATAAATA AAGAACAAAA AACCAAAGAA AAAACATCTG AAAAGCAAGA ATCTGAAAAA
CAAAATATTG AAAAACAAGA GCCTGAAAAA CAGAAACAAA ATGCAGCAAA AATAATCCCT
ACGGTATCAA TTCAAACGGT AGAAATAAGG GAATCAAATC AAATTCCAAA AAGCATTGAG
AAGTACTACA AGCAAGCTTA TCCGATTCAA ACATTCACTC TTGATTTTAG CATCACAAGA
GAAAAGGAAT TTCTAAAACC AGAAGATAAA ATCTTGCCCA CACAGGGGAA AGTGGAGTCT
TTGAGCATCT TAATAAATAA AAAATTGTTA GACTTTAAAG CCCCAGAAAA TCCAAAAAGC
TCAACTTTAA AAAATTTCAA AGAAATTAAA AATATTGAGA ATTTCTTCCA AAATCAAGAC
TTATTATTTG TCTTAACCCT TAAAGATAAA AATAACAACA ACACTATTAA CATCATGCTC
AATCCCCCAA ACGACATCCA AAAACCCAAA GATTATATTT TAAAAGACCT TAAAGACACA
ATTAAAAAGG GTACTGGTGA GAAATACTTA AATCCTATCT ATAGATTTCA AATAAAAAAC
AAAAAAGATT ATCATTCAAT AGATTACAAC AAAGTGACTA TTAGCGAAAA AACAATAGAA
TTGGACCTAC TGCCTCACGA ACAAGTCTTT CAAATGAATA AAAATTTCAC TAAAATTTTA
GACACAATAA CAGACTTAAA TAATCTAAAA TTAGTAATTC AAAAAGAATT AGTGTAA

t4-15.nt

TTGTGATTTATCTATAAATAAAGAACAAAAAACCAAAGAAAAAACATCTGAAAAGCAAGAATCTGAAAAACAAAAT
ATTGAAAAACAAGAGCCTGAAAAACAGAAACAAAATGCAGCAAAAATAATCCCTACGGTATCAATTCAAACGGTAG
AAATAAGGGAATCAAATCAAATTCCAAAAAGCATTGAGAAGTACTACAAGCAAGCTTATCCGATTCAAACATTCAC
TCTTGATTTTAGCATCACAAGAGAAAAGGAATTTCTAAAACCAGAAGATAAAATCTTGCCCACACAGGGGAAAGTG

TABLE 1. Nucleotide and Amino Acid Sequences

GAGTCTTTGAGCATCTTAATAAATAAAAAATTGTTAGACTTTAAAGCCCCAGAAAATCCAAAAAGCTCAACTTTAA
AAAATTTCAAAGAAATTAAAAATATTGAGAATTTCTTCCAAAATCAAGACTTATTATTTGTCTTAACCCTTAAAGA
TAAAAATAACAACAACACTATTAACATCATGCTCAATCCCCCAAACGACATCCAAAAACCCAAAGATTATATTTTA
AAAGACCTTAAAGACACAATTAAAAAGGGTACTGGTGAGAAATACTTAAATCCTATCTATAGATTTCAAATAAAAA
ACAAAAAAGATTATCATTCAATAGATTACAACAAAGTGACTATTAGCGAAAAAACAATAGAATTGGACCTACTGCC
TCACGAACAAGTCTTTCAAATGAATAAAAATTTCACTAAA

f4-15.aa

MSKKVILILL EILILSCDLS INKEQKTKEK TSEKQESEKQ NIEKQEPEKQ KQNAAKIIPT
VSIQTVEIRE SNQIPKSIEK YYKQAYPIQT FTLDFSITRE KEFLKPEDKI LPTQGKVESL
SILINKKLLD FKAPENPKSS TLKNFKEIKN IENFFQNQDL LFVLTLKDKN NNNTINIMLN
PPNDIQKPKD YILKDLKDTI KKGTGEKYLN PIYRFQIKNK KDYHSIDYNK VTISEKTIEL
DLLPHEQVFQ MNKNFTKILD TITDLNNLKL VIQKELV

t4-15.aa

CDLSINKEQKTKEKTSEKQESEKQNIEKQEPEKQKQNAAKIIPTVSIQTVEIRESNQIPKSIEKYYKQAYPIQTFT
LDFSITREKEFLKPEDKILPTQGKVESLSILINKKLLDFKAPENPKSSTLKNFKEIKNIENFFQNQDLLFVLTLKD
KNNNNTINIMLNPPNDIQKPKDYILKDLKDTIKKGTGEKYLNPIYRFQIKNKKDYHSIDYNKVTISEKTIELDLLP
HEQVFQMNKNFTK

f4-50.nt

TAGAAGGAGG AAAAAATGAA AATTGGAAAG CTAAATTCAA TAGTTATAGC CTTGTTTTTT
AAACTATTGG TCGCATGTAG TATTGGATTA GTAGAAAGAA CAAATGCAGC TCTTGAATCG
TCCTCTAAGG ATTTAAAAAA CAAAATTTTA AAAATAAAAA AAGAAGCCAC GGGAAAAGGT
GTACTTTTTG AAGCTTTTAC AGGTCTTAAA ACCGGTTCCA AGGTAACAAG TGGTGGACTA
GCCTTAAGAG AAGCAAAAGT ACAAGCCATT GTTGAAACAG GAAAGTTCCT TAAGATAATA
GAAGAAGAAG CTTTAAAGCT TAAAGAAACT GGAAACAGTG GTCAATTCTT GGCTATGTTT
GACTTAATGC TTGAGGTTGT AGAATCGCTA GAAGACGTTG GAATAATAGG CTTAAAAGCC
CGTGTTTTAG AGGAATCTAA AAATAATCCT ATAAACACAG CTGAAAGATT GCTTGCGGCT
AAAGCTCAAA TAGAAAATCA ACTTAAAGTG GTTAAGGAAA AACAAAATAT TGAAAATGGT
GGAGAGAAAA AAAATAATAA AAGCAAAAAA AAGAAATAA

t4-50.nt

ATGTAGTATTGGATTAGTAGAAAGAACAAATGCAGCTCTTGAATCGTCCTCTAAGGATTTAAAAAACAAAATTTTA
AAAATAAAAAAAGAAGCCACGGGAAAAGGTGTACTTTTTGAAGCTTTTACAGGTCTTAAAACCGGTTCCAAGGTAA
CAAGTGGTGGACTAGCCTTAAGAGAAGCAAAAGTACAAGCCATTGTTGAAACAGGAAAGTTCCTTAAGATAATAGA
AGAAGAAGCTTTAAAGCTTAAAGAAACTGGAAACAGTGGTCAATTCTTGGCTATGTTTGACTTAATGCTTGAGGTT
GTAGAATCGCTAGAAGACGTTGGAATAATAGGCTTAAAAGCCCGTGTTTTAGAGGAATCTAAAAATAATCCTATAA
ACACAGCTGAAAGATTGCTTGCGGCTAAAGCTCAAATAGAAAATCAACTTAAAGTGGTTAAGGAAAAACAAAATAT
TGAAAATGGTGGAGAGAAAAAAAATAATAAAAGCAAAAAAAAGAAA

f4-50.aa

KEEKMKIGKL NSIVIALFFK LLVACSIGLV ERTNAALESS SKDLKNKILK IKKEATGKGV
LFEAFTGLKT GSKVTSGGLA LREAKVQAIV ETGKFLKIIE EEALKLKETG NSGQFLAMFD
LMLEVVESLE DVGIIGLKAR VLEESKNNPI NTAERLLAAK AQIENQLKVV KEKQNIENGG
EKKNNKSKKK K

t4-50.aa

TABLE 1. Nucleotide and Amino Acid Sequences

CSIGLVERTNAALESSSKDLKNKILKIKKEATGKGVLFEAFTGLKTGSKVTSGGLALREAKVQAIVETGKFLKIIE
EEALKLKETGNSGQFLAMFDLMLEVVESLEDVGIIGLKARVLEESKNNPINTAERLLAAKAQIENQLKVVKEKQNI
ENGGEKKNNKSKKKK

f4-66.nt

TAATTTTTAA AATTTAAATA TTTACATAAT AGTAATGTGT GTGGGAGACG TATGAAAAAT
ATTTTATTAT TTGTTATTTT ATTATTCTTT TCTTGTAAAG AATTTAATTA TTCTGATCTT
AGGAGAAGGC CTTCAAAGGT TTTAAATGCT TCTAATGGTG CATCAAATAA AGAACTTAAA
ATTTCTTTTG TAGATTCTTT AAATGATGAT CAAAAAGAAG CTTTGTTTTT TCTTGAACAG
GTAGTTCTTG ATAGCAATCC CGACAAGTTT AATCAAATTT TTAATTTAAA TGAAGAGAAG
GTAAAAGAAA TGCTTGTTAC TGTTGTTAAG TGTTTAAAGG CCAAAAGAAA GGCTAAAATG
GCTCTTGAGA GCTCAAATGT TGCAAATGTT GCCAATGCTA AACAGCAATT GCTACAGGTT
GAAAAAACTT ACATAGATAA TTTGCGACAA TCTTTTATGA CTACTAAAAA CATTGAAGAG
GCTTGTAATC TTGTAAAAAA TTATGATGCA TCTGCTTCGT TTTAA

t4-66.nt

TTGTAAAGAATTTAATTATTCTGATCTTAGGAGAAGGCCTTCAAAGGTTTTAAATGCTTCTAATGGTGCATCAAAT
AAAGAACTTAAAATTTCTTTTGTAGATTCTTTAAATGATGATCAAAAAGAAGCTTTGTTTTTTCTTGAACAGGTAG
TTCTTGATAGCAATCCCGACAAGTTTAATCAAATTTTTAATTTAAATGAAGAGAAGGTAAAAGAAATGCTTGTTAC
TGTTGTTAAGTGTTTAAAGGCCAAAAGAAAGGCTAAAATGGCTCTTGAGAGCTCAAATGTTGCAAATGTTGCCAAT
GCTAAACAGCAATTGCTACAGGTTGAAAAAACTTACATAGATAATTTGCGACAATCTTTTATGACTACTAAAAACA
TTGAAGAGGCTTGTAATCTTGTAAAAAATTATGATGCATCTGCTTCGTTT

f4-66.aa

FLKFKYLHNS NVCGRRMKNI LLFVILLFFS CKEFNYSDLR RRPSKVLNAS NGASNKELKI
SFVDSLNDDQ KEALFFLEQV VLDSNPDKFN QIFNLNEEKV KEMLVTVVKC LKAKRKAKMA
LESSNVANVA NAKQQLLQVE KTYIDNLRQS FMTTKNIEEA CNLVKNYDAS ASF

t4-66.aa

CKEFNYSDLRRRPSKVLNASNGASNKELKISFVDSLNDDQKEALFFLEQVVLDSNPDKFNQIFNLNEEKVKEMLVT
VVKCLKAKRKAKMALESSNVANVANAKQQLLQVEKTYIDNLRQSFMTTKNIEEACNLVKNYDASASF

f42-1.nt

TAATTATTAA AATCTAAGGA GAAGAGATTT ATGAACAAAA AATTTTCTAT TTCATTATTA
TCTACAATAT TAGCCTTCTT GTTAGTATTA GGTTGTGATT TGTCAAGCAA TAATGCTGAA
AACAAAATGG ATGATATTTT TAATTTAGAA AAGAAATACA TGGATAATTC AAATTATAAA
TGTTTAAGTA AAAATGAGGC TATAGTTAAA AATTCTAAAA TTAAATTAGG TGTAAATAAT
ACTAGAAGTC GTTCTTATTC TTCTAGAGAG ACTAATGTTT CGGATTCCTA TAATAAAACC
TATTCATATT GCAAAAGCAA CTGA

t42-1.nt

TTGTGATTTGTCAAGCAATAATGCTGAAAACAAAATGGATGATATTTTTAATTTAGAAAAGAAATACATGGATAAT
TCAAATTATAAATGTTTAAGTAAAAATGAGGCTATAGTTAAAAATTCTAAAATTAAATTAGGTGTAAATAATACTA
GAAGTCGTTCTTATTCTTCTAGAGAGACTAATGTTTCGGATTCCTATAATAAAACCTATTCATATTGCAAAAGCAA
C

f42-1.aa

LLKSKEKRFM NKKFSISLLS TILAFLLVLG CDLSSNNAEN KMDDIFNLEK KYMDNSNYKC
LSKNEAIVKN SKIKLGVNNT RSRSYSSRET NVSDSYNKTY SYCKSN

TABLE 1. Nucleotide and Amino Acid Sequences

t42-1.aa

CDLSSNNAENKMDDIFNLEKKYMDNSNYKCLSKNEAIVKNSKIKLGVNNTRSRSYSSRETNVSDSYNKTYSYCKSN

f43-3.nt

TGAATATTAA TAATAAAAAA AGGAATAANA ATGAAAATTA TCAACATATT ATTTTGTTTA
TTTTTACTAA TGCTAAACAG CTGTAATTCT AATGATACTA ATACTAGCCA AACAAAAAGT
AGACAAAAAC GTGATTTAAC CCAAAAAGAA GCAACACAAG AAAAACCAAA ATCTAAAGAA
GACCTGCTTA GAGAAAAGCT ATCTGAAGAC CAAAAAACAC ATCTTGACTG GTTAAAAACC
GCTTTAACTG GTGCTGGAGA ATTTGATAAA TTTTTAGGAT ATGACGAAGA CAAAATAAAA
GGTGCACTTA ATCATATAAA GAGTGAACTT GATAAGTGTA CTGGGGATAA TTCTGAACAA
CAAAAAAGCA CCTTCAAAGA GGTGGTTAAG GGGGCTCTTG GTGGCGGTAT AGATAGTTTT
GCAACTAGTG CAAGTAGTAC CTGCCAAGCT CAGCAATAA

t43-3.nt

CTGTAATTCTAATGATACTAATACTAGCCAAACAAAAAGTAGACAAAAACGTGATTTAACCCAAAAAGAAGCAACA
CAAGAAAAACCAAAATCTAAAGAAGACCTGCTTAGAGAAAAGCTATCTGAAGACCAAAAAACACATCTTGACTGGT
TAAAAACCGCTTTAACTGGTGCTGGAGAATTTGATAAATTTTTAGGATATGACGAAGACAAAATAAAAGGTGCACT
TAATCATATAAAGAGTGAACTTGATAAGTGTACTGGGGATAATTCTGAACAACAAAAAAGCACCTTCAAAGAGGTG
GTTAAGGGGGCTCTTGGTGGCGGTATAGATAGTTTTGCAACTAGTGCAAGTAGTACCTGCCAAGCTCAGCAA

f43-3.aa

ILIIKKGIXM KIINILFCLF LLMLNSCNSN DTNTSQTKSR QKRDLTQKEA TQEKPKSKED
LLREKLSEDQ KTHLDWLKTA LTGAGEFDKF LGYDEDKIKG ALNHIKSELD KCTGDNSEQQ
KSTFKEVVKG ALGGGIDSFA TSASSTCQAQ Q

t43-3.aa

CNSNDTNTSQTKSRQKRDLTQKEATQEKPKSKEDLLREKLSEDQKTHLDWLKTALTGAGEFDKFLGYDEDKIKGAL
NHIKSELDKCTGDNSEQQKSTFKEVVKGALGGGIDSFATSASSTCQAQQ

f45-2.nt

TAGGAGAGAA TAATTATGAA TAAAAAAACA TTGATTATTT GTGCTGTTTT TGCGCTGATA
ATTTCTTGCA AGAATTTTGC AACTGGTAAA GATATAAAAC AAAATTCAGA AGGGAAAATT
AAAGGATTTG TAAATAAGAT TTTAGATCCA GTAAAGGATA AAATTGCTTC AAGTGGTACA
AAAGTAGATG AAGTAGCAAA AAAATTACAA GAAGAAGAAA AAGAAGAATT AATGCAGGGC
GATGATCCTA ATGGCAGTGG AATAAATCCG CCACCAGTAT TGCCGGAAAA TATTCACAAT
AATGCATTAG TATTAAAAGC AATAGAACAA AGTGATGGTC AACAAGAAAA AAAAGTAGAA
GAAGCTGAAG CTAAAGTTGA AGAAAATAAA GAAAAACAAG AGAATACAGA AGAAAACATT
AAAGAAAAAG AAATAATAGA CGAACAAAAC AAACAAGAAT TAGCTAAAGC TAAAGAAGAA
GAACAACAAA AAGAACAAAA AAGACATCAA GAAGAGCAAC AAAGAAAAGC TAAAGCAGAA
AAAGAAAAAA GAGAAAGAGA AGAGGCAGAA CAACAAAAAC GACAACAAGA AGAGGAAGAA
AAAAGGCAAG TTGATAACCA AATTAAAACA CTTATAGCTA AAATAGATGA GATCAATGAA
AATATTGATG TTATAAAATG GCAAACGACT GTAGGCCCAC AAGGCGTTAT AGATAGAATT
ACTGGGCCTG TGTATGATGA TTTTACCAAT GGCAATAATT CTATACGCGA AACTTGGGAG
GGGTTAGAAG AGGAATCAGA AGACGAAGGA TTAGGAAAAT TATTGAAAGA ATTGAGTGAT
GCTAGGGACG CGCTAAGAAC TAAATTAAAT GAAGGCAATA AACCATATAC TGGTTACGAA
GAGCCTAAGT TAAAAGAAAG TGTAAATGTT AGCGAAATTA AAGAAGATTT AGAAAAATTA
AAATCAAAAT TAGAAGAAGT TAAAAAATAT CTTAAAGATA GTTCTAAATT TGAAGAAATT
AAAGGATACA TCAGTGACAG TCAGTAA

t45-2.nt

TABLE 1. Nucleotide and Amino Acid Sequences

TTGCAAGAATTTTGCAACTGGTAAAGATATAAAACAAAATTCAGAAGGGAAAATTAAAGGATTTGTAAATAAGATT
TTAGATCCAGTAAAGGATAAAATTGCTTCAAGTGGTACAAAAGTAGATGAAGTAGCAAAAAAATTACAAGAAGAAG
AAAAAGAAGAATTAATGCAGGGCGATGATCCTAATGGCAGTGGAATAAATCCGCCACCAGTATTGCCGGAAAATAT
TCACAATAATGCATTAGTATTAAAAGCAATAGAACAAAGTGATGGTCAACAAGAAAAAAAAGTAGAAGAAGCTGAA
GCTAAAGTTGAAGAAAATAAAGAAAAACAAGAGAATACAGAAGAAAACATTAAAGAAAAAGAAATAATAGACGAAC
AAAACAAACAAGAATTAGCTAAAGCTAAAGAAGAAGAACAACAAAAAGAACAAAAAAGACATCAAGAAGAGCAACA
AAGAAAAGCTAAAGCAGAAAAAGAAAAAAGAGAAAGAGAAGAGGCAGAACAACAAAAACGACAACAAGAAGAGGAA
GAAAAAAGGCAAGTTGATAACCAAATTAAAACACTTATAGCTAAAATAGATGAGATCAATGAAAATATTGATGTTA
TAAAATGGCAAACGACTGTAGGCCCACAAGGCGTTATAGATAGAATTACTGGCCCTGTGTATGATGATTTTACCAA
TGGCAATAATTCTATACGCGAAACTTGGGAGGGGTTAGAAGAGGAATCAGAAGACGAAGGATTAGGAAAATTATTG
AAAGAATTGAGTGATGCTAGGGACGCGCTAAGAACTAAATTAAATGAAGGCAATAAACCATATACTGGTTACGAAG
AGCCTAAGTTAAAAGAAAGTGTAAATGTTAGCGAAATTAAAGAAGATTTAGAAAAATTAAAATCAAAATTAGAAGA
AGTTAAAAAATATCTTAAAGATAGTTCTAAATTTGAAGAAATTAAAGGATACATCAGTGACAGTCAG

f45-2.aa

ERIIMNKKTL IICAVFALII SCKNFATGKD IKQNSEGKIK GFVNKILDPV KDKIASSGTK
VDEVAKKLQE EEKEELMQGD DPNGSGINPP PVLPENIHNN ALVLKAIEQS DGQQEKKVEE
AEAKVEENKE KQENTEENIK EKEIIDEQNK QELAKAKEEE QQKEQKRHQE EQQRKAKAEK
EKREREEAEQ QKRQQEEEEK RQVDNQIKTL IAKIDEINEN IDVIKWQTTV GPQGVIDRIT
GPVYDDFTNG NNSIRETWEG LEEESEDEGL GKLLKELSDA RDALRTKLNE GNKPYTGYEE
PKLKESVNVS EIKEDLEKLK SKLEEVKKYL KDSSKFEEIK GYISDSQ

t45-2.aa

CKNFATGKDIKQNSEGKIKGFVNKILDPVKDKIASSGTKVDEVAKKLQEEEKEELMQGDDPNGSGINPPPVLPENI
HNNALVLKAIEQSDGQQEKKVEEAEAKVEENKEKQENTEENIKEKEIIDEQNKQELAKAKEEEQQKEQKRHQEEQQ
RKAKAEKEKREREEAEQQKRQQEEEEKRQVDNQIKTLIAKIDEINENIDVIKWQTTVGPQGVIDRITGPVYDDFTN
GNNSIRETWEGLEEESEDEGLGKLLKELSDARDALRTKLNEGNKPYTGYEEPKLKESVNVSEIKEDLEKLKSKLEE
VKKYLKDSSKFEEIKGYISDSQ

f47-2.nt

TGAATATTAA TAATAAAAAA AGGAGTAACA ATGAAAATCA TCAACATATT ATTTTGTATA
TCTTTGCTAC TACTAAATAG CTGTAATTCC AATGATAATG ACACTTTAAA AAACAATGCC
CAACAAACAA AAAGCAGGAA AAAACGTGAT TTAAGCCAAG AAGAACTGCC ACAACAAGAA
AAAATCACTT TAACATCCGA CGAAGAAAAA ATGTTTACTT CATTAATCAA TGTGTTTAAA
TACACAATTG AAAAATTAAA CAATGAAATA CAAGGGTGCA TGAATGGAAA CAAAAGTAAA
TGTAATGACT TCTTTGATTG GCTTTCTGAA GATATTCAAA AACAAAAAGA ATTAGCTGGT
GCTTTTACCA AGGTTTACAA CTTCTTAAAA TCAAAAGCAC AAAATGAAAC TTTTGATACT
TATATTAAAG GAGCTATTGA TTGTAAAAAA AACACTCCAC AAGATTGTAA TAAAAATAAT
GAAATATGGG GAGGTGGACA ACTTANTAGN GCAATATTTT AG

t47-2.nt

CTGTAATTCCAATGATAATGACACTTTAAAAAACAATGCCCAACAAACAAAAAGCAGGAAAAAACGTGATTTAAGC
CAAGAAGAACTGCCACAACAAGAAAAAATCACTTTAACATCCGACGAAGAAAAAATGTTTACTTCATTAATCAATG
TGTTTAAATACACAATTGAAAAATTAAACAATGAAATACAAGGGTGCATGAATGGAAACAAAAGTAAATGTAATGA
CTTCTTTGATTGGCTTTCTGAAGATATT
CAAAAACAAAAAGAATTAGCTGGTGCTTTTACCAAGGTTTACAACTTCTTAAAATCAAAAGCACAAAATGAAACTT
TTGATACTTATATTAAAGGAGCTATTGATTGTAAAAAAAACACTCCACAAGATTGTAATAAAAATAATGAA

f47-2.aa

ILIIKKGVTM KIINILFCIS LLLLNSCNSN DNDTLKNNAQ QTKSRKKRDL SQEELPQQEK

TABLE 1. Nucleotide and Amino Acid Sequences

ITLTSDEEKM FTSLINVFKY TIEKLNNEIQ GCMNGNKSKC NDFFDWLSED IQKQKELAGA
FTKVYNFLKS KAQNETFDTY IKGAIDCKKN TPQDCNKNNE IWGGGQLXXA IF

t47-2.aa

CNSNDNDTLKNNAQQTKSRKKRDLSQEELPQQEKITLTSDEEKMFTSLINVFKYTIEKLNNEIQGCMNGNKSKCND
FFDWLSEDIQKQKELAGAFTKVYNFLKSKAQNETFDTYIKGAIDCKKNTPQDCNKNNE

f49-2.nt

TAAATGTTCA AAACAATCAT TAAACAAAAA AATATGAAAA AAATTTCAAG TGCAATTTTA
TTAACAACTT TCTTTGTTTT TATTAATTGT AAAAGCCAAG TTGCTGATAA GGCGAGTGTG
ACGGGGATTG CTAAGGGAAT AAAGGAGATT GTTGAAGCTG CTGGGGGGAG TGAAAAGCTG
AAAGTTGCTG CTGCTGAAGG GGAGAATAAT GAAAAGGCAG GGAAGTTGTT TGGGAAGGCT
GGTGCTGGTA ATGCTGGGGA CAGTGAGGCT GCTAGCAAGG CGGCTGGTGC TGTTAGTGCT
GTTAGTGGGG AGCAGATATT AAGTGCGATT GTTAAGGCTG CTGGTGAGGC TGCGCAGGAT
GGAGAGAAGC CTGGGGAGGC TAAAAATCCG ATTGCTGCTG CTATTGGGAA GGGTAATGAG
GATGGTGCGG AGTTTAAGGA TGAGATGAAG AAGGATGATC AGATTGCTGC TGCTATTGCT
TTGAGGGGGA TGGCTAAGGA TGGAAAGTTT GCTGTGAAGA ATGATGAGAA AGGGAAGGCT
GAGGGGGCTA TTAAGGGAGC TGGCGAGTTG TTGGATAAGC TGGTAAAAGC TGTAAAGACA
GCTGAGGGGG CTTCAAGTGG TACTGCTGCA ATTGGAGAAG TTGTGGCTGA TGATAATGCT
GCGAAGGTTG CTGATAAGGC GAGTGTGAAG GGGATTGCTA AGGGGATAAA GGAGATTGTT
GAAGCTGCTG GGGGGAGTAA AAAGCTGAAA GTTGCTGCTG CTAAAGAGGG CAATGAAAAG
GCAGGGAAGT TGTTTGGGAA AGTTGATGCT GCTCATGCTG GGGACAGTGA GGCTGCTAGC
AAGGCGGCTG GTGCTGTTAG TGCTGTTAGT GGGGAGCAGA TATTAAGTGC GATTGTTAAG
GCTGCTGGTG CGGCTGCTGG TGATCAGGAG GGAAAGAAGC CTGGGGATGC TAAAAATCCG
ATTGCTGCTG CTATTGGGAA GGGTGATGCG GAGAATGGTG CGGAGTTTAA TCATGATGGG
ATGAAGAAGG ATGATCAGAT TGCTGCTGCT ATTGCTTTGA GGGGGATGGC TAAGGATGGA
AAGTTTGCTG TGAAGAGTGG TGGTGGTGAG AAAGGGAAGG CTGAGGGGGC TATTAAGGGA
GCTGCTGAGT TGTTGGATAA GCTGGTAAAA GCTGTAAAGA CAGCTGAGGG GGCTTCAAGT
GGTACTGATG CAATTGGAGA AGTTGTGGCT AATGCTGGTG CTGCAAAGGT TGCTGATAAG
GCGAGTGTGA CGGGGATTGC TAAGGGGATA AAGGAGATTG TTGAAGCTGC TGGGGGGAGT
GAAAAGCTGA AAGTTGCTGC TGCTACAGGG GAGAGTAATA AAGGGGCAGG GAAGTTGTTT
GGGAAGGCTG GTGCTGGTGC TAATGCTGGG GACAGTGAGG CTGCTAGCAA GGCGGCTGGT
GCTGTTAGTG CTGTTAGTGG GGAGCAGATA TTAAGTGCGA TTGTTAAGGC TGCTGATGCG
GCTGATCAGG AGGGAAAGAA GCCTGGGGAT GCTANAAATC CGATTGCTGC TGCTATTGGG
AAGGGTNATG NGGAGAATGG TGCGGAGTTT AANNATGANG GATGA

t49-2.nt

TTGTAAAAGCCAAGTTGCTGATAAGGCGAGTGTGACGGGGATTGCTAAGGGAATAAAGGAGATTGTTGAAGCTGCT
GGGGGGAGTGAAAAGCTGAAAGTTGCTGCTGCTGAAGGGGAGAATAATGAAAAGGCAGGGAAGTTGTTTGGGAAGG
CTGGTGCTGGTAATGCTGGGGACAGTGAGGCTGCTAGCAAGGCGGCTGGTGCTGTTAGTGCTGTTAGTGGGGAGCA
GATATTAAGTGCGATTGTTAAGGCTGCTGGTGAGGCTGCGCAGGATGGAGAGAAGCCTGGGGAGGCTAAAAATCCG
ATTGCTGCTGCTATTGGGAAGGGTAATGAGGATGGTGCGGAGTTTAAGGATGAGATGAAGAAGGATGATCAGATTG
CTGCTGCTATTGCTTTGAGGGGGATGGCTAAGGATGGAAAGTTTGCTGTGAAGAATGATGAGAAAGGGAAGGCTGA
GGGGGCTATTAAG

f49-2.aa

MFKTIIKQKN MKKISSAILL TTFFVFINCK SQVADKASVT GIAKGIKEIV EAAGGSEKLK
VAAAEGENNE KAGKLFGKAG AGNAGDSEAA SKAAGAVSAV SGEQILSAIV KAAGEAAQDG
EKPGEAKNPI AAAIGKGNED GAEFKDEMKK DDQIAAAIAL RGMAKDGKFA VKNDEKGKAE
GAIKGAGELL DKLVKAVKTA EGASSGTAAI GEVVADDNAA KVADKASVKG IAKGIKEIVE
AAGGSKKLKV AAAKEGNEKA GKLFGKVDAA HAGDSEAASK AAGAVSAVSG EQILSAIVKA
AGAAAGDQEG KKPGDAKNPI AAAIGKGDAE NGAEFNHDGM KKDDQIAAAI ALRGMAKDGK

TABLE 1. Nucleotide and Amino Acid Sequences

FAVKSGGGEK GKAEGAIKGA AELLDKLVKA VKTAEGASSG TDAIGEVVAN AGAAKVADKA
SVTGIAKGIK EIVEAAGGSE KLKVAAATGE SNKGAGKLFG KAGAGANAGD SEAASKAAGA
VSAVSGEQIL SAIVKAADAA DQEGKKPGDA XNPIAAAIGK GXXENGAEFX XXG

t49-2.aa

CKSQVADKASVTGIAKGIKEIVEAAGGSEKLKVAAAEGENNEKAGKLFGKAGAGNAGDSEAASKAAGAVSAVSGEQ
ILSAIVKAAGEAAQDGEKPGEAKNPIAAAIGKGNEDGAEFKDEMKKDDQIAAAIALRGMAKDGKFAVKNDEKGKAE
GAIK

f5-14.nt

TAGAAATTCA AAACAAAGGA GAAAACAAAA AGTATGAATA AAAAAATATT GATTATTTTT
GCTGTTTTTG CACTTATAAT TTCTTGTAAA AATTATGCAA CTGGTAAAGA TATAAAACAA
AATGCAAAAG GGAAAATTAA AGGATTTTTA GATAAGGTTT TAGATCCAGC AAAAGATAAA
ATTACTTCAA GTAGTTCAAA AGTAGATGAA TTAGCAAAAA AATTACAAGA AGAAGATGAA
GATAATGAAT TAATGCAGGG CGATGATCCT AATAACAGAG CAATAGCACT GTTACCAGTA
TTGCCGGAAA ATAGTCATGA CAATCCACCA GTACCAAAAG TAAAAGCAGC AGCACAAAGT
GGTGGTCAAC AAGAAGACCA AAAAGCAAAA GAATCTAAAG ATAAAGTTGA GGAAGAAAAA
GAAGTTGTAG AGGAGAAAAA AGAAGAACAA GATAGTAAAA AAGAAAAAGT GGAGAAGCAA
AGTCAAAAGC AAAAAGAAGA AGAGAGAAAC TCTAAAGAAG AACAACAAAA ACAAGAAGAA
GCAAAAGCTA GAGCAGATAG AGAAAGAGAA GAACGACTAA AACAACAAGA ACAAAAAAGA
CAACAGGAAG AAGCTAGGGT TAAAGCAGAA AAAGAAAAAC AAGAAAGAGA GGAACAACAA
AAACAAGAAG AAGAAAAGAA AGTTAAATAT AAAATTAAAA CACTTACAGA CAAAATAGAT
GAAATAAATA AGGATATTGA TGGTATAAAT GGTAAAACAA TTGTAGGAGC AGAAGAAGTT
ATAGATAAAA TTACGGGGCC TGTATATGAT GATTTTACTG ATGGGAATAA AGCTATATAC
AAAACTTGGG GAGATTTAGA GGATGAAGAA GGCGAAGAAT TAGGAAAATT ATTGAAAGAA
TTGAGTGATA CTAGACATAA TTTAAGAACC AAATTAAATG AGGGTAATAA AGCATATATT
GTTCTAGAAA AGGAGCCTAA TTTAAAAGAA AATGTAAATG TTAGTGATAT TCAATCAGAT
TTAGAAAAAT TAAAATCAGG ATTAGAAGAA GTTAAAAAAT ATTTTGAAAA TGAAGATAAT
TTTGAAGAAA TTAAAGGATA CATTGAGGAT AGTAATTCAT ATTGA

t5-14.nt

TTGTAAAAATTATGCAACTGGTAAAGATATAAAACAAAATGCAAAAGGGAAAATTAAAGGATTTTTAGATAAGGTT
TTAGATCCAGCAAAAGATAAAATTACTTCAAGTAGTTCAAAAGTAGATGAATTAGCAAAAAAATTACAAGAAGAAG
ATGAAGATAATGAATTAATGCAGGGCGATGATCCTAATAACAGAGCAATAGCACTGTTACCAGTATTGCCGGAAAA
TAGTCATGACAATCCACCAGTACCAAAAGTAAAAGCAGCAGCACAAAGTGGTGGTCAACAAGAAGACCAAAAAGCA
AAAGAATCTAAAGATAAAGTTGAGGAAGAAAAAGAAGTTGTAGAGGAGAAAAAAGAAGAACAAGATAGTAAAAAAG
AAAAAGTGGAGAAGCAAAGTCAAAAGCAAAAAGAAGAAGAGAGAAACTCTAAAGAAGAACAACAAAAACAAGAAGA
AGCAAAAGCTAGAGCAGATAGAGAAAGAGAAGAACGACTAAAACAACAAGAACAAAAAAGACAACAGGAAGAAGCT
AGGGTTAAAGCAGAAAAAGAAAAACAAGAAAGAGAGGAACAACAAAAACAAGAAGAAGAAAAGAAAGTTAAATATA
AAATTAAAACACTTACAGACAAAATAGATGAAATAAATAAGGATATTGATGGTATAAATGGTAAAACAATTGTAGG
AGCAGAAGAAGTTATAGATAAAATTACGGGGCCTGTATATGATGATTTTACTGATGGGAATAAAGCTATATACAAA
ACTTGGGGAGATTTAGAGGATGAAGAAGGCGAAGAATTAGGAAAATTATTGAAAGAATTGAGTGATACTAGACATA
ATTTAAGAACCAAATTAAATGAGGGTAATAAAGCATATATTGTTCTAGAAAAGGAGCCTAATTTAAAAGAAAATGT
AAATGTTAGTGATATTCAATCAGATTTAGAAAAATTAAAATCAGGATTAGAAGAAGTTAAAAAATATTTTGAAAAT
GAAGATAATTTTGAAGAAATTAAAGGATACATTGAGGATAGTAATTCATAT

f5-14.aa

KFKTKEKTKS MNKKILIIFA VFALIISCKN YATGKDIKQN AKGKIKGFLD KVLDPAKDKI
TSSSSKVDEL AKKLQEEDED NELMQGDDPN NRAIALLPVL PENSHDNPPV PKVKAAAQSG
GQQEDQKAKE SKDKVEEEKE VVEEKKEEQD SKKEKVEKQS QKQKEEERNS KEEQQKQEEA
KARADREREE RLKQQEQKRQ QEEARVKAEK EKQEREEQQK QEEEKKVKYK IKTLTDKIDE
INKDIDGING KTIVGAEEVI DKITGPVYDD FTDGNKAIYK TWGDLEDEEG EELGKLLKEL

TABLE 1. Nucleotide and Amino Acid Sequences

SDTRHNLRTK LNEGNKAYIV LEKEPNLKEN VNVSDIQSDL EKLKSGLEEV KKYFENEDNF
EEIKGYIEDS NSY

t5-14.aa

CKNYATGKDIKQNAKGKIKGFLDKVLDPAKDKITSSSSKVDELAKKLQEEDEDNELMQGDDPNNRAIALLPVLPEN
SHDNPPVPKVKAAAQSGGQQEDQKAKESKDKVEEEKEVVEEKKEEQDSKKEKVEKQSQKQKEEERNSKEEQQKQEE
AKARADREREERLKQQEQKRQQEEARVKAEKEKQEREEQQKQEEEKKVKYKIKTLTDKIDEINKDIDGINGKTIVG
AEEVIDKITGPVYDDFTDGNKAIYKTWGDLEDEEGEELGKLLKELSDTRHNLRTKLNEGNKAYIVLEKEPNLKENV
NVSDIQSDLEKLKSGLEEVKKYFENEDNFEEIKGYIEDSNSY

f5-15.nt

TAACTTATGA ATAAGAAAAT GAAAATGTTT ATTATTTGTG CTGTTTTTGC ATTGATGATT
TCTTGCAAGA ATTATGCAAG TGGTGAAAAT CTAAAAAATT CAGAACAAAA TCTAGAAAGT
TCAGAACAAA ATGTAAAAAA AACAGAACAA GAGATAAAAA AACAAGTTGA AGGATTTTTA
GAAATTCTAG AGACAAAAGA TTTATCTAAA TTAGATGAAA AAGATACAAA AGAAATTGAA
AAACAAATTC AAGAATTAAA GAATAAAATA GAAAAATTAG ATTCTAAAAA AACTTCTATT
GAAACATATT CTGAGTATGA AGAAAAAATA AACAAAATAA AAGAAAAATT GAAAGGAAAA
GGACTTGAAG ATAAATTTAA GGAGCTTGAA GAGAGTTTAG CAAAGAAAAA GGGGGAGAGA
AAAAAAGCTT TACAAGAGGC CAAACAGAAA TTTGAAGAAT ATAAAAAACA AGTAGATACT
TCAACTGGGA AAACTCAAGG CGACAGGTCT AAAAACCGAG GTGGTGTTGG AGTGCAAGCT
TGGCAGTGTG CCAATGAATT AGGTTTGGGT GTAAGTTATT CTAATGGCGG CAGTGACAAC
AGCAATACTG ATGAATTAGC AAACAAAGTT ATAGATGATT CTCTTAAAAA GATTGAAGAA
GAACTTAAGG GAATAGAAGA AGATAAAAAA GAATAA

t5-15.nt

TTGCAAGAATTATGCAAGTGGTGAAAATCTAAAAAATTCAGAACAAAATCTAGAAAGTTCAGAACAAAATGTAAAA
AAAACAGAACAAGAGATAAAAAAACAAGTTGAAGGATTTTTAGAAATTCTAGAGACAAAAGATTTATCTAAATTAG
ATGAAAAAGATACAAAAGAAATTGAAAAACAAATTCAAGAATTAAAGAATAAAATAGAAAAATTAGATTCTAAAAA
AACTTCTATTGAAACATATTCTGAGTATGAAGAAAAAATAAACAAAATAAAAGAAAAATTGAAAGGAAAAGGACTT
GAAGATAAATTTAAGGAGCTTGAAGAGAGTTTAGCAAAGAAAAAGGGGGAGAGAAAAAAAGCTTTACAAGAGGCCA
AACAGAAATTTGAAGAATATAAAAAACAAGTAGATACTTCAACTGGGAAAACTCAAGGCGACAGGTCTAAAAACCG
AGGTGGTGTTGGAGTGCAAGCTTGGCAGTGTGCCAATGAATTAGGTTTGGGTGTAAGTTATTCTAATGGCGGCAGT
GACAACAGCAATACTGATGAATTAGCAAACAAAGTTATAGATGATTCTCTTAAAAAGATTGAAGAAGAACTTAAGG
GAATAGAAGAAGATAAAAAAGAA

f5-15.aa

LMNKKMKMFI ICAVFALMIS CKNYASGENL KNSEQNLESS EQNVKKTEQE IKKQVEGFLE
ILETKDLSKL DEKDTKEIEK QIQELKNKIE KLDSKKTSIE TYSEYEEKIN KIKEKLKGKG
LEDKFKELEE SLAKKKGERK KALQEAKQKF EEYKKQVDTS TGKTQGDRSK NRGGVGVQAW
QCANELGLGV SYSNGGSDNS NTDELANKVI DDSLKKIEEE LKGIEEDKKE

t5-15.aa

CKNYASGENLKNSEQNLESSEQNVKKTEQEIKKQVEGFLEILETKDLSKLDEKDTKEIEKQIQELKNKIEKLDSKK
TSIETYSEYEEKINKIKEKLKGKGLEDKFKELEESLAKKKGERKKALQEAKQKFEEYKKQVDTSTGKTQGDRSKNR
GGVGVQAWQCANELGLGVSYSNGGSDNSNTDELANKVIDDSLKKIEEELKGIEEDKKE

f51-2.nt

TAATTGTTTG GGGTTGTGGT AAACTTAAGG CTTATGGAGT GGATTATGAA TAAAAAAATG
AAAATATTTA TTATTTGTGC TGTATTTGTG CTGATAAGTT CTTGCAAGAT TGATGCAACT
GGTAAAGATG CAACTGGTAA AGATGCAACT GGTAAAGATG CAACTGGTAA AGATGCAACT
GGTAAAAATG CAGAACAAAA TATAAAAGGG AAAGTTCAAG GATTTTTAGA AAAGATTTTA

TABLE 1. Nucleotide and Amino Acid Sequences

GATCCAGTAA AGGATAAAAT TGCTTCAAAT GGTCCAATAG CAGATGAATT GGCAAAAAAA
TTACAAGAAG AAGAAAAGGT AAATAACGGG GAAGAAGAAA ATGATAAAGC TGTCTTTTTA
GGAGAAGAAT CAAAAGAGGA TGAAGAAGAA AATGAGCAAG CTGTTAATTT AGAAGAAAAA
AATGCGGAAG AGGATAAGAA AGTTGTTAAT TTAGAAGAGA AAGAATTAGA AGTTAAAAAA
GAGACTGAAG AAGATGAAGA TAAAGAAGAA ATAGAGAAAC AAAAACAAGA AGTGGAAAAA
GCACAAGAAA GAAAACAACG ACAAGAAGAA AAGAAACGAA AAAAACAAGA ACAGCAAGAA
GAAAAGAAAC GAAAACGACA AGAACAAAGA AAAGAAAGGA GAGCTAAAAA CAAAATTAAA
AAACTTGCGG ATAAAATAGA TGAGATAAGT TGGAATATTG ATGGTATAGA AAGTCAAACA
AGTGTAAAAC CGAAAGCAGT TATAGATAAA ATTACGGGGC CTGTATATGA TTATTTTACC
GATGACAACA AAAAAGCTAT ATATAAAACA TGGGGAGATT TAGAAGATGA AGAAGGCGAA
GGATTGGGAA AATTATTGAA AGAATTGAGT GATACTAGAG ATGAGTTAAG AACCAAATTA
AATAAAGATA ATAAAAAATA TTATGCCCAT GAAAATGAGC CTCCTCTAAA AGAAAATGTA
GATGTCAGCG AAATTAAAGA AGATTTAGAA AAAGTAAAAT CAGGATTAGA AAAGGTTAAA
GAATATCTTA AAGACAATTC TAAATTTGAA GAAATTAAAG GATACATCAG TTACAGTCAG
TAA

t51-2.nt

TTGCAAGATTGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCA
ACTGGTAAAAAATGCAGAACAAAATATAAAAGGGAAAGTTCAAGGATTTTTAGAAAAGATTTTAGATCCAGTAAAGG
ATAAAATTGCTTCAAATGGTCCAATAGCAGATGAATTGGCAAAAAAATTACAAGAAGAAGAAAAGGTAAATAACGG
GGAAGAAGAAAATGATAAAGCTGTCTTTTTAGGAGAAGAATCAAAAGAGGATGAAGAAGAAAATGAGCAAGCTGTT
AATTTAGAAGAAAAAAATGCGGAAGAGGATAAGAAAGTTGTTAATTTAGAAGAGAAAGAATTAGAAGTTAAAAAAG
AGACTGAAGAAGATGAAGATAAAGAAGAAATAGAGAAACAAAAACAAGAAGTGGAAAAAGCACAAGAAAGAAAACA
ACGACAAGAAGAAAAGAAACGAAAAAAACAAGAACAGCAAGAAGAAAAGAAACGAAAACGACAAGAACAAAGAAAA
GAAAGGAGAGCTAAAAACAAAATTAAAAAACTTGCGGATAAAATAGATGAGATAAGTTGGAATATTGATGGTATAG
AAAGTCAAACAAGTGTAAAACCGAAAGCAGTTATAGATAAAATTACGGGGCCTGTATATGATTATTTTACCGATGA
CAACAAAAAAGCTATATATAAAACATGGGGAGATTTAGAAGATGAAGAAGGCGAAGGATTGGGAAAATTATTGAAA
GAATTGAGTGATACTAGAGATGAGTTAAGAACCAAATTAAATAAAGATAATAAAAAATATTATGCCCATGAAAATG
AGCCTCCTCTAAAAGAAAATGTAGATGTCAGCGAAATTAAAGAAGATTTAGAAAAAGTAAAATCAGGATTAGAAAA
GGTTAAAGAATATCTTAAAGACAATTCTAAATTTGAAGAAATTAAAGGATACATCAGTTACAGTCAG

f51-2.aa

LFGVVVNLRL MEWIMNKKMK IFIICAVFVL ISSCKIDATG KDATGKDATG KDATGKDATG
KNAEQNIKGK VQGFLEKILD PVKDKIASNG PIADELAKKL QEEEKVNNGE EENDKAVFLG
EESKEDEEEN EQAVNLEEKN AEEDKKVVNL EEKELEVKKE TEEDEDKEEI EKQKQEVEKA
QERKQRQEEK KRKKQEQQEE KKRKRQEQRK ERRAKNKIKK LADKIDEISW NIDGIESQTS
VKPKAVIDKI TGPVYDYFTD DNKKAIYKTW GDLEDEEGEG LGKLLKELSD TRDELRTKLN
KDNKKYYAHE NEPPLKENVD VSEIKEDLEK VKSGLEKVKE YLKDNSKFEE IKGYISYSQ

t51-2.aa

CKIDATGKDATGKDATGKDATGKDATGKNAEQNIKGKVQGFLEKILDPVKDKIASNGPIADELAKKLQEEEKVNNG
EEENDKAVFLGEESKEDEEENEQAVNLEEKNAEEDKKVVNLEEKELEVKKETEEDEDKEEIEKQKQEVEKAQERKQ
RQEEKKRKKQEQQEEKKRKRQEQRKERRAKNKIKKLADKIDEISWNIDGIESQTSVKPKAVIDKITGPVYDYFTDD
NKKAIYKTWGDLEDEEGEGLGKLLKELSDTRDELRTKLNKDNKKYYAHENEPPLKENVDVSEIKEDLEKVKSGLEK
VKEYLKDNSKFEEIKGYISYSQ

f6-21.nt

TAGGCAAAAT TTAAATTTAT AAAAACTTGT AAGGATGCTT GTATGAAAAT ATTGATAAAA
AAGTTAAAAG TTGTATTATT TCTCAATTTA ATTTTACTTA TTTCTTGTGT TAATGAAAGT
AATAGAAACA AATTGGTTTT TAAGCTAAAT ATTGGAAGTG AGCCTGCTAC TTTAGATGCT
CAATTAATAA ACGATACGGT TGGATCAGGG ATTGTAAGCC AAATGTTTCT TGGCATTTTA
GATGGAGATC CCAGGACTGG AGGATACAGA CCGGGACTTG CTAAAAGTTG GGATATTTCT

TABLE 1. Nucleotide and Amino Acid Sequences

GATGACGGAG TAGTTTATAC GTTTCATTTA AGAGATAATC TTGTTTGGAG TGATGGAGTT
TCCATTACTG CCGAAGAATA A

t6-21.nt

TTGTGTTAATGAAAGTAATAGAAACAAATTGGTTTTTAAGCTAAATATTGGAAGTGAGCCTGCTACTTTAGATGCT
CAATTAATAAACGATACGGTTGGATCAGGGATTGTAAGCCAAATGTTTCTTGGCATTTTAGATGGAGATCCCAGGA
CTGGAGGATACAGACCGGGACTTGCTAAAAGTTGGGATATTTCTGATGACGGAGTAGTTTATACGTTTCATTTAAG
AGATAATCTTGTTTGGAGTGATGGAGTTTCCATTACTGCCGAAGAA

f6-21.aa

AKFKFIKTCK DACMKILIKK LKVVLFLNLI LLISCVNESN RNKLVFKLNI GSEPATLDAQ
LINDTVGSGI VSQMFLGILD GDPRTGGYRP GLAKSWDISD DGVVYTFHLR DNLVWSDGVS
ITAEE

t6-21.aa

CVNESNRNKLVFKLNIGSEPATLDAQLINDTVGSGIVSQMFLGILDGDPRTGGYRPGLAKSWDISDDGVVYTFHLR
DNLVWSDGVSITAEE

f6-27.nt

TAAAGAAAAG CTTGCATAAA AAGTATAACA AATTCTTTAA TAATTAAAAT CAAAAAGAAT
ATAATTATTG CACTAAAATT AAATTTATAC AGTTATATAG AATCACTTAA GGAACAAAAA
ATGAAATACC TTAAAAACAT TTCCTTATTT TTGTTAATTT TAGGTTGCAA ATCCATCCCA
AATGGTAATT TCAATCTACA CGATACAAAC CATAAATTAG GAAAACTAAA ATTTCAAGAA
GACTCGATAA TAAGCAGAAA TTATGATAAT AAAATATCCA TTGTGGGAGT ATACAACCCT
TTAACAGAAA AAGAAAATTT TAAAGTCAAT ATTTTCATCA AAAAAAAAGG ATTACAAATA
GATCCTGAAA ATATTTTGAT AAATGAAGAA AAAATTAATT ATTCAAAATA TAAAGCAGAA
CTCAAAGTAA AATCTAGCTT TAATAAAAGC ATTATCAGTA TTTCACTAAC TAATTCAAGA
GATCTATTAA CCTACATTTA CGATAAAAGC ACAGGGAAAT ACATTAACAT TGACTTTAAG
GACAATTGGA ACGTATCGCA CAGTATAAAA TTTAATAAGG AGTATATTTT AGCATATATA
ACAGATTTTG ATAAAGAAAT TAAAATATCT AAAAATATTT TGCAAAAACG TATTGATAAT
AGAAAAATTG AAATTGAAAA AACAGAGCTT AAAACAGAAT ATAATGAAAT AGAGGATTAT
TACATCTACA GTATGAAAAT TCCAAAATTA TTTGAAAAAT CAGACGCTCC CTCTGAAACT
TACGAAACAT TTGTTATAGC AAATTATTAC CCCTGTGAAA ATTTAAATAT ACTGTTTTTG
AATTTAAGCT TATACTCTGA TAAATTACGC TTTCTAAACT CTATTTATGA TGAGAATGAT
AGAAAATTAA AAATGGAGCC TCCTGTGAGA GCCTTAAAGA ATTCAAAAAC AATAAAAGAA
ACATTAAATA TAGTATTAAG TCCTCAAAAA ATAATAGAGC TAGCAAAAAA CATTGAAAAA
GATATTACTC TAAAATTAAA ATCTTACGGA GAAAAGGGAG AATTCACATT TGAAATATAT
AAACCACTTC TTTTAAAATT CTTAAAAGAA GTAGATCATT GCATAAAAAA TTTGCAATCA
AGTAGGCATA AATTTTAA

t6-27.nt

TTGCAAATCCATCCCAAATGGTAATTTCAATCTACACGATACAAACCATAAATTAGGAAAACTAAAATTTCAAGAA
GACTCGATAATAAGCAGAAATTATGATAATAAAATATCCATTGTGGGAGTATACAACCCTTTAACAGAAAAAGAAA
ATTTTAAAGTCAATATTTTCATCAAAAAAAAAGGATTACAAATAGATCCTGAAAATATTTTGATAAATGAAGAAAA
AATTAATTATTCAAAATATAAAGCAGAACTCAAAGTAAAATCTAGCTTTAATAAAAGCATTATCAGTATTTCACTA
ACTAATTCAAGAGATCTATTAACCTACATTTACGATAAAAGCACAGGGAAATACATTAACATTGACTTTAAGGACA
ATTGGAACGTATCGCACAGTATAAAATTTAATAAGGAGTATATTTTAGCATATATAACAGATTTTGATAAAGAAAT
TAAAATATCTAAAAATATTTTGCAAAAACGTATTGATAATAGAAAAATTGAAATTGAAAAAACAGAGCTTAAAACA
GAATATAATGAAATAGAGGATTATTACATCTACAGTATGAAAATTCCAAAATTATTTGAAAAATCAGACGCTCCCT
CTGAAACTTACGAAACATTTGTTATAGCAAATTATTACCCCTGTGAAAATTTAAATATACTGTTTTTGAATTTAAG
CTTATACTCTGATAAATTACGCTTTCTAAACTCTATTTATGATGAGAATGATAGAAAATTAAAAATGGAGCCTCCT

TABLE 1. Nucleotide and Amino Acid Sequences

GTGAGAGCCTTAAAGAATTCAAAAACAATAAAAGAAACATTAAATATAGTATTAAGTCCTCAAAAAATAATAGAGC
TAGCAAAAAACATTGAAAAAGATATTACTCTAAAATTAAAATCTTACGGAGAAAAGGGAGAATTCACATTTGAAAT
ATATAAACCACTTCTTTTAAAATTCTTAAAAGAAGTAGATCATTGCATAAAAAATTTGCAATCAAGTAGGCATAAA
TTT

f6-27.aa

RKACIKSITN SLIIKIKKNI IIALKLNLYS YIESLKEQKM KYLKNISLFL LILGCKSIPN
GNFNLHDTNH KLGKLKFQED SIISRNYDNK ISIVGVYNPL TEKENFKVNI FIKKKGLQID
PENILINEEK INYSKYKAEL KVKSSFNKSI ISISLTNSRD LLTYIYDKST GKYINIDFKD
NWNVSHSIKF NKEYILAYIT DFDKEIKISK NILQKRIDNR KIEIEKTELK TEYNEIEDYY
IYSMKIPKLF EKSDAPSETY ETFVIANYYP CENLNILFLN LSLYSDKLRF LNSIYDENDR
KLKMEPPVRA LKNSKTIKET LNIVLSPQKI IELAKNIEKD ITLKLKSYGE KGEFTFEIYK
PLLLKFLKEV DHCIKNLQSS RHKF

t6-27.aa

CKSIPNGNFNLHDTNHKLGKLKFQEDSIISRNYDNKISIVGVYNPLTEKENFKVNIFIKKKGLQIDPENILINEEK
INYSKYKAELKVKSSFNKSIISISLTNSRDLLTYIYDKSTGKYINIDFKDNWNVSHSIKFNKEYILAYITDFDKEI
KISKNILQKRIDNRKIEIEKTELKTEYNEIEDYYIYSMKIPKLFEKSDAPSETYETFVIANYYPCENLNILFLNLS
LYSDKLRFLNSIYDENDRKLKMEPPVRALKNSKTIKETLNIVLSPQKIIELAKNIEKDITLKLKSYGEKGEFTFEI
YKPLLLKFLKEVDHCIKNLQSSRHKF

f6-5.nt

TAAATGAAGA AGTTTTTAAT ATCCGTTTAT TTTTTATTGT TTTATGGTTG TTCAACTATA
TCTTTGGTAA AAATACCAGA AAAAGATAAA ATAAATTTAA CTGTTTTATC ATCTTTAATG
AATTATCCTG ATTTGAAGAT TTCAAATTTT AAAATAAAAG ACTACGAACA TTTGCATTAT
TCATCTGATT TTGAAAGCTT GAGTGATACT AAAAATAGTG CTTATATTTA CGTTGATGAA
TCTAGTTTCA ATAATAATAT TAATTTTATT AAAGATCTTT TTATTTATAA TAAGAAATTA
TATAGAATAC TTATTGCTTA TAGCTTGACC CAAGGTGCAT CTTTTAAGGC AGAAGTTTTA
TCTTATCTTG AAAAACAAAA AATTATGAAA AATTTTTCAT TGAAAATAAA TTTTCCAACT
GCTAAAAAAT TTATGGATAA TAAGTATTGG ATTGTAATTG CAAAAAACCA TTTAGATTCT
CTTGTTAAGA GTAAAAATTA TTTAGTCTTG GCGAATGTAA AGATGGAATA TATACTCAAA
AAGTTTTTAA CTTGA

t6-5.nt

TTGTTCAACTATATCTTTGGTAAAAATACCAGAAAAAGATAAAATAAATTTAACTGTTTTATCATCTTTAATGAAT
TATCCTGATTTGAAGATTTCAAATTTTAAAATAAAAGACTACGAACATTTGCATTATTCATCTGATTTTGAAAGCT
TGAGTGATACTAAAAATAGTGCTTATATTTACGTTGATGAATCTAGTTTCAATAATAATATTAATTTTATTAAAGA
TCTTTTTATTTATAATAAGAAATTATATAGAATACTTATTGCTTATAGCTTGACCCAAGGTGCATCTTTTAAGGCA
GAAGTTTTATCTTATCTTGAAAAACAAAAAATTATGAAAAATTTTTCATTGAAAATAAATTTTCCAACTGCTAAAA
AATTTATGGATAATAAGTATTGGATTGTAATTGCAAAAAACCATTTAGATTCTCTTGTTAAGAGTAAAAAT

f6-5.aa

MKKFLISVYF LLFYGCSTIS LVKIPEKDKI NLTVLSSLMN YPDLKISNFK IKDYEHLHYS
SDFESLSDTK NSAYIYVDES SFNNNINFIK DLFIYNKKLY RILIAYSLTQ GASFKAEVLS
YLEKQKIMKN FSLKINFPTA KKFMDNKYWI VIAKNHLDSL VKSKNYLVLA NVKMEYILKK
FLT

t6-5.aa

CSTISLVKIPEKDKINLTVLSSLMNYPDLKISNFKIKDYEHLHYSSDFESLSDTKNSAYIYVDESSFNNNINFIKD
LFIYNKKLYRILIAYSLTQGASFKAEVLSYLEKQKIMKNFSLKINFPTAKKFMDNKYWIVIAKNHLDSLVKSKN

TABLE 1. Nucleotide and Amino Acid Sequences

f7-30.nt

TAGAGACGAA GTCACAAGCA AAATGTTAAA AGATTTACAA AATCAAGTTC AAGGGGGCAA
ATAATGAAAA ATTTAAAGAC AAAAATTAAT TTTTTAGGGA TATTTTGGCT ACTGTTACTA
TTTCTTTCTT GCGAATCAAT ACCATCACTT CCCCAAAAAC CAACCCTAAC AAACAAAGAA
GATATTGAAA ATTTAATGCT CGATGAAGCA GAACTTTTTA GATACTCAAC CGCACTAAAT
GTTTGGCTTT TGACTGTAAA ATCTTATGTG ATCAAATACT ATCCTAATGA CAAATTTCCT
GTGTTTGAAA ATTTTGATCC CGTGTTTGGC GATGAAAATG GAACTAAAGA AACAAATATA
CTAAAAAATC GAATTACCTA CTACAATCGA TACATAGAAA AAACCGAACC GATTGTATTT
GGGTGTTACA AAAAATACAG CAGAAGATAA

t7-30.nt

TTGCGAATCAATACCATCACTTCCCCAAAAACCAACCCTAACAAACAAAGAAGATATTGAAAATTTAATGCTCGAT
GAAGCAGAACTTTTTAGATACTCAACCGCACTAAATGTTTGGCTTTTGACTGTAAAATCTTATGTGATCAAATACT
ATCCTAATGACAAATTTCCTGTGTTTGAAAATTTTGATCCCGTGTTTGGCGATGAAAATGGAACTAAAGAAACAAA
TATACTAAAAAATCGAATTACCTACTACAATCGATACATAGAAAAAACCGAACCGATTGTATTTGGGTGTTACAAA
AAATACAGCAGAAGA

f7-30.aa

RRSHKQNVKR FTKSSSRGQI MKNLKTKINF LGIFWLLLLF LSCESIPSLP QKPTLTNKED
IENLMLDEAE LFRYSTALNV WLLTVKSYVI KYYPNDKFPV FENFDPVFGD ENGTKETNIL
KNRITYYNRY IEKTEPIVFG CYKKYSRR

t7-30.aa

CESIPSLPQKPTLTNKEDIENLMLDEAELFRYSTALNVWLLTVKSYVIKYYPNDKFPVFENFDPVFGDENGTKETN
ILKNRITYYNRYIEKTEPIVFGCYKKYSRR

f76-1.nt

TGAATATTAA TAATAAAAAA AGGAGTAACA ATGAAAATTA TCAACATATT ATTTTGTTTG
TTTTTACTAA TGCTAAACGG CTGTAATTCT AATGATACAA ATACCAAGCA GACAAAAAGC
AGACAAAAGC GTGATTTAAC CCAAAAAGAA GCAACACAAG AAAAACCTAA ATCTAAATCT
AAAGAAGACC TGCTTAGAGA AAAGCTATCT GATGATCAAA AAACACAACT TGACTGGTTA
AAAACCGCTT TAACTGGTGT TGGAAAATTT GATAAATTCT TAGAAAATGA TGAAGGCAAA
ATTAAATCAG CACTTGAACA TATAAAGACT GAACTTGATA AATGTAATGG AAATGATGAA
GGAAAAAACA CCTTCAAAAC TACCGTTCAA GGGTTTTTTA GCGGCGGCAA TATAGATAAT
TTTGCAGATC AAGCAACTGC TACCTGCAAT TAA

t76-1.nt

CTGTAATTCTAATGATACAAATACCAAGCAGACAAAAAGCAGACAAAAGCGTGATTTAACCCAAAAAGAAGCAACA
CAAGAAAAACCTAAATCTAAATCTAAAGAAGACCTGCTTAGAGAAAAGCTATCTGATGATCAAAAAACACAACTTG
ACTGGTTAAAAACCGCTTTAACTGGTGTTGGAAAATTTGATAAATTCTTAGAAAATGATGAAGGCAAAATTAAATC
AGCACTTGAACATATAAAGACTGAACTTGATAAATGTAATGGAAATGATGAAGGAAAAAACACCTTCAAAACTACC
GTTCAAGGGTTTTTTAGCGGCGGCAATATAGATAATTTTGCAGATCAAGCAACTGCTACCTGCAAT

f76-1.aa

ILIIKKGVTM KIINILFCLF LLMLNGCNSN DTNTKQTKSR QKRDLTQKEA TQEKPKSKSK
EDLLREKLSD DQKTQLDWLK TALTGVGKFD KFLENDEGKI KSALEHIKTE LDKCNGNDEG
KNTFKTTVQG FFSGGNIDNF ADQATATCN

t76-1.aa

TABLE 1. Nucleotide and Amino Acid Sequences

CNSNDTNTKQTKSRQKRDLTQKEATQEKPKSKSKEDLLREKLSDDQKTQLDWLKTALTGVGKFDKFLENDEGKIKS
ALEHIKTELDKCNGNDEGKNTFKTTVQGFFSGGNIDNFADQATATCN

f8-10.nt

TAAGTAAGGA GAATATTTAT GAAATATAAT ACGATTATAA GCATATTTGT TTGTTTGTTT
TTAACTGCTT GCAATCCAGA TTTTAACACA AATAAGAAAA GAACTCTAAG TAAGGGGATA
ATTTCAAATC AAGATGCAGA TTCTGATAAA ATAATAAAAA ATAAATTACT TGATGATTTA
ATAAATTTAA TAGAAAAAGC GAATGCAGAT AGAGAAAAAT ATGTAAAAAA AATGGAAGAA
GAACCTTCGG ATCAATATGG AATGTTGGCT GTTTTTGGAG GTATGTATTG GGCAGAATCA
CCACGGGAAT TAATATCTGA TACAGGTAGT GAGAGATCTA TTAGGTATAG AAGGCGTGTT
TATAGTATTT TATTAAATGC TATTGAAACT AATGAATTAA AGAAATTTTC AGAAATTAGA
ATACTGTCAA TAAAAGTACT AGAAATATTT AGCCTATTTA ATCTATTTGG AAGTACTCTT
GATGATGTGG TTGTTCACTT ATATTCCAAA AAGATACTC TAGGTAAACT AGATATTTCA
AATTTAAAAA GACTTAAAAA TTTGTTTGAA AAATTATTAT CTATAAAAAC AATCGTTTCA
AAGATGTCAA AACGTCTTTT ATTGGATTAT CAAAATAATG AAAATTTTAT AAAAACAGAT
AACGCCAAGC TTGGATCTTA TGTGGTTGCA CTTTCCAATC AAATTCAAGA AAAATATAAT
GAAGCAGAAA GGCTGAAAAG CGAGATAATT TTAATATATA CCCTTTAA

t8-10.nt

TTGCAATCCAGATTTTAACACAAATAAGAAAAGAACTCTAAGTAAGGGGATAATTTCAAATCAAGATGCAGATTCT
GATAAAATAATAAAAAATAAATTACTTGATGATTTAATAAATTTAATAGAAAAAGCGAATGCAGATAGAGAAAAAT
ATGTAAAAAAAATGGAAGAAGAACCTTCGGATCAATATGGAATGTTGGCTGTTTTTGGAGGTATGTATTGGGCAGA
ATCACCACGGGAATTAATATCTGATACAGGTAGTGAGAGATCTATTAGGTATAGAAGGCGTGTTTATAGTATTTTA
TTAAATGCTATTGAAACTAATGAATTAAAGAAATTTTCAGAAATTAGAATACTGTCAATAAAAGTACTAGAAATAT
TTAGCCTATTTAATCTATTTGGAAGTACTCTTGATGATGTGGTTGTTCACTTATATTCCAAAAAAGATACTCTAGG
TAAACTAGATATTTCAAATTTAAAAAGACTTAAAAATTTGTTTGAAAAATTATTATCTATAAAAACAATCGTTTCA
AAGATGTCAAAACGTCTTTTATTGGATTATCAAAATAATGAAAATTTTATAAAAACAGATAACGCCAAGCTTGGAT
CTTATGTGGTTGCACTTTCCAATCAAATTCAAGAAAAATATAATGAAGCAGAAAGGCTGAAA

f8-10.aa

VRRIFMKYNT IISIFVCLFL TACNPDFNTN KKRTLSKGII SNQDADSDKI IKNKLLDDLI
NLIEKANADR EKYVKKMEEE PSDQYGMLAV FGGMYWAESP RELISDTGSE RSIRYRRRVY
SILLNAIETN ELKKFSEIRI LSIKVLEIFS LFNLFGSTLD DVVVHLYSKK DTLGKLDISN
LKRLKNLFEK LLSIKTIVSK MSKRLLLDYQ NNENFIKTDN AKLGSYVVAL SNQIQEKYNE
AERLKSEIIL IYTL

t8-10.aa

CNPDFNTNKKRTLSKGIISNQDADSDKIIKNKLLDDLINLIEKANADREKYVKKMEEEPSDQYGMLAVFGGMYWAE
SPRELISDTGSERSIRYRRRVYSILLNAIETNELKKFSEIRILSIKVLEIFSLFNLFGSTLDDVVVHLYSKKDTLG
KLDISNLKRLKNLFEKLLSIKTIVSKMSKRLLLDYQNNENFIKTDNAKLGSYVVALSNQIQEKYNEAERLK

f8-14.nt

TAATATATAT TCTTGATTAA GGGAAAGGAG AGTATTTTTA TGAAAAAAAA AATGTTTTTA
TATACATTGT TAACGATAGG ATTGATGTCT TGTAATCTAA ATTCTAAATT ATCTGGTAAT
AAAGAGGAAC AAAAAAATAA CAATGATATA AAAGAAGCTT TAAATGGCGT TCAAGAAAAT
GCTATTAATA ATTTATATGG AAATAAAAAA GAAAAAAAAG ATTTTATTAA AAATTCGGAA
AAATTGAAAG ACAAGGGTTT AGACGTGACC ACCCTCCCCT TAGAACCTGT AGTGGCGCCC
TCCGTAGAAT CTGCGGTGTC TTTAGGAGAA TCTAATAATA GGATTGGTAT ACCAACCATT
TCAATTGAGC ATAATCAAAA AAAAGAGATA AAAGAAGAGG ATTTTTTCCC TTCTACTGAG
GAAGAAAAGC AAGCGGATAA AGCAATTAAA GATATAGAGA ATCTTATTGG AGAATCTGGA

TABLE 1. Nucleotide and Amino Acid Sequences

TTTCCCGAGT TAATTGAGAA TGTGTGCTCA CTTAAACATG AATATACTTT AATAAGAAGT
GATTTTTATG ATGTGATAAC TAAGATTCAG AATAAAAAAA TATCACTAAT GAAAAATTCT
CATAATAATA GAAATAAAAT AAGGGAACTA GTACAATTGC AAAATAATTT AAAGATAGGA
GACGAACTTG ATAAAATTAT GGGTTGCATT GATACTGCAG AACAAGAGAT AAGATCTGCC
GCTTTCTTTT TTGATGAAGC TAAGGAAAGC TTAAAAGAAG GTATTATTAA AAGATTGGAA
AAAAGTAAAA ATAGGGCAGC ATCACAATTA TCTAAAAAGG CTTTAAATAG AGCAGAGGAT
GCTTTAAGGT GCTTAGAAAA TTATTCTTCT AAAAAAGGTG AGGCAATAGG AAGAAGAAGC
TTTATAAAAG AAGTTGTTGA ACAGGCAAAA AATGCTTTAA GTAAGTCTTA A

t8-14.nt

TTGTAATCTAAATTCTAAATTATCTGGTAATAAAGAGGAACAAAAAAATAACAATGATATAAAAGAAGCTTTAAAT
GGCGTTCAAGAAAATGCTATTAATAATTTATATGGAAATAAAAAAGAAAAAAAAGATTTTATTAAAAATTCGGAAA
AATTGAAAGACAAGGGTTTAGACGTGACCACCCTCCCCTTAGAACCTGTAGTGGCGCCCTCCGTAGAATCTGCGGT
GTCTTTAGGAGAATCTAATAATAGGATTGGTATACCAACCATTTCAATTGAGCATAATCAAAAAAAAGAGATAAAA
GAAGAGGATTTTTTCCCTTCTACTGAGGAAGAAAAGCAAGCGGATAAAGCAATTAAAGATATAGAGAATCTTATTG
GAGAATCTGGATTTCCCGAGTTAATTGAGAATGTGTGCTCACTTAAACATGAATATACTTTAATAAGAAGTGATTT
TTATGATGTGATAACTAAGATTCAGAATAAAAAAATATCACTAATGAAAAATTCTCATAATAATAGAAATAAAATA
AGGGAACTAGTACAATTGCAAAATAATTTAAAGATAGGAGACGAACTTGATAAAATTATGGGTTGCATTGATACTG
CAGAACAAGAGATAAGATCTGCCGCTTTCTTTTTTGATGAAGCTAAGGAAAGCTTAAAAGAAGGTATTATTAAAAG
ATTGGAAAAAAGTAAAAATAGGGCAGCATCACAATTATCTAAAAAGGCTTTAAATAGAGCAGAGGATGCTTTAAGG
TGCTTAGAAAATTATTCTTCTAAAAAAGGTGAGGCAATAGGAAGAAGAAGCTTTATAAAAGAAGTTGTTGAACAGG
CAAAAAATGCTTTAAGTAAGTCT

f8-14.aa

YIFLIKGKES IFMKKKMFLY TLLTIGLMSC NLNSKLSGNK EEQKNNNDIK EALNGVQENA
INNLYGNKKE KKDFIKNSEK LKDKGLDVTT LPLEPVVAPS VESAVSLGES NNRIGIPTIS
IEHNQKKEIK EEDFFPSTEE EKQADKAIKD IENLIGESGF PELIENVCSL KHEYTLIRSD
FYDVITKIQN KKISLMKNSH NNRNKIRELV QLQNNLKIGD ELDKIMGCID TAEQEIRSAA
FFFDEAKESL KEGIIKRLEK SKNRAASQLS KKALNRAEDA LRCLENYSSK KGEAIGRRSF
IKEVVEQAKN ALSKS

t8-14.aa

CNLNSKLSGNKEEQKNNNDIKEALNGVQENAINNLYGNKKEKKDFIKNSEKLKDKGLDVTTLPLEPVVAPSVESAV
SLGESNNRIGIPTISIEHNQKKEIKEEDFFPSTEEEKQADKAIKDIENLIGESGFPELIENVCSLKHEYTLIRSDF
YDVITKIQNKKISLMKNSHNNRNKIRELVQLQNNLKIGDELDKIMGCIDTAEQEIRSAAFFFDEAKESLKEGIIKR
LEKSKNRAASQLSKKALNRAEDALRCLENYSSKKGEAIGRRSFIKEVVEQAKNALSKS

f01A.nt BB001

TGATTAATTTTTTTTAAGGATTACGTTTTGAAAAGAAACAAAATTTGGAAAACGTTAAAACTGTTTCAAATAACTT
TACTGTTCTCATGCTCTTTTTATTCTAAATCAAACAACACAGAAGCGATAAGTGAATTACAATCAAGCCCTATTAA
ACTTGGAAAAATTAAAGTTTTACAAAAAACAGAAAAGATTGTAAGCACCCAAAATCTTCAAAACTTACAACAAAGC
CAGTTCTTTAAAAATGAAAAAGAAAAAATAATTAAAAAAATTGCACAAGAATTTGATGAGAATGAAAAATTGATTA
ATAAAATAGGTCCAAATATCGAAATGTTTGCTCAAACAATAAACACGGATATTCAAAAAATCGAACCTAATGATCA
ATTTGGAATAAATAAAACTTTATTCACAGAAAAAAAAGACAATAATATTGACTTTATGTTAAAAGACAATCGACTT
AGAAGATTATTTTACTCATCTTTAAATTATGATGAAAATAAAATCAAAAAATTAGCCACAATACTCGCGCAAACAT
CAAGCTCAAACGACTACCATTACACACTTATTGGTTTAATTTTTTGGACAGGATTTAAAATCCAAGAAGCATTTGA
AAGCGCTGTTAATATTTTAACTAAAGACGAGCAAAAGCGCCTAATTTTTAATTTTAGAACAAAAACAGTAAAAGAG
ATTCAGGAAAATTTTGAAAAACTAATGCAAGAGAGAAATTCATGGATAAAAATCGTCGATAACATTATTGGCGAAT
ATGACAAAAATACGGGAGGATGCAAAGCTGATGGAAAAATTCTCGGAGAAGTAATAAGGGTTGGATACGAGCATGA
ACTCGACTCAAATAAAAGTATGCAAATTTTAAACAATATTGAAACACCGCTAAAAACCTGTTGTGACCACATACAC
TACTAA

TABLE 1. Nucleotide and Amino Acid Sequences

t01A.nt BB001

TGCTCTTTTTATTCTAAATCAAACAACACAGAAGCGATAAGTGAATTACAATCAAGCCCTATTAAACTTGGAAAAA
TTAAAGTTTTACAAAAAACAGAAAAGATTGTAAGCACCCAAAATCTTCAAAACTTACAACAAAGCCAGTTCTTTAA
AAATGAAAAAGAAAAAATAATTAAAAAAATTGCACAAGAATTTGATGAGAATGAAAAATTGATTAATAAAATAGGT
CCAAATATCGAAATGTTTGCTCAAACAATAAACACGGATATTCAAAAAATCGAACCTAATGATCAATTTGGAATAA
ATAAAACTTTATTCACAGAAAAAAAAGACAATAATATTGACTTTATGTTAAAAGACAATCGACTTAGAAGATTATT
TTACTCATCTTTAAATTATGATGAAAATAAAATCAAAAAATTAGCCACAATACTCGCGCAAACATCAAGCTCAAAC
GACTACCATTACACACTTATTGGTTTAATTTTTTGGACAGGATTTAAAATCCAAGAAGCATTTGAAAGCGCTGTTA
ATATTTTAACTAAAGACGAGCAAAAGCGCCTAATTTTTAATTTTAGAACAAAAACAGTAAAAGAGATTCAGGAAAA
TTTTGAAAAACTAATGCAAGAGAGAAATTCATGGATAAAAATCGTCGATAACATTATTGGCGAATATGACAAAAAT
ACGGGAGGATGCAAAGCTGATGGAAAAATTCTCGGAGAAGTAATAAGGGTTGGATACGAGCATGAACTCGACTCAA
ATAAAAGTATGCAAATTTTAAACAATATTGAAACACCGCTAAAAACCTGTTGTGACCACATACACTAC

f01A.aa BB001

LIFFKDYVLKRNKIWKTLKLFQITLLFSCSFYSKSNNTEAISELQSSPIKLGKIKVLQKTEKIVSTQNLQNLQQSQ
FFKNEKEKIIKKIAQEFDENEKLINKIGPNIEMFAQTINTDIQKIEPNDQFGINKTLFTEKKDNNIDFMLKDNRLR
RLFYSSLNYDENKIKKLATILAQTSSSNDYHYTLIGLIFWTGFKIQEAFESAVNILTKDEQKRLIFNFRTKTVKEI
QENFEKLMQERNSWIKIVDNIIGEYDKNTGGCKADGKILGEVIRVGYEHELDSNKSMQILNNIETPLKTCCDHIHY

t01A.aa BB001

CSFYSKSNNTEAISELQSSPIKLGKIKVLQKTEKIVSTQNLQNLQQSQFFKNEKEKIIKKIAQEFDENEKLINKIG
PNIEMFAQTINTDIQKIEPNDQFGINKTLFTEKKDNNIDFMLKDNRLRRLFYSSLNYDENKIKKLATILAQTSSSN
DYHYTLIGLIFWTGFKIQEAFESAVNILTKDEQKRLIFNFRTKTVKEIQENFEKLMQERNSWIKIVDNIIGEYDKN
TGGCKADGKILGEVIRVGYEHELDSNKSMQILNNIETPLKTCCDHIHY

f02A.nt BB002

TAATTAATACTGGTTTTAATTTATAAGGAGAGTATTTTGAAAAAAGCCAAACTAAATATAATCAAGATTAATATTA
TTACAATGATATTAACTTTAATTTGCATCTCATGTGCACCTTTTAACAAAATCAATCCCAAGGCAAATGAAAACAC
CAAGCTTAAAAAAAACACCAGACTGAAAAAACCCGCCAATCCAGGGGAAAACATCCAAAATTTTAAAGATAAATCT
GGAGACCTTGGCGCTTCTGATGAAAAATTTATGGGAACTACCGCTTCAGAGCTAAAAGCAATTGGTAAGGAGCTAG
AAGATCGAAAAAATCAATACGATATACAAATAGCCAAAATTACTAATGAAGAATCTAACCTATTAGATACTTATAT
TCGGGCTTATGAACTAGCTAACGAAAATGAAAAAATGCTTTTAAAAAGATTTCTTCTTTCATCTTTAGATTATAAA
AAAGAAAACATAGAGACATTAAAAGAAATTCTTGAAAAACTCATAAATAATTACGAAAACGACCCCAAAATTGCTG
CAAATTTCCTTTATCGCATAGCGCTGGATATTCAATTAAAACTGGAAAAGCACTTAAAATCAATAAATGAAAAACT
GGACACTCTAAGCAAAGAAAATTCAAAAGAAGATTTAGAGGCGTTGCTAGAACAAGTAAAATCTGCCTTACAGCTA
CAAGAAAAGTTTAAAAAAACCCTAAACAAAACTCTTGAAGATTACCGTAAAAATACTAACAACATTCAAGAAAATA
AAGTACTAGCAGAACACTTTAATAAATATTACAAAGACTCTGATTCTTTACAATCTGCCTTTTATTAA

t02A.nt BB002

TGTGCACCTTTTAACAAAATCAATCCCAAGGCAAATGAAAACACCAAGCTTAAAAAAAACACCAGACTGAAAAAAC
CCGCCAATCCAGGGGAAAACATCCAAAATTTTAAAGATAAATCTGGAGACCTTGGCGCTTCTGATGAAAAATTTAT
GGGAACTACCGCTTCAGAGCTAAAAGCAATTGGTAAGGAGCTAGAAGATCGAAAAAATCAATACGATATACAAATA
GCCAAAATTACTAATGAAGAATCTAACCTATTAGATACTTATATTCGGGCTTATGAACTAGCTAACGAAAATGAAA
AAATGCTTTTAAAAAGATTTCTTCTTTCATCTTTAGATTATAAAAAAGAAAACATAGAGACATTAAAAGAAATTCT
TGAAAAACTCATAAATAATTACGAAAACGACCCCAAAATTGCTGCAAATTTCCTTTATCGCATAGCGCTGGATATT
CAATTAAAACTGGAAAAGCACTTAAAATCAATAAATGAAAAACTGGACACTCTAAGCAAAGAAAATTCAAAAGAAG
ATTTAGAGGCGTTGCTAGAACAAGTAAAATCTGCCTTACAGCTACAAGAAAAGTTTAAAAAAACCCTAAACAAAAC
TCTTGAAGATTACCGTAAAAATACTAACAACATTCAAGAAAATAAAGTACTAGCAGAACACTTTAATAAATATTAC
AAAGACTCTGATTCTTTACAATCTGCCTTTTAT

f02A.aa BB002

TABLE 1. Nucleotide and Amino Acid Sequences

LILVLIYKESILKKAKLNIIKINIITMILTLICISCAPFNKINPKANENTKLKKNTRLKKPANPGENIQNFKDKSG
DLGASDEKFMGTTASELKAIGKELEDRKNQYDIQIAKITNEESNLLDTYIRAYELANENEKMLLKRFLLSSLDYKK
ENIETLKEILEKLINNYENDPKIAANFLYRIALDIQLKLEKHLKSINEKLDTLSKENSKEDLEALLEQVKSALQLQ
EKFKKTLNKTLEDYRKNTNNIQENKVLAEHFNKYYKDSDSLQSAFY

t02A.aa BB002

CAPFNKINPKANENTKLKKNTRLKKPANPGENIQNFKDKSGDLGASDEKFMGTTASELKAIGKELEDRKNQYDIQI
AKITNEESNLLDTYIRAYELANENEKMLLKRFLLSSLDYKKENIETLKEILEKLINNYENDPKIAANFLYRIALDI
QLKLEKHLKSINEKLDTLSKENSKEDLEALLEQVKSALQLQEKFKKTLNKTLEDYRKNTNNIQENKVLAEHFNKYY
KDSDSLQSAFY

f03A.nt BB006

TGATTTAATGTAAATTTTAATTACCGCCTAAAAAAGGCTTTAAATGGTATAAAGGAAGAAGATCTAATGGTATTTA
GAACATATAAACATTTGGAACTAATAATGCTGCCCATGTTAATGCTGAGTTGCGCTTTTTTTAAGAAACCACAATC
TGTACATCAAGACAGCAATACTGGCAAACCAATAAGCGATGAAAAATTACATTTAATATCAGGCAAAATTTCAAAT
AAAAAATTGCCAATCATAAATAGTAATCATGACGTAACTTGGATAAAAACAAAGGCAATGACAATCTTAGGCGAAG
ATGGAAAAGAAATACCAGAATTTAAAAACAAATTTGGATATTCTTATATAATATCTCCTGTAAAAATGGATGGAAA
ATATAGTTATTACGCGTCATTATTAATACTTTTTGAAACAACTAAAAATGGAGATGATGAATATGAAATTGAAGAT
GTTAAATTTGTAACAGCTGGTTCCACCCTAGAACTTAAAAATTCTCTTTTAGCTGTTGAAAATTCACAAGAAGAAG
GATATGTTACTGCATACCCATTTGGAATATTGATGAGTGACGAGATTAAAAATGCTTTTAAATTAACATATAAAAA
TGGTCATTGGAATTATATGCTTGCAGATTTAACTGTCAAAAATAAACTTACTCAAGAAACTAAAATTTATAAAATT
TCTCTTAATTCAAAATTAATTATTGAATTTTTAAAAGAAGTGCTAAAAGAAAATTCTATATTAAAAGACATAGCTG
GAGATTTATTTGAAGATATATAA

t03A.nt BB006

TGCGCTTTTTTTAAGAAACCACAATCTGTACATCAAGACAGCAATACTGGCAAACCAATAAGCGATGAAAAATTAC
ATTTAATATCAGGCAAAATTTCAAATAAAAAATTGCCAATCATAAATAGTAATCATGACGTAACTTGGATAAAAAC
AAAGGCAATGACAATCTTAGGCGAAGATGGAAAAGAAATACCAGAATTTAAAAACAAATTTGGATATTCTTATATA
ATATCTCCTGTAAAAATGGATGGAAAATATAGTTATTACGCGTCATTATTAATACTTTTTGAAACAACTAAAAATG
GAGATGATGAATATGAAATTGAAGATGTTAAATTTGTAACAGCTGGTTCCACCCTAGAACTTAAAAATTCTCTTTT
AGCTGTTGAAAATTCACAAGAAGAAGGATATGTTACTGCATACCCATTTGGAATATTGATGAGTGACGAGATTAAA
AATGCTTTTAAATTAACATATAAAAATGGTCATTGGAATTATATGCTTGCAGATTTAACTGTCAAAAATAAACTTA
CTCAAGAAACTAAAATTTATAAAATTTCTCTTAATTCAAAATTAATTATTGAATTTTTAAAAGAAGTGCTAAAAGA
AAATTCTATATTAAAAGACATAGCTGGAGATTTATTTGAAGATATA

f03A.aa BB006

FNVNFNYRLKKALNGIKEEDLMVFRTYKHLELIMLPMLMLSCAFFKKPQSVHQDSNTGKPISDEKLHLISGKISNK
KLPIINSNHDVTWIKTKAMTILGEDGKEIPEFKNKFGYSYIISPVKMDGKYSYYASLLILFETTKNGDDEYEIEDV
KFVTAGSTLELKNSLLAVENSQEEGYVTAYPFGILMSDEIKNAFKLTYKNGHWNYMLADLTVKNKLTQETKIYKIS
LNSKLIIEFLKEVLKENSILKDIAGDLFEDI

t03A.aa BB006

CAFFKKPQSVHQDSNTGKPISDEKLHLISGKISNKKLPIINSNHDVTWIKTKAMTILGEDGKEIPEFKNKFGYSYI
ISPVKMDGKYSYYASLLILFETTKNGDDEYEIEDVKFVTAGSTLELKNSLLAVENSQEEGYVTAYPFGILMSDEIK
NAFKLTYKNGHWNYMLADLTVKNKLTQETKIYKISLNSKLIIEFLKEVLKENSILKDIAGDLFEDI

f04A.nt BB011

TAATTACCAAAGATAAGTAAACTTGCAAATAAAACTACACGTATTGAAAGTAGATTTGAAATTTCCATTATATTTA
TATATAATGGCACTAAATATCTGAAAATGAAGGAGAAGCGGGTGGGCAATAAAATTTTTTATATTTCAGTGGTTTT
AATTTTAATAGTTGGTTGCGACTGGGGAACTATTAAAGATAAAAGTACAGAAATTTCCAAGCTATTAAGAACGGAC

TABLE 1. Nucleotide and Amino Acid Sequences

AAAGATAAGACTAAAAATCAAGATAGAATAGAATTGGGTGAAGATAATTTTGTATCTAAAAATAATATGTCTACTA
CTGATACGGGCATTACTAGTTTAGGAAGTCTAAACAACTTGGATTTAATTAATCGTTCACAGCGGGTCAGTGAACC
ACCTATAATCTCAAATGAGAAAGCCATAGCTACTCAAGCAAAAGTAGATTTAATGAACAACATTAATGTTACTATA
ATAAACCCAAAACCAGCTCAAAATTTGGGAAATTCTTTAAACAATACTACTACTGAAGATAGTGTGAAGTTTTTAT
CAATTGAAAACCAAGAGTGGCTTATTAGTAAAAAGATTTTGCCCAGTAAGTTGGAAAATTTAGAAAGCTTTCTAAA
AACACAACACGAAAAAGAAGCTTTTAAGACGGCTAAAACTATACAAAGTCTCATTAGTAATTCCAATATGGGTAAA
GAAATTATTAAGTTTAAGGAAGAATATTACAAACTTTATAATTTGTTTGAAGGCATACAACAAAAATTCCATAGTC
AAAGGAATTCATTTATAAAAGATACTAAATTTGGGGAAAATAGACAAAAAAATGCAGTTATATTTAAATCCTTTTC
ATCTATAGAGAAAGAAATTAGAGATTTGAATTATAAGTTGNGTGAAATCCAAAGTAATTTTCAAATTGCAGATGTT
AGCTGGAATAATGCAAACTCTCTTTTAAAAGAATCTATAGAAAAATTAATTCAGGCAATTGAAAAAAGGTATGACA
ATGAGAGTAGAAAGCAAGGTCAAATTGGTGGACCTGCTAATAGATGGGATAAAAATCAAGCTGACAATTTTGCTAA
GGATGCAAAGTATAAGGCAGAACATTCAGCAAATGATTTGGAAAATGCAGCCAACTATTTTAGATATAGTTGTTCA
AATGAAAAAGAAGCTAAAAAGCTATTAGAAGAAATTAAAAAAAGATTTGTACGAATTGGTATTAGCCTATAA

t04A.nt BB011

TGCGACTGGGGAACTATTAAAGATAAAAGTACAGAAATTTCCAAGCTATTAAGAACGGACAAAGATAAGACTAAAA
ATCAAGATAGAATAGAATTGGGTGAAGATAATTTTGTATCTAAAAATAATATGTCTACTACTGATACGGGCATTAC
TAGTTTAGGAAGTCTAAACAACTTGGATTTAATTAATCGTTCACAGCGGGTCAGTGAACCACCTATAATCTCAAAT
GAGAAAGCCATAGCTACTCAAGCAAAAGTAGATTTAATGAACAACATTAATGTTACTATAATAAACCCAAAACCAG
CTCAAAATTTGGGAAATTCTTTAAACAATACTACTACTGAAGATAGTGTGAAGTTTTTATCAATTGAAAACCAAGA
GTGGCTTATTAGTAAAAAGATTTTGCCCAGTAAGTTGGAAAATTTAGAAAGCTTTCTAAAAACACAACACGAAAAA
GAAGCTTTTAAGACGGCTAAAACTATACAAAGTCTCATTAGTAATTCCAATATGGGTAAAGAAATTATTAAGTTTA
AGGAAGAATATTACAAACTTTATAATTTGTTTGAAGGCATACAACAAAAATTCCATAGTCAAAGGAATTCATTTAT
AAAAGATACTAAATTTGGGGAAAATAGACAAAAAAATGCAGTTATATTTAAATCCTTTTCATCTATAGAGAAAGAA
ATTAGAGATTTGAATTATAAGTTGNGTGAAATCCAAAGTAATTTTCAAATTGCAGATGTTAGCTGGAATAATGCAA
ACTCTCTTTTAAAAGAATCTATAGAAAAATTAATTCAGGCAATTGAAAAAAGGTATGACAATGAGAGTAGAAAGCA
AGGTCAAATTGGTGGACCTGCTAATAGATGGGATAAAAATCAAGCTGACAATTTTGCTAAGGATGCAAAGTATAAG
GCAGAACATTCAGCAAATGATTTGGAAAATGCAGCCAACTATTTTAGATATAGTTGTTCAAATGAAAAAGAAGCTA
AAAAGCTATTAGAAGAAATTAAAAAAAGATTTGTACGAATTGGTATTAGCCTA

f04A.aa BB011

LPKISKLANKTTRIESRFEISIIFIYNGTKYLKMKEKRVGNKIFYISVVLILIVGCDWGTIKDKSTEISKLLRTDK
DKTKNQDRIELGEDNFVSKNNMSTTDTGITSLGSLNNLDLINRSQRVSEPPIISNEKAIATQAKVDLMNNINVTII
NPKPAQNLGNSLNNTTTEDSVKFLSIENQEWLISKKILPSKLENLESFLKTQHEKEAFKTAKTIQSLISNSNMGKE
IIKFKEEYYKLYNLFEGIQQKFHSQRNSFIKDTKFGENRQKNAVIFKSFSSIEKEIRDLNYKLXEIQSNFQIADVS
WNNANSLLKESIEKLIQAIEKRYDNESRKQGQIGGPANRWDKNQADNFAKDAKYKAEHSANDLENAANYFRYSCSN
EKEAKKLLEEIKKRFVRIGISL

t04A.aa BB011

CDWGTIKDKSTEISKLLRTDKDKTKNQDRIELGEDNFVSKNNMSTTDTGITSLGSLNNLDLINRSQRVSEPPIISN
EKAIATQAKVDLMNNINVTIINPKPAQNLGNSLNNTTTEDSVKFLSIENQEWLISKKILPSKLENLESFLKTQHEK
EAFKTAKTIQSLISNSNMGKEIIKFKEEYYKLYNLFEGIQQKFHSQRNSFIKDTKFGENRQKNAVIFKSFSSIEKE
IRDLNYKLXEIQSNFQIADVSWNNANSLLKESIEKLIQAIEKRYDNESRKQGQIGGPANRWDKNQADNFAKDAKYK
AEHSANDLENAANYFRYSCSNEKEAKKLLEEIKKRFVRIGISL

f05A.nt BB009

TAAATAAATTGTAGGATAAAAATGAAACAAAAATACGAAAACTATTTTAAAAAAAGATTAATTTTAAACCTATTAA
TATTTTTACTACTAGCATGCTCAAGCGAATCCATATTTTCACAATTAGGAAATCTGCAAAAAATAAAACATGAATA
CAATATTTTGGGCAGTTCAAGTCCAAGAGGAATTTCTCTAGTAGGAGAAACTCTCTACATTGCAGCCATGCATTTA
TTTAAAAAAGAAAACGGCAAGATTGAAAAAATTGATTTGAGCAATTCTTATGAGTTTATAAACGACATTGTAAATA
TATCTGGAAAAACCTATCTTTTAGCGCAAAACAAAGAAGAAGAATTAGAAGTTTGCGAGCTAAATGGAAAAGATTG
GACATTAAAATTTAAAAAACCGCTAAAAGCATATAAATTCTTAAAATCCGTAGAAGAGATGGCGTAA

TABLE 1. Nucleotide and Amino Acid Sequences

t05A.nt BB009

TGCTCAAGCGAATCCATATTTTCACAATTAGGAAATCTGCAAAAAATAAAACATGAATACAATATTTTGGGCAGTT
CAAGTCCAAGAGGAATTTCTCTAGTAGGAGAAACTCTCTACATTGCAGCCATGCATTTATTTAAAAAAGAAAACGG
CAAGATTGAAAAAATTGATTTGAGCAATTCTTATGAGTTTATAAACGACATTGTAAATATATCTGGAAAAAACCTAT
CTTTTAGCGCAAAACAAAGAAGAAGAATTAGAAGTTTGCGAGCTAAATGGAAAAGATTGGACATTAAAATTTAAAA
AACCGCTAAAAGCATATAAATTCTTAAAATCCGTAGAAGAGATGGCG

f05A.aa BB009

INCRIKMKQKYENYFKKRLILNLLIFLLLACSSESIFSQLGNLQKIKHEYNILGSSSPRGISLVGETLYIAAMHLF
KKENGKIEKIDLSNSYEFINDIVNISGKTYLLAQNKEEELEVCELNGKDWTLKFKKPLKAYKFLKSVEEMA

t05A.aa BB009

CSSESIFSQLGNLQKIKHEYNILGSSSPRGISLVGETLYIAAMHLFKKENGKIEKIDLSNSYEFINDIVNISGKTY
LLAQNKEEELEVCELNGKDWTLKFKKPLKAYKFLKSVEEMA

f06A.nt BB014

TAAGGAGCATATATGAGGATTTTGGTTGGCGTTTGTATAATAGCATTGGCTTTATTGGGTTGTTATTTGCCTGATA
ATCAGGAACAAGCTGTTCAAACTTTTTTTGAGAATTCGGAAAGTAGTGATATGGGTTCCGATGAGATTGTTACTGA
AGGCATATTTTCTAGTTTAAAATTATATGCGTCTGAACATCGTTTATTGGTTGAGATAAAAAAGACTTTAATTAGT
TTAAAAGATCCTAATTATCNNGNTGTAGTACNCCCAGTGAGTGACTATAATGAGGAGTATTTTAATAAATTCTTTC
TAGATTTAGGGTCTGAGCAATCTAAAGACCTGATTAAGTTGTTTATTATGGTAAAAAATGAGCAGAACAATAATAA
ATTTATGCGTATAGTTCGTTGGCTGTATTCATGTATAGAGGAGTTATATTCTCTAGATATTAAGTATTCTGGCGAG
GGAGCCATGAGTATAATCGTAATATGCCTAGACCCACTGCTTATGAACAATATTTAAAAGTGAAGAGGTATGATT
ATAATAGCCCAGTTTCTATTTTACCTACATAA

t06A.nt BB014

TGTTATTTGCCTGATAATCAGGAACAAGCTGTTCAAACTTTTTTTGAGAATTCGGAAAGTAGTGATATGGGTTCCG
ATGAGATTGTTACTGAAGGCATATTTTCTAGTTTAAAATTATATGCGTCTGAACATCGTTTATTGGTTGAGATAAA
AAAGACTTTAATTAGTTTAAAAGATCCTAATTATCNNGNTGTAGTACNCCCAGTGAGTGACTATAATGAGGAGTAT
TTTAATAAATTCTTTCTAGATTTAGGGTCTGAGCAATCTAAAGACCTGATTAAGTTGTTTATTATGGTAAAAAATG
AGCAGAACAATAATAAATTTATGCGTATAGTTCGTTGGCTGTATTCATGTATAGAGGAGTTATATTCTCTAGATAT
TAAGTATTCTGGCGAGGGGAGCCATGAGTATAATCGTAATATGCCTAGACCCACTGCTTATGAACAATATTTAAAA
GTGAAGAGGTATGATTATAAT

f06A.aa BB014

GAYMRILVGVCIIALALLGCYLPDNQEQAVQTFFENSESSDMGSDEIVTEGIFSSLKLYASEHRLLVEIKKTLISL
KDPNYXXVVXPVSDYNEEYFNKFFLDLGSEQSKDLIKLFIMVKNEQNNNKFMRIVRWLYSCIEELYSLDIKYSGEG
SHEYNRNMPRPTAYEQYLKVKRYDYNSPVSILPT

t06A.aa BB014

CYLPDNQEQAVQTFFENSESSDMGSDEIVTEGIFSSLKLYASEHRLLVEIKKTLISLKDPNYXXVVXPVSDYNEEY
FNKFFLDLGSEQSKDLIKLFIMVKNEQNNNKFMRIVRWLYSCIEELYSLDIKYSGEGSHEYNRNMPRPTAYEQYLK
VKRYDYN

f07A.nt BB023

TAAAGTATTTTATTTTTTTTATTATCCACTGTTCTTTTTGCTCAAGAGACTGATGGATTAGCAGAGGGTTCTAAAA
GGGCAGAGCCTGGAGAATTAGTTTTAGATTTTGCCGAGCTTGCAAGAGATCCAAGTTCAACTAGACTTGATCTTAC

TABLE 1. Nucleotide and Amino Acid Sequences

AAATTATGTTGATTATGTATATTCGGGCGCTTCTGGTATTGTTAAGCCGGAAGATATGGTTGTAGATCTTGGGATA
AATAATTGGAGCGTTTTACTTACTCCTTCTGCAAGGTTGCAGGCTTACGTTAAAAATTCAGTTGTTGCGCCCGCTG
TTGTTAAGAGTGAGTCAAAAAGGTACGCAGGTGATACTATTTTAGGGGTAAGAGTTTTGTTTCCAAGCTATTCTCA
ATCATCTGCTATGATTATGCCACCATTTAAAATTCCTTTTTATTCAGGGGAAAGTGGCAATCAATTTTTAGGCAAA
GGTCTTATTGATAACATTAAAACCATGAAAGAAATTAAGGTATCTGTTTATAGTTTAGGGTATGAGATAGATCTTG
AGGTTTTATTTGAAGATATGAATGNCATGGAATATGCTTNNTCTATGGGTACTTTAAAGTTTAAAGGGTGGGCTGA
TTTAATTTGGTCAAATCCTAACTATATTCCTAATATATCATCCAGAATTATTAAAGACGATGTTCCAAATTATCCT
CTTGCTTCAAGTAAAATGAGATTTAAGGCTTTTAGAGTTTCAAAGTCACACAGTTCAAAAGAGCAAAATTTCATCT
TTTATGTTAAAGATTTAAGAGTTCTTTATGATAAGTTGAGTGTTTCAATAGATTCTGATATTGACAGTGAGTCTGT
ATTTAAAGTTTATGAGACTAGCGGAACTGAATCCCTTCGTAAATTAAAGGCACACGNAACNTTTAAAAGNGTTTTA
AAGCTTAGAGAAAAAATTTCTATGCCTGAAGGCTCTTTCCAAAACTTTGTAGAAAAGATTGAGAGTGAAAAACCTG
AAGAATCATCTCCGAAAAATTAG

t07A.nt BB023

GAGGGTTCTAAAAGGGCAGAGCCTGGAGAATTAGTTTTAGATTTTGCCGAGCTTGCAAGAGATCCAAGTTCAACTA
GACTTGATCTTACAAATTATGTTGATTATGTATATTCGGGCGCTTCTGGTATTGTTAAGCCGGAAGATATGGTTGT
AGATCTTGGGATAAATAATTGGAGCGTTTTACTTACTCCTTCTGCAAGGTTGCAGGCTTACGTTAAAAATTCAGTT
GTTGCGCCCGCTGTTGTTAAGAGTGAGTCAAAAAGGTACGCAGGTGATACTATTTTAGGGGTAAGAGTTTTGTTTC
CAAGCTATTCTCAATCATCTGCTATGATTATGCCACCATTTAAAATTCCTTTTTATTCAGGGGAAAGTGGCAATCA
ATTTTTAGGCAAAGGTCTTATTGATAACATTAAAACCATGAAAGAAATTAAGGTATCTGTTTATAGTTTAGGGTAT
GAGATAGATCTTGAGGTTTTATTTGAAGATATGAATGNCATGGAATATGCTTNNTCTATGGGTACTTTAAAGTTTA
AAGGGTGGGCTGATTTAATTTGGTCAAATCCTAACTATATTCCTAATATATCATCCAGAATTATTAAAGACGATGT
TCCAAATTATCCTCTTGCTTCAAGTAAAATGAGATTTAAGGCTTTTAGAGTTTCAAAGTCACACAGTTCAAAAGAG
CAAAATTTCATCTTTTATGTTAAAGATTTAAGAGTTCTTTATGATAAGTTGAGTGTTTCAATAGATTCTGATATTG
ACAGTGAGTCTGTATTTAAAGTTTATGAGACTAGCGGAACTGAATCCCTTCGTAAATTAAAGGCACACGNAACNTT
TAAAAGNGTTTTAAAGCTTAGAGAAAAAATTTCTATGCCTGAAGGCTCTTTCCAAAACTTTGTAGAAAAGATTGAG
AGTGAAAAACCTGAAGAATCATCTCCGAAAAAT

f07A.aa BB023

SILFFLLSTVLFAQETDGLAEGSKRAEPGELVLDFAELARDPSSTRLDLTNYVDYVYSGASGIVKPEDMVVDLGIN
NWSVLLTPSARLQAYVKNSVVAPAVVKSESKRYAGDTILGVRVLFPSYSQSSAMIMPPFKIPFYSGESGNQFLGKG
LIDNIKTMKEIKVSVYSLGYEIDLEVLFEDMNXMEYAXSMGTLKFKGWADLIWSNPNYIPNISSRIIKDDVPNYPL
ASSKMRFKAFRVSKSHSSKEQNFIFYVKDLRVLYDKLSVSIDSDIDSESVFKVYETSGTESLRKLKAHXTFKXVLK
LREKISMPEGSFQNFVEKIESEKPEESSPKN

t07A.aa BB023

EGSKRAEPGELVLDFAELARDPSSTRLDLTNYVDYVYSGASGIVKPEDMVVDLGINNWSVLLTPSARLQAYVKNSV
VAPAVVKSESKRYAGDTILGVRVLFPSYSQSSAMIMPPFKIPFYSGESGNQFLGKGLIDNIKTMKEIKVSVYSLGY
EIDLEVLFEDMNXMEYAXSMGTLKFKGWADLIWSNPNYIPNISSRIIKDDVPNYPLASSKMRFKAFRVSKSHSSKE
QNFIFYVKDLRVLYDKLSVSIDSDIDSESVFKVYETSGTESLRKLKAHXTFKXVLKLREKISMPEGSFQNFVEKIE
SEKPEESSPKN

f08A.nt BB024

TGAATATTAATAATAAAAAAAGGAGTAACAATGAAAATCATCAACATATTATTTTGTTTATTTTTACTAATGCTAA
ACGGCTGTAATTCTAATGATAATGACACTTTAAAAAACAATGCCCAACAAACAAAAAGACGGGGAAAGCGTGATTT
AACCCAAAAAGAAACAACACAAGAAAAACCAAAATCTAAAGAAGAACTACTTAGAGAAAAGCTATCTGACGATCAA
AAAACACATCTTGACTGGTTAAAACCCGCTTTAACTGGTGCTGGAGAATTTGACAAATTCTTAGAAAATGATGATG
ATAAAATAAAATCAGCACTTGATCATATAAAAACTCAACTTGATAGTTGTAATGGTGATCAAGCAGAACAACAAAA
AACCACTTTCAAAACTGTGGTTACAGAATTCTTTAAAAATGGTGATATAGATAATTTTGCAACTGGAGCGGTTAGT
AACTGCAATAATGGTGGCTAA

t08A.nt BB024

TABLE 1. Nucleotide and Amino Acid Sequences

TGTAATTCTAATGATAATGACACTTTAAAAAACAATGCCCAACAAACAAAAAGACGGGGAAAGCGTGATTTAACCC
AAAAAGAAACAACACAAGAAAAACCAAAATCTAAAGAAGAACTACTTAGAGAAAAGCTATCTGACGATCAAAAAAC
ACATCTTGACTGGTTAAAACCCGCTTTAACTGGTGCTGGAGAATTTGACAAATTCTTAGAAAATGATGATGATAAA
ATAAAATCAGCACTTGATCATATAAAAACTCAACTTGATAGTTGTAATGGTGATCAAGCAGAACAACAAAAAAACCA
CTTTCAAAACTGTGGTTACAGAATTCTTTAAAAATGGTGATATAGATAATTTTGCAACTGGAGCGGTTAGTAACTG
CAATAATGGTGGC

f08A.aa BB024

ILIIKKGVTMKIINILFCLFLLMLNGCNSNDNDTLKNNAQQTKRRGKRDLTQKETTQEKPKSKEELLREKLSDDQK
THLDWLKPALTGAGEFDKFLENDDDKIKSALDHIKTQLDSCNGDQAEQQKTTFKTVVTEFFKNGDIDNFATGAVSN
CNNGG

t08A.aa BB024

CNSNDNDTLKNNAQQTKRRGKRDL51TQKETTQEKPKSKEELLREKLSDDQKTHLDWLKPALTGAGEFDKFLENDD
DKIKSALDHIKTQLDSCNGDQAEQQKTTFKTVVTEFFKNGDIDNFATGAVSNCNNGG

f09A.nt BB025

TGAATATTAATAATAAAAAAAGGAATAATAATGAAAATTATCAACATATTATTTTGTTTATTTTTACTAATGCTAA
ACGGCTGTAATTCTAATGATACTAATAATAGCCAAACAAAAAGTAGACAAAAACGTGATTTAACCCAAAAAGAAGC
AACACAAGAAAAACCTAAATCTAAAGAAGAACTTCTTAGAGAAAAGCTAAATGATAATCAAAAAACACACCTTGAC
TGGTTAAAAGAAGCTCTGGGCAATGATGGAGAATTTAATAAATTTTTAGGATATGATGAAAGCAAAATAAAATCTG
CACTTGATCATATAAAGAGTGAACTTGACAGTTGTACTGGAGATAAGGTTGAAAATAAAAATACCTTCAAGCAGGT
CGTTCAGGAGGCCCTTAAAGGGGGCATAGACGGCTTTGAAAATACTGCAAGTAGTACGTGCAAAAATTCATAA

t09A.nt BB025

TGTAATTCTAATGATACTAATAATAGCCAAACAAAAAGTAGACAAAAACGTGATTTAACCCAAAAAGAAGCAACAC
AAGAAAAACCTAAATCTAAAGAAGAACTTCTTAGAGAAAAGCTAAATGATAATCAAAAAACACACCTTGACTGGTT
AAAAGAAGCTCTGGGCAATGATGGAGAATTTAATAAATTTTTAGGATATGATGAAAGCAAAATAAAATCTGCACTT
GATCATATAAAGAGTGAACTTGACAGTTGTACTGGAGATAAGGTTGAAAATAAAAATACCTTCAAGCAGGTCGTTC
AGGAGGCCCTTAAAGGGGGCATAGACGGCTTTGAAAATACTGCAAGTAGTACGTGCAAAAATTCA

f09A.aa BB025

ILIIKKGIIMKIINILFCLFLLMLNGCNSNDTNNSQTKSRQKRDLTQKEATQEKPKSKEELLREKLNDNQKTHLDW
LKEALGNDGEFNKFLGYDESKIKSALDHIKSELDSCTGDKVENKNTFKQVVQEALKGGIDGFENTASSTCKNS

t09A.aa BB025

CNSNDTNNSQTKSRQKRDLTQKEA51TQEKPKSKEELLREKLNDNQKTHLDWLKEALGNDGEFNKFLGYDESKIKS
ALDHIKSELDSCTGDKVENKNTFKQVVQEALKGGIDGFENTASSTCKNS
1

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

Query	GenSeq Access No.	GenSeq Gene Description	BLAST Score	BLAST P-Value
f01A.aa	gil2690256	(AE000790) antigen, P35, putative [Borrelia burgdorferi]	1523	5.90E-206
f02A.aa	gil2690286	(AE000790) B. burgdorferi predicted coding region BBA69 [Borrelia	1320	2.10E-174
f02A.aa	gil2690285	(AE000790) B. burgdorferi predicted coding region BBA68 [Borrelia	278	7.50E-71
f02A.aa	gil2690105	(AE000789) B. burgdorferi predicted coding region BBI38 [Borrelia	151	8.40E-54
f02A.aa	gil2690092	(AE000789) antigen, P35, putative [Borrelia burgdorferi]	151	2.70E-48
f02A.aa	gil2690183	(AE000787) antigen, P35, putative [Borrelia burgdorferi]	155	4.20E-22
f02A.aa	gil2690106	(AE000789) B. burgdorferi predicted coding region BBI39 [Borrelia	154	1.30E-21
f03A.aa	gil2688051	(AE001127) antigen, S2, putative [Borrelia burgdorferi]	1223	7.60E-164
f03A.aa	gil1063419	S2 gene product [Borrelia burgdorferi]	116	3.00E-22
f03A.aa	gil2690227	(AE000790) antigen, S2 [Borrelia burgdorferi] >pirlD70207lD70207	116	9.70E-22
f03A.aa	gil2690128	(AE000788) protein p23 [Borrelia burgdorferi] >pirlC70257lC70257	110	5.70E-19
f03A.aa	gil2689956	(AE000785) protein p23 [Borrelia burgdorferi] >pirlD70225lD70225	104	7.90E-15
f04A.aa	gil2690078	(AE000784) B. burgdorferi predicted coding region BBH18 [Borrelia	1873	5.60E-250
f04A.aa	gil2690192	(AE000787) B. burgdorferi predicted coding region BBJ13 [Borrelia	167	1.40E-15
f05A.aa	gil2687919	(AE001117) B. burgdorferi predicted coding region BB0028 [Borrelia	696	4.20E-92
f06A.aa	gil2690129	(AE000788) outer membrane protein [Borrelia burgdorferi]	884	4.80E-124
f06A.aa	gil2690089	(AE000789) conserved hypothetical protein [Borrelia burgdorferi]	731	2.20E-118
f06A.aa	gil520783	unknown [Borrelia burgdorferi] >gil551742 unknown [Borrelia	337	4.30E-58
f07A.aa	gil2688608	(AE001168) flagellar filament outer layer protein (flaA) [Borrelia	1668	2.50E-224
f07A.aa	gil1575447	FlaA protein [Borrelia burgdorferi] >gil1019754 orf [Borrelia	1645	3.60E-221
f07A.aa	gil152896	flagellar filament surface antigen [Spirochaeta aurantia]	144	1.70E-38
f07A.aa	gil155059	endoflagellar sheath protein [Treponema pallidum]	139	3.80E-28
f07A.aa	gil433524	flagellin FlaA1 [Serpulina hyodysenteriae] >gil904393 endoflagellar	119	3.00E-26
f07A.aa	pirlA32814l A32814	flagellar filament surface antigen - Spirochaeta aurantia	116	9.40E-11
f08A.aa	gil1209837	lipoprotein [Borrelia burgdorferi]	508	2.10E-78
f08A.aa	gil2121280	(AF000270) lipoprotein [Borrelia burgdorferi] >gil3095109	547	4.00E-70
f08A.aa	gil1209873	lipoprotein [Borrelia burgdorferi]	303	3.70E-51

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f08A.aa	gil1209843	lipoprotein [Borrelia burgdorferi]	395	2.20E-49
f08A.aa	gil1209849	lipoprotein [Borrelia burgdorferi]	219	2.60E-27
f08A.aa	gil3095105	(AF046998) 2.9-8 lipoprotein [Borrelia burgdorferi]	234	4.30E-27
f08A.aa	gil1209831	lipoprotein [Borrelia burgdorferi]	209	1.10E-22
f08A.aa	gil3095107	(AF046999) 2.9-9 lipoprotein [Borrelia burgdorferi]	200	1.80E-22
f08A.aa	gil1209857	lipoprotein [Borrelia burgdorferi]	200	2.50E-21
f08A.aa	gnllPIDle268244	surface-exposed lipoprotein [Borrelia afzelii]	142	1.80E-11
f09A.aa	gil1209843	lipoprotein [Borrelia burgdorferi]	453	8.60E-67
f09A.aa	gil2121280	(AF000270) lipoprotein [Borrelia burgdorferi] >gil3095109	379	1.00E-56
f09A.aa	gil1209873	lipoprotein [Borrelia burgdorferi]	282	1.10E-45
f09A.aa	gil1209837	lipoprotein [Borrelia burgdorferi]	357	7.10E-44
f09A.aa	gil1209849	lipoprotein [Borrelia burgdorferi]	143	1.60E-13
f09A.aa	gnllPIDle268244	surface-exposed lipoprotein [Borrelia afzelii]	111	3.60E-13
f09A.aa	gil3095105	(AF046998) 2.9-8 lipoprotein [Borrelia burgdorferi]	142	5.40E-13
f101.aa	gil2688708	(AE001176) conserved hypothetical protein [Borrelia burgdorferi]	1099	4.50E-152
f105.aa	gil2688693	(AE001175) B. burgdorferi predicted coding region BB0758 [Borrelia	1276	2.20E-177
f11-12.aa	gil2690139	(AE000788) B. burgdorferi predicted coding region BBK01 [Borrelia	1473	4.70E-193
f11-12.aa	gil2690030	(AE000786) B. burgdorferi predicted coding region BBG01 [Borrelia	1066	1.40E-138
f11-12.aa	gil2690074	(AE000784) B. burgdorferi predicted coding region BBH37 [Borrelia	173	6.20E-93
f11-12.aa	gil2690188	(AE000787) B. burgdorferi predicted coding region BBJ08 [Borrelia	192	2.70E-75
f11-4.aa	gil2690150	(AE000788) B. burgdorferi predicted coding region BBK12 [Borrelia	1144	2.70E-147
f11-4.aa	gil2690145	(AE000788) B. burgdorferi predicted coding region BBK07 [Borrelia	852	5.70E-127
f11-4.aa	gil2690095	(AE000789) B. burgdorferi predicted coding region BBI10 [Borrelia	153	1.30E-34
f11-4.aa	gil2690197	(AE000787) B. burgdorferi predicted coding region BBJ31 [Borrelia	115	1.40E-12
f11-4.aa	gil2690219	(AE000787) B. burgdorferi predicted coding region BBJ45 [Borrelia	115	1.40E-12
f112-1.aa	gil2690054	(AE000784) B. burgdorferi predicted coding region BBH06 [Borrelia	573	7.00E-75
f12.aa	gil2688785	(AE001182) B. burgdorferi predicted coding region BB0838 [Borrelia	6008	0
f129.aa	gil2688685	(AE001174) B. burgdorferi predicted coding region BB0739 [Borrelia	987	6.20E-133
f14-8.aa	gil2689955	(AE000785) antigen, P35, putative [Borrelia burgdorferi]	385	2.70E-75

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f14-8.aa	gi|2690120	(AE000789) B. burgdorferi predicted coding region BBI34 [Borrelia	330	2.60E-66
f14-8.aa	gi|2690052	(AE000784) antigen, P35, putative [Borrelia burgdorferi]	287	4.00E-64
f14-8.aa	gi|2690100	(AE000789) B. burgdorferi predicted coding region BBI16 [Borrelia	172	1.10E-38
f14-8.aa	gi|2690115	(AE000789) B. burgdorferi predicted coding region BBI28 [Borrelia	173	1.70E-28
f14-8.aa	gi|2690116	(AE000789) B. burgdorferi predicted coding region BBI29 [Borrelia	163	8.20E-24
f14-8.aa	gi|2690207	(AE000787) B. burgdorferi predicted coding region BBJ02 [Borrelia	220	1.90E-23
f14-8.aa	gi|2690099	(AE000789) B. burgdorferi predicted coding region BBI15 [Borrelia	140	3.60E-12
f14-8.aa	gi|2690125	(AE000788) antigen, P35, putative [Borrelia burgdorferi]	111	1.00E-11
f142.aa	gi|2688655	(AE001172) glutamate transporter (gltP) [Borrelia burgdorferi]	2233	7.19999999999982e-311
f142.aa	gnl|PID|e233874	hypothetical protein [Bacillus subtilis] >gnl|PID|e1182902	727	2.60E-156
f142.aa	gnl|PID|d1016231	Proton/sodium-glutamate symport protein (Glutamate-aspartate	762	6.60E-146
f142.aa	gi|1574711	proton glutamate symport protein (gltP) [Haemophilus influenzae]	903	2.10E-131
f142.aa	gi|2983758	(AE000735) proton/sodium-glutamate symport protein [Aquifex	111	8.40E-36
f142.aa	gi|143000	proton glutamate symport protein [Bacillus stearothermophilus]	125	1.20E-30
f142.aa	gi|143002	proton glutamate symport protein [Bacillus caldotenax]	125	1.90E-28
f142.aa	gnl|PID|e1183024	proton/sodium-glutamate symport protein [Bacillus subtilis]	122	2.20E-25
f142.aa	gnl|PID|d1022697	glutamate transporter [Caenorhabditis elegans]	121	1.80E-22
f142.aa	gi|1255318	coded for by C. elegans cDNA cm08h9; coded for by C. elegans cDNA	121	2.10E-22
f142.aa	gi|2388712	(AF017105) amino acid transporter [Chlamydia psittaci]	135	3.60E-22
f142.aa	gi|2655021	(AF018259) glutamate transporter 5A [Ambystoma tigrinum]	125	7.70E-22
f142.aa	gnl|PID|e149542	gluT-R gene product [Clostridium perfringens]	199	4.60E-21
f142.aa	gi|396412	gltP [Escherichia coli] >gi|147160 proton-glutamate [Escherichia	109	7.90E-21
f147.aa	gi|2688656	(AE001172) NADH oxidase, water-forming (nox) [Borrelia burgdorferi]	2245	7.20E-303
f147.aa	gi|642030	NADH oxidase [Serpulina hyodysenteriae]	318	9.20E-105
f147.aa	gi|2650234	(AE001077) NADH oxidase (noxA-2) [Archaeoglobus fulgidus]	303	2.90E-93

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f147.aa	gi|2792490	(AF041467) coenzyme A disulfide reductase [Staphylococcus aureus]	194	2.60E-90
f147.aa	gi|2650383	(AE001088) NADH oxidase (noxA-1) [Archaeoglobus fulgidus]	286	3.30E-88
f147.aa	gnl|PID|d1009320	H2O-forming NADH Oxidase [Streptococcus mutans]	369	4.30E-85
f147.aa	gi|49023	NADH peroxidase [Enterococcus faecalis] >pir|S18332|S18332 NADH	638	3.20E-83
f147.aa	gi|1591361	NADH oxidase (nox) [Methanococcus jannaschii] >pir|A64381|A64381	535	4.80E-83
f147.aa	gi|2622461	(AE000898) NADH oxidase [Methanobacterium thermoautotrophicum]	303	8.40E-72
f147.aa	gi|47045	NADH oxidase [Enterococcus faecalis] >pir|S26965|S26965 NADH oxidase	547	8.80E-71
f147.aa	gi|2650233	(AE001077) NADH oxidase (noxA-3) [Archaeoglobus fulgidus]	312	2.00E-63
f147.aa	gi|1674132	(AE000044) Mycoplasma pneumoniae, NADH oxidase; similar to	175	7.00E-61
f147.aa	gi|1045969	NADH oxidase [Mycoplasma genitalium] >pir|D64230|D64230 NADH	164	4.10E-51
f147.aa	gi|2648692	(AE000975) NADH oxidase (noxA-5) [Archaeoglobus fulgidus]	143	2.00E-40
f147.aa	gi|2983379	(AE000709) NADH oxidase [Aquifex aeolicus]	162	5.50E-30
f150.aa	gi|2688659	(AE001172) conserved hypothetical protein [Borrelia burgdorferi]	1319	2.70E-179
f150.aa	gi|2983887	(AE000743) hypothetical protein [Aquifex aeolicus]	238	1.40E-25
f150.aa	gi|2581796	(AF001974) putative TrkA [Thermoanaerobacter ethanolicus]	175	5.80E-23
f150.aa	gi|1377829	unknown [Bacillus subtilis] >gnl|PID|d1007628 orf4 [Bacillus	212	1.50E-21
f150.aa	gnl|PID|e1185982	similar to hypothetical proteins [Bacillus subtilis]	181	6.00E-17
f150.aa	gnl|PID|d1011497	hypothetical protein [Synechocystis sp.] >pir|S75999|S75999	128	3.70E-11
f152.aa	gi|2688660	(AE001172) K+ transport protein (ntpJ) [Borrelia burgdorferi]	2200	2.40000000001213e-313
f152.aa	gi|2983882	(AE000743) K+ transport protein homolog [Aquifex aeolicus]	239	3.60E-106
f152.aa	gnl|PID|e1184940	similar to Na+-transporting ATP synthase [Bacillus subtilis]	158	6.60E-64
f152.aa	gnl|PID|e1185983	similar to Na+-transporting ATP synthase [Bacillus subtilis]	131	3.40E-62
f152.aa	gnl|PID|d1018749	Na+ -ATPase subunit J [Synechocystis sp.] >pir|S75455|S75455	141	1.70E-55

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f152.aa	gnl|PID|d10 04799	Na+ -ATPase subunit J [Enterococcus hirae]	209	4.00E-45
f152.aa	gi|2581795	(AF001974) putative TrkG [Thermoanaerobacter ethanolicus]	149	2.20E-29
f152.aa	gi|1674061	(AE000036) Mycoplasma pneumoniae, Na(+) translocating ATPase	104	4.00E-28
f152.aa	gi|1046024	Na+ ATPase subunit J [Mycoplasma genitalium] >pir|F64235|F64235 Na+	114	2.80E-27
f152.aa	gi|567062	HKT1 [Triticum aestivum] >pir|S47582|S47582 high-affinity potassium	137	2.00E-17
f154.aa	gi|2688664	(AE001172) B. burgdorferi predicted coding region BB0722 [Borrelia	2456	0
f157.aa	gi|2688641	(AE001171) rod shape-determining protein (mreB-2) [Borrelia	2300	0
f157.aa	gi|143657	endospore forming protein [Bacillus subtilis]	224	2.60E-61
f157.aa	gi|580938	internal open reading frame (AA 1-290) [Bacillus subtilis]	224	2.60E-61
f157.aa	gi|2982781	(AE000670) rod shape determining protein RodA [Aquifex aeolicus]	333	5.40E-61
f157.aa	gi|580937	spoVE gene product (AA 1-366) [Bacillus subtilis] >gnl|PID|e1185111	224	7.70E-59
f157.aa	gi|147695	rod-shape-determining protein [Escherichia coli] >gi|1778551	340	6.10E-58
f157.aa	gnl|PID|e32 8589	sfr [Streptomyces coelicolor]	362	6.40E-58
f157.aa	gi|1572976	rod shape-determining protein (mreB) [Haemophilus influenzae]	307	4.00E-56
f157.aa	gnl|PID|e11 85075	similar to cell-division protein [Bacillus subtilis]	203	2.60E-45
f157.aa	gi|1469784	putative cell division protein ftsW [Enterococcus hirae]	231	6.90E-45
f157.aa	gi|1016213	strong sequence similarity to FtsW, RodA, and SpoV-E [Cyanophora	206	3.00E-41
f157.aa	gnl|PID|d10 19002	rod-shape-determining protein [Synechocystis sp.]	184	1.60E-38
f157.aa	gi|146039	cell division protein [Escherichia coli] >gi|40857 FtsW protein	104	8.30E-35
f157.aa	gi|1574692	cell division protein (ftsW) [Haemophilus influenzae]	114	3.30E-33
f157.aa	gi|1165286	FtsW [Borrelia burgdorferi] >gi|2688164 (AE001137) cell division	170	6.20E-32
f17-6.aa	gi|2690100	(AE000789) B. burgdorferi predicted coding region BBI16 [Borrelia	1250	1.70E-164
f17-6.aa	gi|2690120	(AE000789) B. burgdorferi predicted coding region BBI34 [Borrelia	142	3.40E-59
f17-6.aa	gi|2690115	(AE000789) B. burgdorferi predicted coding region BBI28 [Borrelia	447	6.70E-56
f17-6.aa	gi|2690052	(AE000784) antigen, P35, putative [Borrelia burgdorferi]	182	1.10E-34
f17-6.aa	gi|2689955	(AE000785) antigen, P35, putative [Borrelia burgdorferi]	196	6.60E-34

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f17-6.aa	gil2690114	(AE000789) B. burgdorferi predicted coding region BBI27 [Borrelia	176	1.00E-16
f17-6.aa	gnllPIDld10 12343	gene required for phosphoylation of oligosaccharides/ has	178	2.80E-15
f17-6.aa	gil2690207	(AE000787) B. burgdorferi predicted coding region BBJ02 [Borrelia	114	3.50E-13
f17-6.aa	gnllPIDle32 9895	(AJ000496) cyclic nucleotide-gated channel beta subunit	152	1.10E-11
f170.aa	gil2688652	(AE001171) B. burgdorferi predicted coding region BB0708 [Borrelia	524	2.60E-73
f186.aa	gil2688622	(AE001169) B. burgdorferi predicted coding region BB0689 [Borrelia	792	1.80E-105
f186.aa	gil2688622	(AE001169) B. burgdorferi predicted coding region BB0689 [Borrelia	792	1.80E-105
f19-2.aa	gil2690120	(AE000789) B. burgdorferi predicted coding region BBI34 [Borrelia	1341	2.70E-177
f19-2.aa	gil2689955	(AE000785) antigen, P35, putative [Borrelia burgdorferi]	347	7.00E-53
f19-2.aa	gil2690052	(AE000784) antigen, P35, putative [Borrelia burgdorferi]	254	7.70E-53
f19-2.aa	gil2690100	(AE000789) B. burgdorferi predicted coding region BBI16 [Borrelia	142	6.60E-50
f19-2.aa	gil2690115	(AE000789) B. burgdorferi predicted coding region BBI28 [Borrelia	144	7.60E-34
f19-2.aa	gil2690116	(AE000789) B. burgdorferi predicted coding region BBI29 [Borrelia	183	2.20E-21
f19-2.aa	gil2690207	(AE000787) B. burgdorferi predicted coding region BBJ02 [Borrelia	171	2.00E-16
f19-2.aa	gil2690099	(AE000789) B. burgdorferi predicted coding region BBI15 [Borrelia	166	1.20E-15
f19-2.aa	gil2690125	(AE000788) antigen, P35, putative [Borrelia burgdorferi]	122	5.70E-14
f19-4.aa	gil2690116	(AE000789) B. burgdorferi predicted coding region BBI29 [Borrelia	1129	1.30E-150
f19-4.aa	gil2690099	(AE000789) B. burgdorferi predicted coding region BBI15 [Borrelia	260	3.00E-30
f19-4.aa	gil2689955	(AE000785) antigen, P35, putative [Borrelia burgdorferi]	180	1.80E-23
f19-4.aa	gil2690120	(AE000789) B. burgdorferi predicted coding region BBI34 [Borrelia	183	1.50E-21
f19-4.aa	gil2690052	(AE000784) antigen, P35, putative [Borrelia burgdorferi]	192	1.20E-19
f19-4.aa	gil2690207	(AE000787) B. burgdorferi predicted coding region BBJ02 [Borrelia	149	8.90E-14
f19-4.aa	gil2690098	(AE000789) B. burgdorferi predicted coding region BBI14 [Borrelia	138	8.00E-12
f19-6.aa	gil2690115	(AE000789) B. burgdorferi predicted coding region BBI28 [Borrelia	995	1.20E-131
f19-6.aa	gil2690100	(AE000789) B. burgdorferi predicted coding region BBI16 [Borrelia	447	3.00E-55
f19-6.aa	gil2689955	(AE000785) antigen, P35, putative [Borrelia burgdorferi]	219	2.00E-36
f19-6.aa	gil2690120	(AE000789) B. burgdorferi predicted coding region BBI34 [Borrelia	144	3.50E-34
f19-6.aa	gil2690052	(AE000784) antigen, P35, putative [Borrelia burgdorferi]	130	6.30E-12
f196.aa	gil2688620	(AE001169) methyl-accepting chemotaxis protein (mcp-5) [Borrelia	3093	0

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f196.aa	gi|2688621	(AE001169) methyl-accepting chemotaxis protein (mcp-4) [Borrelia	615	1.90E-83
f196.aa	gi|496484	tlpC gene product [Bacillus subtilis] >pir|I40496|I40496 methylation	180	6.90E-28
f196.aa	gnl|PID|d10 07002	methyl-accepting chemotaxis protein TlpC [Bacillus subtilis]	180	4.90E-27
f196.aa	gnl|PID|e11 73493	methyl-accepting chemotaxis protein [Bacillus subtilis]	162	5.10E-25
f196.aa	gi|882594	ORF_f506 [Escherichia coli] >gi|1789453 (AE000389) aerotaxis	204	1.70E-24
f196.aa	gi|148350	tas [Enterobacter aerogenes] >pir|D32302|D32302 probable aspartate	179	1.80E-24
f196.aa	gi|1066850	putative [Rhodobacter capsulatus] >pir|JC4735|JC4735	207	1.80E-24
f196.aa	gi|154381	chemoreceptor [Salmonella typhimurium] >pir|A47178|A47178	230	2.00E-24
f196.aa	gi|459690	transmembrane receptor [Bacillus subtilis] >gnl|PID|e1185997	212	1.40E-23
f196.aa	gi|805015	MCPA protein [Rhodobacter sphaeroides] >pir|S70094|S54262	237	2.10E-23
f196.aa	gi|40424	mcpA gene product [Caulobacter crescentus] >pir|S23064|S23064 mcpA	238	7.30E-23
f196.aa	gi|144913	sensory transducer protein [Clostridium thermocellum]	227	8.90E-23
f196.aa	gi|1061063	Trg sensory transducer protein [Escherichia coli]	211	2.40E-20
f196.aa	gnl|PID|d10 15762	Methyl-accepting chemotaxis protein III (MCP-III) (Ribose and	211	2.50E-20
f197.aa	gi|2688621	(AE001169) methyl-accepting chemotaxis protein (mcp-4) [Borrelia	3724	0
f197.aa	gi|2688620	(AE001169) methyl-accepting chemotaxis protein (mcp-5) [Borrelia	615	8.40E-83
f197.aa	gi|1066850	putative [Rhodobacter capsulatus] >pir|JC4735|JC4735	227	9.80E-27
f197.aa	gi|882594	ORF_f506 [Escherichia coli] >gi|1789453 (AE000389) aerotaxis	217	1.00E-26
f197.aa	gi|154381	chemoreceptor [Salmonella typhimurium] >pir|A47178|A47178	239	2.80E-25
f197.aa	gi|496484	tlpC gene product [Bacillus subtilis] >pir|I40496|I40496 methylation	202	5.10E-25
f197.aa	gnl|PID|d10 07002	methyl-accepting chemotaxis protein TlpC [Bacillus subtilis]	202	5.10E-25
f197.aa	gi|2564665	(AF022807) putative methyl accepting chemotaxis protein [Rhizobium	212	7.20E-24
f197.aa	gi|459691	transmembrane receptor [Bacillus subtilis] >gnl|PID|e1185996	215	1.10E-23
f197.aa	gi|43218	serine chemoreceptor [Escherichia coli] >bbs|127562 serine	236	2.80E-23
f197.aa	gi|537197	CG Site No. 63; alternate gene name cheD [Escherichia coli]	236	2.90E-23
f197.aa	gi|148077	methyl-accepting chemotaxis protein I [Escherichia coli] >gi|2367378	236	2.90E-23
f197.aa	gnl|PID|d10	transducer [Pseudomonas aeruginosa]	178	4.20E-23

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

	09948			
f197.aa	gil148349	tse [Enterobacter aerogenes] >pirlC32302lC32302 serine transducer	234	5.50E-23
f197.aa	gil2626835	chemotactic transducer [Pseudomonas aeruginosa]	177	5.70E-23
f200.aa	gil2688600	(AE001168) ribose/galactose ABC transporter, permease protein	1887	5.10E-266
f200.aa	gnllPIDle311453	unknown [Bacillus subtilis] >gnllPIDle1184234 similar to	283	1.50E-63
f200.aa	gil2649711	(AE001042) ribose ABC transporter, permease protein (rbsC-1)	202	1.10E-47
f200.aa	gil2130609	(AF000308) putative polytopic protein [Mycoplasma fermentans]	119	2.10E-27
f200.aa	gnllPIDle311493	unknown [Bacillus subtilis] >gnllPIDle1184235 similar to	112	1.10E-18
f200.aa	gil950073	membrane forming protein [Mycoplasma capricolum] >pirlS77790lS77790	161	5.60E-16
f200.aa	gil2688599	(AE001168) ribose/galactose ABC transporter, permease protein	108	2.00E-14
f208.aa	gil2688610	(AE001168) B. burgdorferi predicted coding region BB0674 [Borrelia	1726	6.70E-244
f21-4.aa	gil1197833	Bbk2.11 [Borrelia burgdorferi] >pirlS70531lS70531 bbk2.11 protein	474	3.00E-70
f21-4.aa	gil2627267	ErpL [Borrelia burgdorferi]	477	6.30E-69
f21-4.aa	gil1707281	putative outer membrane protein [Borrelia burgdorferi]	503	6.60E-66
f21-4.aa	gil896042	OspF [Borrelia burgdorferi] >pirlS70532lS70532 outer surface protein	503	6.60E-66
f21-4.aa	gil1707287	putative outer membrane protein [Borrelia burgdorferi]	489	3.00E-60
f21-4.aa	gil1707290	putative outer surface protein [Borrelia burgdorferi]	342	3.20E-49
f21-4.aa	gil1663633	ErpK [Borrelia burgdorferi]	268	1.70E-48
f21-4.aa	gil466482	outer surface protein F [Borrelia burgdorferi] >pirlI40287lI40287	321	3.80E-38
f21-4.aa	gil896038	BbK2.10 precursor [Borrelia burgdorferi] >pirlS70534lS70534 bbK2.10	121	3.90E-34
f21-4.aa	gil896040	BbK2.10 precursor [Borrelia burgdorferi] >pirlS70533lS70533 bbK2.10	118	2.30E-33
f21-4.aa	gil1051120	outer surface protein G [Borrelia burgdorferi] >gil1373118 ErpG	107	3.30E-33
f21-4.aa	gil2444428	(AF020657) ErpX protein [Borrelia burgdorferi]	118	6.00E-14
f210.aa	gil2688603	(AE001168) conserved hypothetical protein [Borrelia burgdorferi]	867	2.60E-116
f210.aa	gil2688604	(AE001168) chemotaxis response regulator (cheY-3) [Borrelia	733	1.40E-97
f210.aa	gil1408274	CheY [Borrelia burgdorferi]	720	9.00E-96
f210.aa	gil1765976	chemotaxis protein CheY [Treponema pallidum]	405	6.60E-52
f210.aa	gil142682	chemotactic response protein [Bacillus subtilis] >gnllPIDle1185224	184	8.00E-30
f210.aa	gil940149	CheY [Thermotoga maritima]	171	1.50E-27

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f210.aa	gi|2649557	(AE001031) chemotaxis response regulator (cheY) [Archaeoglobus	168	1.50E-26
f210.aa	gi|620085	cheY gene product [Listeria monocytogenes]	183	3.00E-26
f210.aa	gnl|PID|e249646	YneI [Bacillus subtilis] >gi|870926 response regulator	166	4.00E-24
f210.aa	gi|149620	ORF2 [Leptospira borgpetersenii] >sp|P24086|YLB3_LEPIN HYPOTHETICAL	121	4.70E-22
f210.aa	gi|1408275	orfX; putative OrfX protein [Borrelia burgdorferi]	208	9.20E-22
f210.aa	gi|994802	cheY gene product [Halobacterium salinarium] >pir|S58645|S58645 CheY	139	8.90E-18
f210.aa	gi|143598	spo0F [Bacillus subtilis] >gi|143601 Spo0F protein [Bacillus	113	4.70E-11
f216.aa	gi|2688586	(AE001167) conserved hypothetical protein [Borrelia burgdorferi]	804	1.20E-109
f216.aa	gi|1575446	orfA [Borrelia burgdorferi]	472	1.10E-91
f219.aa	gi|2688594	(AE001167) B. burgdorferi predicted coding region BB0664 [Borrelia	1122	3.10E-148
f22.aa	gi|2688779	(AE001181) B. burgdorferi predicted coding region BB0832 [Borrelia	1400	4.90E-188
f22.aa	gi|2688779	(AE001181) B. burgdorferi predicted coding region BB0832 [Borrelia	1400	4.90E-188
f221.aa	gi|2688596	(AE001167) B. burgdorferi predicted coding region BB0662 [Borrelia	692	2.60E-93
f229.aa	gi|2688591	(AE001167) oxygen-independent coproporphyrinogen III oxidase,	863	7.80E-120
f24-1.aa	gi|2039285	putative vls recombination cassette Vls6 [Borrelia burgdorferi]	924	1.80E-114
f24-1.aa	gi|2039284	putative vls recombination cassette Vls5 [Borrelia burgdorferi]	867	6.30E-107
f24-1.aa	gi|2039287	putative vls recombination cassette Vls8 [Borrelia burgdorferi]	824	1.50E-104
f24-1.aa	gi|2039289	putative vls recombination cassette Vls10 [Borrelia burgdorferi]	829	7.50E-102
f24-1.aa	gi|2039320	vmp-like sequence protein VlsE [Borrelia burgdorferi]	644	1.10E-98
f24-1.aa	gi|2039288	putative vls recombination cassette Vls9 [Borrelia burgdorferi]	783	8.20E-96
f24-1.aa	gi|2039330	vmp-like sequence protein VlsE [Borrelia burgdorferi]	742	6.30E-95
f24-1.aa	gi|2039336	vmp-like sequence protein VlsE [Borrelia burgdorferi]	509	1.50E-92
f24-1.aa	gi|2039286	putative vls recombination cassette Vls7 [Borrelia burgdorferi]	754	6.60E-92
f24-1.aa	gi|2039324	vmp-like sequence protein VlsE [Borrelia burgdorferi]	488	8.10E-86
f24-1.aa	gi|2039316	vmp-like sequence protein VlsE [Borrelia burgdorferi]	531	1.70E-85
f24-1.aa	gi|2039312	vmp-like sequence protein VlsE [Borrelia burgdorferi]	531	1.20E-83
f24-1.aa	gi|2039326	vmp-like sequence protein VlsE [Borrelia burgdorferi]	476	2.00E-82
f24-1.aa	gi|2039332	vmp-like sequence protein VlsE [Borrelia burgdorferi]	474	5.10E-82
f24-1.aa	gi|2039328	vmp-like sequence protein VlsE [Borrelia burgdorferi]	420	3.50E-59

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f253.aa	gi|2688567	(AE001165) Na+/H+ antiporter (nhaC-1) [Borrelia burgdorferi]	2247	0
f253.aa	gi|2688566	(AE001165) Na+/H+ antiporter (nhaC-2) [Borrelia burgdorferi]	609	6.40E-155
f253.aa	gi|2209268	Na+/H+ antiporter [Bacillus firmus] >pir|A41594|A41594	158	9.40E-15
f253.aa	gi|1574661	Na+/H+ antiporter (nhaC) [Haemophilus influenzae]	143	4.20E-14
f253.aa	gnl|PID|e1185625	similar to Na+/H+ antiporter [Bacillus subtilis]	137	1.20E-11
f253.aa	gnl|PID|e324972	hypothetical protein [Bacillus subtilis] >gnl|PID|e1182969	133	2.00E-11
f265.aa	gi|2688555	(AE001164) conserved hypothetical protein [Borrelia burgdorferi]	1196	9.90E-161
f269.aa	gi|2688560	(AE001164) B. burgdorferi predicted coding region BB0624 [Borrelia	1654	5.50E-226
f28-2.aa	gi|2690174	(AE000788) B. burgdorferi predicted coding region BBK47 [Borrelia	1683	2.80E-222
f28-2.aa	gi|2690161	(AE000788) B. burgdorferi predicted coding region BBK49 [Borrelia	1068	2.20E-163
f28-3.aa	gi|2690138	(AE000788) immunogenic protein P37, putative [Borrelia burgdorferi]	281	6.00E-48
f28-3.aa	gi|2690127	(AE000788) immunogenic protein P37 [Borrelia burgdorferi]	209	3.20E-28
f28-3.aa	gi|2459605	immunogenic protein P37 [Borrelia burgdorferi]	208	4.50E-28
f28-3.aa	gi|2690137	(AE000788) immunogenic protein P37, putative [Borrelia burgdorferi]	172	5.50E-17
f29.aa	gi|2688764	(AE001180) B. burgdorferi predicted coding region BB0826 [Borrelia	869	8.20E-116
f290.aa	gi|2688537	(AE001162) serine-type D-Ala-D-Ala carboxypeptidase (dacA)	2046	1.50E-281
f290.aa	gi|143439	DD-carboxypeptidase [Bacillus subtilis] >pir|B42708|B42708	161	6.60E-36
f290.aa	gnl|PID|e1185617	D-alanyl-D-alanine carboxypeptidase (penicilin binding	161	6.60E-36
f290.aa	gnl|PID|d1016562	Probable penicillin-binding protein. [Escherichia coli]	131	3.30E-28
f290.aa	sp|P37604|DACD_SALTY	PENICILLIN-BINDING PROTEIN 6B PRECURSOR	135	9.10E-28
f290.aa	gi|1572974	penicillin-binding protein 5 (dacA) [Haemophilus influenzae]	145	3.00E-27
f290.aa	gi|580849	D-alanine carboxypeptidase [Bacillus stearothermophilus]	170	4.10E-27
f290.aa	gi|1778549	penicillin-binding protein 5 [Escherichia coli] >gi|41212 precursor	152	3.20E-26
f290.aa	gi|142820	penicillin-binding protein 5 [Bacillus subtilis]	137	4.60E-26
f290.aa	gi|410134	penicillin-binding protein [Bacillus subtilis] >gnl|PID|e1185588	137	4.60E-26
f290.aa	gi|41218	precursor [Escherichia coli]	136	1.30E-25

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f290.aa	gnl|PID|d10 15262	Penicillin-binding protein 6 precursor (D-alanyl-D-alanine	136	1.30E-25
f290.aa	gi|1864022	pencillin binding protein 4 [Staphylococcus aureus]	155	5.10E-22
f290.aa	gnl|PID|e15 4145	penicillin binding protein 4 [Staphylococcus aureus]	155	5.10E-22
f290.aa	gnl|PID|e26 4682	penicillin-binding protein 4 [Staphylococcus aureus]	155	5.10E-22
f291.aa	gi|2688538	(AE001162) L-lactate permease (lctP) [Borrelia burgdorferi]	2473	0
f291.aa	gnl|PID|e27 4704	lactate premease [Streptococcus iniae]	586	1.20E-132
f291.aa	gi|882504	ORF_f560 [Escherichia coli] >gi|1789347 (AE000380) f560; This 560 aa	345	3.60E-95
f291.aa	gi|2313225	(AE000535) L-lactate permease (lctP) [Helicobacter pylori]	359	1.10E-94
f291.aa	gi|2313224	(AE000535) L-lactate permease (lctP) [Helicobacter pylori]	348	2.90E-93
f291.aa	gi|404693	L-lactate permease [Escherichia coli] >gi|466741 aug is 3rd start	331	7.20E-82
f291.aa	gnl|PID|e31 3006	hypothetical protein [Bacillus subtilis] >gnl|PID|e1186107	330	9.00E-80
f291.aa	gnl|PID|d10 22632	lactate permease [Bacillus subtilis]	300	1.70E-61
f291.aa	gnl|PID|e11 82258	L-lactate permease [Bacillus subtilis] >pir|F69649|F69649	300	1.10E-60
f291.aa	gnl|PID|d10 09575	homologue of L-lactate permease of E. coli [Bacillus	265	6.40E-56
f291.aa	gi|2649804	(AE001049) L-lactate permease (lctP) [Archaeoglobus fulgidus]	170	1.50E-47
f291.aa	gnl|PID|e28 3914	L-lactate permease [Sulfolobus solfataricus]	163	2.60E-44
f291.aa	gi|1574148	L-lactate permease (lctP) [Haemophilus influenzae]	173	6.00E-35
f296.aa	gi|2688517	(AE001161) chaperonin, putative [Borrelia burgdorferi]	1276	4.40E-177
f296.aa	gi|840643	mucZ gene product [Coxiella burnetii] >pir|I40852|I40852 mucZ	101	7.90E-12
f3.aa	gi|2688797	(AE001183) B. burgdorferi predicted coding region BB0844 [Borrelia	1604	1.40E-211
f30.aa	gi|2688765	(AE001180) B. burgdorferi predicted coding region BB0825 [Borrelia	1343	2.00E-181
f301.aa	gi|2688521	(AE001161) methyl-accepting chemotaxis protein (mcp-3) [Borrelia	2756	0
f301.aa	gi|1805311	methyl-accepting chemotaxis protein B [Treponema denticola]	211	7.00E-20

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

<table>
<tr><td>f301.aa</td><td>gi|2688522</td><td>(AE001161) methyl-accepting chemotaxis protein (mcp-2) [Borrelia</td><td>189</td><td>2.80E-18</td></tr>
<tr><td>f301.aa</td><td>gi|2367665</td><td>(AF016689) Mcp-2 [Treponema pallidum]</td><td>189</td><td>3.50E-17</td></tr>
<tr><td>f301.aa</td><td>gi|2352917</td><td>(AF012922) methyl-accepting chemotaxis protein [Treponema</td><td>187</td><td>5.70E-17</td></tr>
<tr><td>f301.aa</td><td>gi|1354776</td><td>MCP-1 [Treponema pallidum]</td><td>189</td><td>5.90E-17</td></tr>
<tr><td>f301.aa</td><td>gi|2619023</td><td>(AF027868) YoaH [Bacillus subtilis] >gnl|PID|e1185333 similar to</td><td>184</td><td>2.80E-16</td></tr>
<tr><td>f301.aa</td><td>gi|1654421</td><td>transducer HtB protein [Halobacterium salinarum]</td><td>177</td><td>2.20E-15</td></tr>
<tr><td>f301.aa</td><td>gi|415694</td><td>chemoreceptor [Desulfovibrio vulgaris] >pir|G36943|G36943</td><td>163</td><td>3.50E-15</td></tr>
<tr><td>f301.aa</td><td>gi|459691</td><td>transmembrane receptor [Bacillus subtilis] >gnl|PID|e1185996</td><td>163</td><td>4.90E-15</td></tr>
<tr><td>f301.aa</td><td>gi|2104730</td><td>ORF2 [Desulfurococcus sp. SY]</td><td>173</td><td>5.80E-15</td></tr>
<tr><td>f301.aa</td><td>gi|2914132</td><td>methyl accepting chemotaxis homolog [Treponema denticola]</td><td>170</td><td>1.10E-14</td></tr>
<tr><td>f301.aa</td><td>gi|459689</td><td>transmembrane receptor [Bacillus subtilis] >gnl|PID|e1185998</td><td>164</td><td>1.30E-14</td></tr>
<tr><td>f301.aa</td><td>gi|496484</td><td>tlpC gene product [Bacillus subtilis] >pir|I40496|I40496 methylation</td><td>170</td><td>3.80E-14</td></tr>
<tr><td>f301.aa</td><td>gi|2313163</td><td>(AE000530) methyl-accepting chemotaxis transducer (tlpC)</td><td>170</td><td>6.30E-14</td></tr>
<tr><td>f308.aa</td><td>gi|2688527</td><td>(AE001161) B. burgdorferi predicted coding region BB0592 [Borrelia</td><td>1227</td><td>1.70E-176</td></tr>
<tr><td>f31-2.aa</td><td>gi|2690202</td><td>(AE000787) B. burgdorferi predicted coding region BBJ36 [Borrelia</td><td>1771</td><td>7.20E-235</td></tr>
<tr><td>f31-2.aa</td><td>gi|2690200</td><td>(AE000787) B. burgdorferi predicted coding region BBJ34 [Borrelia</td><td>423</td><td>4.60E-88</td></tr>
<tr><td>f31.aa</td><td>gi|2688766</td><td>(AE001180) B. burgdorferi predicted coding region BB0824 [Borrelia</td><td>957</td><td>7.80E-133</td></tr>
<tr><td>f314.aa</td><td>gi|2688509</td><td>(AE001160) pfs protein (pfs-2) [Borrelia burgdorferi]</td><td>1329</td><td>7.40E-180</td></tr>
<tr><td>f314.aa</td><td>gi|2690087</td><td>(AE000789) pfs protein (pfs) [Borrelia burgdorferi]</td><td>335</td><td>1.50E-77</td></tr>
<tr><td>f314.aa</td><td>gi|2688288</td><td>(AE001143) pfs protein (pfs-1) [Borrelia burgdorferi]</td><td>266</td><td>1.00E-65</td></tr>
<tr><td>f314.aa</td><td>gi|2738591</td><td>(AF012886) Pfs [Buchnera aphidicola]</td><td>115</td><td>1.70E-52</td></tr>
<tr><td>f314.aa</td><td>gi|1552737</td><td>similar to purine nucleoside phosphorylase (deoD) [Escherichia</td><td>133</td><td>6.90E-52</td></tr>
<tr><td>f314.aa</td><td>gnl|PID|e11
83957</td><td>similar to purine nucleoside phosphorylase [Bacillus</td><td>157</td><td>1.20E-49</td></tr>
<tr><td>f314.aa</td><td>gi|147158</td><td>pfs [Escherichia coli] >gi|457107 ORF [Escherichia coli] {SUB 9-219}</td><td>133</td><td>2.50E-42</td></tr>
<tr><td>f314.aa</td><td>gi|1574146</td><td>pfs protein (pfs) [Haemophilus influenzae] >pir|C64169|C64169 pfs</td><td>110</td><td>2.70E-37</td></tr>
<tr><td>f314.aa</td><td>gi|2267164</td><td>(AF009177) pfs protein homolog [Helicobacter pylori]</td><td>118</td><td>3.30E-23</td></tr>
<tr><td>f314.aa</td><td>gi|2313168</td><td>(AE000530) pfs protein (pfs) [Helicobacter pylori]</td><td>115</td><td>1.00E-22</td></tr>
<tr><td>f314.aa</td><td>gi|1777939</td><td>Pfs [Treponema pallidum]</td><td>102</td><td>1.90E-20</td></tr>
<tr><td>f314.aa</td><td>gi|2689970</td><td>(AE000785) B. burgdorferi predicted coding region BBE07 [Borrelia</td><td>191</td><td>1.50E-19</td></tr>
<tr><td>f314.aa</td><td>gnl|PID|e24</td><td>unknown [Mycobacterium tuberculosis] >sp|Q10889|Y05A_MYCTU</td><td>105</td><td>7.60E-16</td></tr>
</table>

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

	9405			
f32-4.aa	gil2690221	(AE000787) B. burgdorferi predicted coding region BBJ47 [Borrelia	1192	4.00E-163
f32-4.aa	gil2689979	(AE000785) B. burgdorferi predicted coding region BBE16 [Borrelia	103	4.10E-11
f32.aa	gil2688767	(AE001180) B. burgdorferi predicted coding region BB0823 [Borrelia	623	1.80E-81
f32.aa	gil2688767	(AE001180) B. burgdorferi predicted coding region BB0823 [Borrelia	623	1.80E-81
f320.aa	gil2688497	(AE001159) carboxypeptidase, putative [Borrelia burgdorferi]	1373	6.40E-186
f320.aa	gil2529473	(AF006665) YokZ [Bacillus subtilis]	136	9.80E-28
f320.aa	gil2415396	(AF015775) carboxypeptidase [Bacillus subtilis] >gnllPIDle1185433	136	1.90E-27
f320.aa	gil1209528	D,D-carboxypeptidase [Enterococcus faecalis] >splQ47746lVANY_ENTFA	148	3.30E-16
f320.aa	gil155044	vanY [Transposon Tn1546] >gil149126 D,D-carboxypeptidase [Plasmid	142	1.60E-13
f328.aa	gil2688502	(AE001159) CTP synthase (pyrG) [Borrelia burgdorferi]	869	6.10E-119
f328.aa	gil1591801	CTP synthase (pyrG) [Methanococcus jannaschii] >pirlE64446lE64446	325	6.20E-59
f328.aa	gil2650385	(AE001088) CTP synthase (pyrG) [Archaeoglobus fulgidus]	304	4.20E-54
f328.aa	gil1399854	CTP synthetase [Synechococcus PCC7942] >splQ54775lPYRG_SYNP7 CTP	313	3.30E-52
f328.aa	gnllPIDld10 19032	CTP synthetase [Synechocystis sp.] >pirlS75840lS75840 CTP	295	1.80E-50
f328.aa	gil143597	CTP synthetase [Bacillus subtilis] >gil853762 CTP synthase [Bacillus	274	1.60E-49
f328.aa	gil2983754	(AE000735) CTP synthetase [Aquifex aeolicus]	271	1.50E-46
f328.aa	gil1574630	CTP synthetase (pyrG) [Haemophilus influenzae] >pirlF64181lF64181	234	1.90E-44
f328.aa	gil413755	CTP synthetase [Spiroplasma citri] >splP52200lPYRG_SPICI CTP	231	3.00E-44
f328.aa	gil2621483	(AE000826) CTP synthase [Methanobacterium thermoautotrophicum]	257	2.80E-40
f328.aa	gil950067	CTP synthase [Mycoplasma capricolum] >pirlS77767lS77767 CTP synthase	220	4.10E-39
f328.aa	gil904007	cytidine triphosphate synthetase precursor [Giardia intestinalis]	219	2.00E-38
f328.aa	gil147478	CTP synthetase (EC 6.3.4.2) [Escherichia coli]	217	2.90E-38
f328.aa	gil882674	CTP synthetase [Escherichia coli] >gil1789142 (AE000361) CTP	214	7.70E-38
f328.aa	gil38688	CTP synthase [Azospirillum brasilense] >pirlI39496lS25101 CTP	132	3.20E-37
f342.aa	gil2688495	(AE001158) B. burgdorferi predicted coding region BB0563 [Borrelia	944	5.30E-130
f346.aa	gil1272356	phosphotransferase enzyme II [Borrelia burgdorferi] >gil2688474	828	1.10E-108

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f346.aa	gi|145603	PTS enzyme III glc [Escherichia coli] >gi|145605 PTS enzyme III glc	385	8.80E-53
f346.aa	gi|1314675	glucose-specific component IIA of the PTS system [Escherichia coli]	385	9.30E-53
f346.aa	gi|47658	III(Glc) (crr) (AA 1 - 169) [Salmonella typhimurium]	382	2.30E-52
f346.aa	gi|1574566	glucose phosphotransferase enzyme III-glc (crr) [Haemophilus	397	8.70E-50
f346.aa	gi|43819	nagE gene product [Klebsiella pneumoniae] >pir|S18607|S18607	349	2.80E-41
f346.aa	gi|146913	N-acetylglucosamine transport protein [Escherichia coli]	334	3.20E-39
f346.aa	gi|1072418	glcA [Staphylococcus carnosus] >pir|S46952|S46952	317	7.20E-37
f346.aa	gi|1072419	glcB [Staphylococcus carnosus] >pir|S63606|S46953	315	1.40E-36
f346.aa	gi|1146177	phosphotransferase system glucose-specific enzyme II [Bacillus	295	7.30E-36
f346.aa	gi|529001	PTS glucose-specific permease [Bacillus stearothermophilus]	294	8.80E-36
f346.aa	gnl|PID|e1182187	alternate gene name: yzfA; similar to phosphotransferase	293	1.40E-33
f346.aa	gi|580912	enzyme III-glucose [Bacillus subtilis]	257	1.20E-30
f346.aa	gi|602681	phosphocarrier protein (enzyme IIA) [Mycoplasma capricolum]	243	1.00E-28
f346.aa	gi|1432153	cellobiose-specific PTS permease [Klebsiella oxytoca]	257	1.20E-28
f352.aa	gi|2688482	(AE001157) B. burgdorferi predicted coding region BB0553 [Borrelia	2547	0
f352.aa	gi|2688482	(AE001157) B. burgdorferi predicted coding region BB0553 [Borrelia	1005	1.30E-132
f363.aa	gi|2688468	(AE001156) B. burgdorferi predicted coding region BB0543 [Borrelia	1109	5.40E-153
f368.aa	gi|2688450	(AE001155) conserved hypothetical integral membrane protein	1133	4.10E-157
f368.aa	gi|1787004	(AE000181) o234; This 234 aa ORF is 26 pct identical (15 gaps) to	417	1.40E-67
f368.aa	gi|2314055	(AE000601) conserved hypothetical integral membrane protein	129	3.50E-16
f368.aa	gnl|PID|e1289272	S1R [Cowpox virus]	135	1.80E-14
f368.aa	gnl|PID|d1003176	24K membrane protein [Pseudomonas aeruginosa]	108	9.00E-13
f368.aa	gi|41284	put. 23.5-kd protein [Escherichia coli] >gi|1787205 (AE000199)	101	1.00E-11
f371.aa	gi|2688452	(AE001155) conserved hypothetical protein [Borrelia burgdorferi]	1066	3.60E-143
f371.aa	gi|2196997	Orf256 [Treponema pallidum]	154	1.10E-15
f373.aa	gi|2688453	(AE001155) zinc protease, putative [Borrelia burgdorferi]	3663	0
f373.aa	gi|1574200	hypothetical [Haemophilus influenzae] >pir|E64171|E64171	295	2.70E-67
f373.aa	gi|1787770	(AE000246) f931; residues 5-650 are 99 pct identical to YDDC_ECOLI	289	1.10E-57

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f373.aa	gi|535004	cds106 gene product [Escherichia coli]	289	3.20E-57
f373.aa	gi|799369	metalloendopeptidase [Pisum sativum]	148	7.10E-28
f373.aa	gi|2827039	(AF008444) chloroplast processing enzyme [Arabidopsis thaliana]	150	1.70E-26
f373.aa	gi|2983709	(AE000732) processing protease [Aquifex aeolicus]	136	4.30E-24
f373.aa	gi|2314155	(AE000609) protease (pqqE) [Helicobacter pylori] >pir|D64646|D64646	115	5.30E-23
f378.aa	gi|2688458	(AE001155) B. burgdorferi predicted coding region BB0531 [Borrelia	1030	1.30E-136
f384.aa	gi|2688435	(AE001154) inositol monophosphatase [Borrelia burgdorferi]	1470	3.80E-201
f4-15.aa	gi|2690238	(AE000790) surface lipoprotein P27 [Borrelia burgdorferi]	1400	1.50E-185
f4-15.aa	gi|144008	P27 [Borrelia burgdorferi] >pir|S34995|S34995 surface lipoprotein	462	2.40E-96
f4-50.aa	gi|2690243	(AE000790) decorin binding protein B (dbpB) [Borrelia burgdorferi]	900	6.30E-117
f4-50.aa	gi|2062381	decorin binding protein B [Borrelia burgdorferi]	897	1.60E-116
f4-50.aa	gi|2809217	(AF042796) putative decorin-binding protein precursor [Borrelia	887	3.60E-115
f4-50.aa	gi|2809218	(AF042796) decorin-binding protein precursor [Borrelia burgdorferi]	172	2.00E-33
f4-50.aa	gi|2690249	(AE000790) decorin binding protein A (dbpA) [Borrelia burgdorferi]	176	9.50E-33
f4-50.aa	gi|2062379	decorin binding protein A [Borrelia burgdorferi]	177	6.10E-32
f4-66.aa	gi|2690229	(AE000790) chpAI protein, putative [Borrelia burgdorferi]	807	1.60E-107
f4.aa	gi|2688787	(AE001183) conserved hypothetical integral membrane protein	2408	0
f4.aa	gi|2697115	(AF008219) unknown [Borrelia afzelii]	1138	1.90E-305
f4.aa	gi|1573583	H. influenzae predicted coding region HI0594 [Haemophilus	337	2.10E-109
f4.aa	gi|1788636	(AE000319) o513; This 513 aa ORF is 31 pct identical (30 gaps) to	327	9.10E-80
f4.aa	gnl|PID|d1009571	homologue of hypothetical protein HI10594 of H. influenzae	357	5.40E-69
f42-1.aa	gi|2689993	(AE000794) conserved hypothetical protein [Borrelia burgdorferi]	495	2.70E-62
f42-1.aa	gi|2689934	(AE000793) conserved hypothetical protein [Borrelia burgdorferi]	312	1.00E-37
f43-3.aa	gi|1209843	lipoprotein [Borrelia burgdorferi]	546	1.50E-69
f43-3.aa	gi|2121280	(AF000270) lipoprotein [Borrelia burgdorferi] >gi|3095109	442	1.80E-55
f43-3.aa	gi|1209837	lipoprotein [Borrelia burgdorferi]	365	3.10E-55
f43-3.aa	gi|1209873	lipoprotein [Borrelia burgdorferi]	269	5.30E-32
f43-3.aa	gi|1209849	lipoprotein [Borrelia burgdorferi]	141	1.70E-13
f43-3.aa	gi|3095105	(AF046998) 2.9-8 lipoprotein [Borrelia burgdorferi]	140	9.60E-13
f43-3.aa	gi|3095107	(AF046999) 2.9-9 lipoprotein [Borrelia burgdorferi]	132	1.40E-11

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f43.aa	gi|2688752	(AE001179) B. burgdorferi predicted coding region BB0811 [Borrelia	2337	6.60000000084856e-315
f446.aa	gi|2688383	(AE001151) B. burgdorferi predicted coding region BB0464 [Borrelia	920	7.20E-124
f45-2.aa	gi|1699017	ErpB2 [Borrelia burgdorferi] >gi|1373133 ErpB [Borrelia	364	7.50E-78
f45-2.aa	gi|2627270	ErpJ [Borrelia burgdorferi]	364	2.50E-77
f45-2.aa	gi|2627268	ErpM [Borrelia burgdorferi]	452	9.70E-60
f45-2.aa	gi|1373144	ErpD [Borrelia burgdorferi]	316	1.60E-58
f45-2.aa	gi|2444428	(AF020657) ErpX protein [Borrelia burgdorferi]	380	2.80E-55
f45-2.aa	gi|1051120	outer surface protein G [Borrelia burgdorferi] >gi|1373118 ErpG	213	7.10E-35
f45-2.aa	gi|1663633	ErpK [Borrelia burgdorferi]	152	1.60E-21
f45-2.aa	gnl|PID|e329895	(AJ000496) cyclic nucleotide-gated channel beta subunit	198	2.80E-16
f45-2.aa	gi|466482	outer surface protein F [Borrelia burgdorferi] >pir|I40287|I40287	111	5.70E-14
f45-2.aa	gi|2246532	ORF 73, contains large complex repeat CR 73 [Kaposi's	174	5.90E-14
f45-2.aa	gi|160299	glutamic acid-rich protein [Plasmodium falciparum]	169	1.00E-13
f45-2.aa	gi|1707287	putative outer membrane protein [Borrelia burgdorferi]	101	2.20E-13
f45-2.aa	gi|1633572	Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated	175	4.10E-13
f45-2.aa	gnl|PID|d1012343	gene required for phosphoylation of oligosaccharides/ has	166	5.60E-13
f45-2.aa	gi|2690100	(AE000789) B. burgdorferi predicted coding region BBI16 [Borrelia	161	2.70E-12
f457.aa	gi|2688369	(AE001150) B. burgdorferi predicted coding region BB0456 [Borrelia	1021	6.20E-139
f469.aa	gi|2688368	(AE001150) Na+/H+ antiporter (napA) [Borrelia burgdorferi]	1544	1.10E-211
f47-2.aa	gi|1209849	lipoprotein [Borrelia burgdorferi]	742	2.30E-97
f47-2.aa	gi|1209857	lipoprotein [Borrelia burgdorferi]	407	7.80E-86
f47-2.aa	gi|1209831	lipoprotein [Borrelia burgdorferi]	393	5.00E-82
f47-2.aa	gnl|PID|e268245	surface-exposed lipoprotein [Borrelia burgdorferi]	321	2.60E-73
f47-2.aa	gi|1209874	lipoprotein [Borrelia burgdorferi]	348	1.10E-64
f47-2.aa	gnl|PID|e268239	surface-exposed lipoprotein [Borrelia garinii]	333	1.40E-57
f47-2.aa	gnl|PID|e26	surface-exposed lipoprotein [Borrelia afzelii]	292	9.60E-44

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

	8244			
f47-2.aa	gi|3095107	(AF046999) 2.9-9 lipoprotein [Borrelia burgdorferi]	328	3.80E-40
f47-2.aa	gnl|PID|e268242	surface-exposed lipoprotein [Borrelia garinii]	320	1.70E-39
f47-2.aa	gi|1209837	lipoprotein [Borrelia burgdorferi]	210	4.80E-29
f47-2.aa	gi|2121280	(AF000270) lipoprotein [Borrelia burgdorferi] >gi|3095109	205	1.10E-27
f47-2.aa	gi|3095105	(AF046998) 2.9-8 lipoprotein [Borrelia burgdorferi]	217	6.30E-25
f47-2.aa	gi|1209873	lipoprotein [Borrelia burgdorferi]	113	2.40E-11
f477.aa	gi|2688350	(AE001149) fructose-bisphosphate aldolase (fba) [Borrelia	1506	3.60E-202
f477.aa	gi|882454	fructose 1,6-bisphosphate aldolase [Escherichia coli] >gi|41423	651	1.10E-131
f477.aa	gi|2708661	(AF037440) fructose 1,6-bisphosphate aldolase [Edwardsiella	593	1.40E-124
f477.aa	gi|1573507	fructose-bisphosphate aldolase (fba) [Haemophilus influenzae]	560	8.50E-120
f477.aa	gi|671841	fructose 1,6-bisphosphate aldolase [Campylobacter jejuni]	856	3.80E-113
f477.aa	gnl|PID|d1004756	fructose 1,6-bisphosphate aldolase [Schizosaccharomyces	749	1.70E-98
f477.aa	gi|433637	yeast fructose-bisphate-aldolase [Saccharomyces cerevisiae] >gi|3696	459	1.20E-92
f477.aa	gnl|PID|e190134	fructose-1,6-bisphosphate aldolase [Euglena gracilis]	701	6.30E-92
f477.aa	gi|1334980	fructose 1,6 bisphosphate-aldolase [Neurospora crassa]	647	1.50E-84
f477.aa	gi|40495	fructose-bisphosphate aldolase [Corynebacterium glutamicum]	204	6.80E-37
f477.aa	gnl|PID|e315480	Fba [Mycobacterium tuberculosis]	207	1.50E-35
f477.aa	gi|1045692	fructose-bisphosphate aldolase [Mycoplasma genitalium]	108	2.10E-23
f477.aa	gnl|PID|d1003809	hypothetical protein [Bacillus subtilis] >gnl|PID|e1184692	102	2.70E-15
f488.aa	gi|2688338	(AE001148) DNA gyrase, subunit A (gyrA) [Borrelia burgdorferi]	3222	0
f488.aa	gi|1790876	DNA gyrase subunit A [Clostridium acetobutylicum]	822	1.80E-171
f488.aa	gi|2650163	(AE001072) DNA gyrase, subunit A (gyrA) [Archaeoglobus fulgidus]	483	1.10E-162
f488.aa	gi|40019	ORF 821 (aa 1-821) [Bacillus subtilis] >gnl|PID|d1005785 A subunit of	836	6.10E-159
f488.aa	gi|459929	gyrase A subunit [Pseudomonas aeruginosa] >sp|P48372|GYRA_PSEAE DNA	418	7.00E-155
f488.aa	gi|144206	DNA gyrase A [Campylobacter jejuni] >pir|A48902|A48902 DNA gyrase	508	7.50E-154

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f488.aa	gi|466275	gyrase A [Mycobacterium tuberculosis] >sp|Q07702|GYRA_MYCTU DNA	395	3.50E-152
f488.aa	gnl|PID|e266924	GyrA [Mycobacterium tuberculosis]	395	2.00E-151
f488.aa	gi|43485	DNA gyrase A subunit [Haloferax] >pir|S30571|S30571 DNA topoisomerase	275	6.10E-151
f488.aa	gnl|PID|d1025098	(AB010081) A subunit of DNA gyrase [Bacillus sp.]	549	1.20E-150
f488.aa	gnl|PID|e214031	DNA gyrase subunit A [Mycobacterium smegmatis]	388	5.90E-150
f488.aa	gi|2731385	DNA gyrase [Serratia marcescens]	378	6.00E-148
f488.aa	gnl|PID|e137038	DNA topoisomerase (ATP-hydrolysing) [Mycobacterium smegmatis]	388	7.30E-147
f488.aa	gi|41634	gyrA gene product (AA 1-875) [Escherichia coli] >gi|41636 DNA gyrase	383	2.40E-146
f488.aa	gi|497648	DNA gyrase subunit A [Mycoplasma genitalium]	514	5.20E-146
f49-2.aa	gi|2039282	putative vls recombination cassette Vls3 [Borrelia burgdorferi]	943	2.30E-120
f49-2.aa	gi|2547241	vmp-like sequence protein VlsE [Borrelia burgdorferi]	434	4.10E-106
f49-2.aa	gi|2039324	vmp-like sequence protein VlsE [Borrelia burgdorferi]	458	3.00E-104
f49-2.aa	gi|2039281	putative vls recombination cassette Vls2 [Borrelia burgdorferi]	793	1.80E-100
f49-2.aa	gi|2039283	putative vls recombination cassette Vls4 [Borrelia burgdorferi]	729	4.60E-92
f49-2.aa	gi|2039308	vmp-like sequence protein VlsE [Borrelia burgdorferi]	652	1.40E-88
f49-2.aa	gi|2039288	putative vls recombination cassette Vls9 [Borrelia burgdorferi]	352	1.80E-88
f49-2.aa	gi|2039332	vmp-like sequence protein VlsE [Borrelia burgdorferi]	550	4.40E-88
f49-2.aa	gi|2039328	vmp-like sequence protein VlsE [Borrelia burgdorferi]	629	1.50E-85
f49-2.aa	gi|2039336	vmp-like sequence protein VlsE [Borrelia burgdorferi]	460	1.40E-82
f49-2.aa	gi|2039318	vmp-like sequence protein VlsE [Borrelia burgdorferi]	367	6.20E-82
f49-2.aa	gi|2039320	vmp-like sequence protein VlsE [Borrelia burgdorferi]	449	1.80E-77
f49-2.aa	gi|2483796	VlsE1 [Borrelia burgdorferi]	497	8.20E-76
f49-2.aa	gi|2039326	vmp-like sequence protein VlsE [Borrelia burgdorferi]	427	2.50E-64
f49-2.aa	gi|2039291	putative vls recombination cassette Vls13 [Borrelia burgdorferi]	409	1.30E-47
f494.aa	gi|2688346	(AE001148) B. burgdorferi predicted coding region BB0428 [Borrelia	547	8.20E-74
f5-14.aa	gi|2627268	ErpM [Borrelia burgdorferi]	1836	2.60E-236

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f5-14.aa	gi|1373144	ErpD [Borrelia burgdorferi]	543	4.40E-87
f5-14.aa	gi|2627270	ErpJ [Borrelia burgdorferi]	503	4.30E-83
f5-14.aa	gi|1699017	ErpB2 [Borrelia burgdorferi] >gi|1373133 ErpB [Borrelia	503	2.60E-82
f5-14.aa	gi|2444428	(AF020657) ErpX protein [Borrelia burgdorferi]	399	9.30E-57
f5-14.aa	gnl|PID|e329895	(AJ000496) cyclic nucleotide-gated channel beta subunit	228	1.50E-20
f5-14.aa	gnl|PID|d1012343	gene required for phosphoylation of oligosaccharides/ has	203	8.70E-18
f5-14.aa	gi|2246532	ORF 73, contains large complex repeat CR 73 [Kaposi's	197	3.30E-17
f5-14.aa	gi|1633572	Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated	192	1.20E-16
f5-14.aa	gi|3068583	(AF000580) Rep-like [Dictyostelium discoideum]	197	3.60E-16
f5-14.aa	gi|2690100	(AE000789) B. burgdorferi predicted coding region BBI16 [Borrelia	183	2.90E-15
f5-14.aa	gi|1825739	No definition line found [Caenorhabditis elegans]	168	1.60E-14
f5-14.aa	gi|3044185	(AF056936) mature parasite-infected erythrocyte surface antigen	166	2.00E-14
f5-14.aa	gnl|PID|e349084	E02A10.2 [Caenorhabditis elegans]	176	2.30E-14
f5-14.aa	gi|1051120	outer surface protein G [Borrelia burgdorferi] >gi|1373118 ErpG	157	3.30E-12
f5-15.aa	gi|2627267	ErpL [Borrelia burgdorferi]	1152	4.40E-147
f5-15.aa	gi|1197833	Bbk2.11 [Borrelia burgdorferi] >pir|S70531|S70531 bbk2.11 protein	856	3.30E-108
f5-15.aa	gi|896042	OspF [Borrelia burgdorferi] >pir|S70532|S70532 outer surface protein	325	1.00E-72
f5-15.aa	gi|1707281	putative outer membrane protein [Borrelia burgdorferi]	323	1.80E-72
f5-15.aa	gi|1707287	putative outer membrane protein [Borrelia burgdorferi]	322	6.60E-70
f5-15.aa	gi|466482	outer surface protein F [Borrelia burgdorferi] >pir|I40287|I40287	448	6.80E-68
f5-15.aa	gi|1707290	putative outer surface protein [Borrelia burgdorferi]	290	1.90E-52
f5-15.aa	gi|1663633	ErpK [Borrelia burgdorferi]	172	8.70E-43
f5-15.aa	gi|896038	BbK2.10 precursor [Borrelia burgdorferi] >pir|S70534|S70534 bbK2.10	153	1.10E-42
f5-15.aa	gi|896040	BbK2.10 precursor [Borrelia burgdorferi] >pir|S70533|S70533 bbK2.10	124	4.30E-39
f5-15.aa	gi|1051120	outer surface protein G [Borrelia burgdorferi] >gi|1373118 ErpG	105	3.10E-23
f5-15.aa	gi|1373144	ErpD [Borrelia burgdorferi]	103	1.10E-14
f50.aa	gi|2688754	(AE001179) B. burgdorferi predicted coding region BB0806 [Borrelia	2651	0
f502.aa	gi|2688313	(AE001146) sensory transduction histidine kinase, putative	7570	0

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f502.aa	gnl|PID|d10 25877	(AB006363) homologue of histidine kinase [Candida albicans]	296	3.80E-58
f502.aa	gi|1354473	Os-1p [Neurospora crassa]	275	3.30E-57
f502.aa	gi|1679757	two-component histidine kinase CHK-1 [Glomerella cingulata]	382	4.20E-57
f502.aa	gi|1262208	Nik-1 [Neurospora crassa] >gi|1262210 Nik-1 [Neurospora crassa]	273	6.30E-57
f502.aa	gi|2460283	(AF024654) hybrid histidine kinase DHKB [Dictyostelium discoideum]	273	3.90E-55
f502.aa	gnl|PID|d10 17789	sensory transduction histidine kinase [Synechocystis sp.]	288	8.50E-54
f502.aa	gi|2623815	(AF030352) two component sensor [Pseudomonas aeruginosa]	252	4.00E-52
f502.aa	gi|939724	putative sensor kinase; regulatory protein for production of	252	1.80E-50
f502.aa	gi|151329	regulatory protein [Pseudomonas syringae] >sp|P48027|LEMA_PSESY	248	1.20E-49
f502.aa	pir|B41863| B41863	two-component regulatory protein lemA - Pseudomonas syringae	248	1.30E-49
f502.aa	gnl|PID|d10 18725	sensory transduction histidine kinase [Synechocystis sp.]	252	2.10E-49
f502.aa	gnl|PID|d10 02185	sensor-regulator protein [Escherichia coli] >gi|1789149	262	6.20E-49
f502.aa	gi|463195	pectate lyase [Pseudomonas viridiflava]	247	7.50E-49
f502.aa	gnl|PID|d10 18731	sensory transduction histidine kinase [Synechocystis sp.]	244	1.00E-48
f51-2.aa	gi|2444428	(AF020657) ErpX protein [Borrelia burgdorferi]	1755	2.20E-227
f51-2.aa	gi|2627268	ErpM [Borrelia burgdorferi]	399	3.20E-57
f51-2.aa	gi|1373144	ErpD [Borrelia burgdorferi]	282	2.20E-50
f51-2.aa	gi|2627270	ErpJ [Borrelia burgdorferi]	271	6.00E-34
f51-2.aa	gi|1699017	ErpB2 [Borrelia burgdorferi] >gi|1373133 ErpB [Borrelia	271	2.50E-33
f51-2.aa	gi|1051120	outer surface protein G [Borrelia burgdorferi] >gi|1373118 ErpG	109	3.70E-22
f51-2.aa	gnl|PID|d10 12343	gene required for phosphoylation of oligosaccharides/ has	203	5.40E-18
f51-2.aa	gi|1707287	putative outer membrane protein [Borrelia burgdorferi]	111	7.50E-18
f51-2.aa	gi|896042	OspF [Borrelia burgdorferi] >pir|S70532|S70532 outer surface protein	111	2.10E-17
f51-2.aa	gi|1707281	putative outer membrane protein [Borrelia burgdorferi]	111	7.50E-17
f51-2.aa	gnl|PID|e32	(AJ000496) cyclic nucleotide-gated channel beta subunit	198	1.60E-16

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

	9895			
f51-2.aa	gil2246532	ORF 73, contains large complex repeat CR 73 [Kaposi's	176	2.30E-14
f51-2.aa	gnllPIDle349084	E02A10.2 [Caenorhabditis elegans]	170	2.10E-13
f51-2.aa	gil160299	glutamic acid-rich protein [Plasmodium falciparum]	157	7.30E-12
f516.aa	gil2688326	(AE001146) B. burgdorferi predicted coding region BB0409 [Borrelia	1096	2.00E-150
f517.aa	gil2688320	(AE001146) PTS system, fructose-specific IIABC component (fruA-1)	1637	2.30E-228
f517.aa	gnllPIDle1183221	similar to fructose phosphotransferase system enzyme II	256	4.00E-88
f517.aa	gil396296	similar to phosphotransferase system enzyme II [Escherichia coli]	305	9.10E-86
f517.aa	gil405893	fructose-specific IIBC component [Escherichia coli] >gil450372	224	4.30E-84
f517.aa	gil151932	fructose enzyme II [Rhodobacter capsulatus] >gil46021 fructose	222	4.70E-79
f517.aa	gil1573422	fructose-permease IIBC component (fruA) [Haemophilus influenzae]	225	6.90E-69
f517.aa	gil2688554	(AE001164) PTS system, fructose-specific IIABC component (fruA-2)	236	8.20E-66
f517.aa	gnllPIDle1185030	phosphotransferase system (PTS) fructose-specific enzyme IIBC	195	2.80E-65
f517.aa	gil155369	PTS enzyme-II fructose [Xanthomonas campestris] >pirlB40944lB40944	187	8.10E-62
f517.aa	gil305003	similar to fructose-specific phosphotransferase enzyme II	145	1.90E-39
f517.aa	gnllPIDld1011544	HrsA [Escherichia coli] >gil1786951 (AE000176)	148	2.80E-39
f517.aa	gil1813488	phosphotransferase enzyme II [Bacillus firmus]	226	3.90E-39
f517.aa	gil757734	fruA gene product [Bacillus amyloliquefaciens] >pirlS59965lS59965	177	2.50E-36
f517.aa	gnllPIDld1016984	PTS SYSTEM, FRUCTOSE-SPECIFIC IIBC COMPONENT (EIIBC-FRU)	173	1.10E-34
f517.aa	gil1673731	(AE000010) Mycoplasma pneumoniae, fructose-permease IIBC component;	143	9.00E-33
f519.aa	gil2688327	(AE001146) B. burgdorferi predicted coding region BB0406 [Borrelia	1060	5.70E-145
f519.aa	gil2688328	(AE001146) B. burgdorferi predicted coding region BB0405 [Borrelia	261	1.20E-47
f520.aa	gil2688328	(AE001146) B. burgdorferi predicted coding region BB0405 [Borrelia	1022	3.90E-138
f520.aa	gil2688327	(AE001146) B. burgdorferi predicted coding region BB0406 [Borrelia	261	4.00E-47
f523.aa	gil2688300	(AE001145) glutamate transporter, putative [Borrelia burgdorferi]	2007	9.90E-284
f526.aa	gil2688309	(AE001145) B. burgdorferi predicted coding region BB0399 [Borrelia	1087	1.60E-145

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f527.aa	gi|2688310	(AE001145) B. burgdorferi predicted coding region BB0398 [Borrelia	1814	7.60E-249
f541.aa	gi|508421	antigen P39 [Borrelia burgdorferi] >gi|2688281 (AE001143) basic	1706	5.40E-230
f541.aa	gi|1753225	BmpA protein [Borrelia burgdorferi]	1698	6.80E-229
f541.aa	gnl|PID|e1172833	bmpA(p39,ORF1) [Borrelia burgdorferi]	1695	1.70E-228
f541.aa	gnl|PID|e1172835	membrane protein A [Borrelia burgdorferi] >gi|516592 membrane	1642	3.40E-221
f541.aa	gnl|PID|e1172834	membrane protein A [Borrelia burgdorferi]	1638	1.20E-220
f541.aa	gnl|PID|e1172828	bmpA(p39,ORF1) [Borrelia burgdorferi]	1551	1.00E-208
f541.aa	gnl|PID|e1172829	membrane protein A [Borrelia afzelii]	1502	5.60E-202
f541.aa	gnl|PID|e1172831	membrane protein A [Borrelia afzelii]	1499	1.40E-201
f541.aa	gnl|PID|e1172837	membrane protein A [Borrelia garinii]	1496	3.70E-201
f541.aa	gnl|PID|e1172830	membrane protein A [Borrelia afzelii]	1493	9.60E-201
f541.aa	gnl|PID|e1172838	membrane protein A [Borrelia garinii]	1488	4.60E-200
f541.aa	gnl|PID|e237214	membrane protein A [Borrelia garinii]	1216	1.20E-162
f541.aa	gnl|PID|e237209	membrane protein A [Borrelia garinii]	1211	5.90E-162
f541.aa	gnl|PID|e237236	membrane protein A [Borrelia garinii]	1098	2.00E-146
f541.aa	gi|2688282	(AE001143) basic membrane protein B (bmpB) [Borrelia burgdorferi]	518	1.20E-123
f542.aa	gi|508422	[Borrelia burgdorferi immunodominant antigen P39 gene, complete	711	1.70E-95
f542.aa	gi|2688282	(AE001143) basic membrane protein B (bmpB) [Borrelia burgdorferi]	711	1.70E-95
f542.aa	gi|551744	membrane lipoprotein [Borrelia burgdorferi]	708	8.60E-95
f542.aa	gnl|PID|e11	bmpB(p39,ORF2) [Borrelia burgdorferi]	699	8.20E-94

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

	72836			
f542.aa	gnllPIDle11 72832	bmpB(p39,ORF2) [Borrelia afzelii]	634	1.00E-84
f542.aa	gnllPIDle11 72839	bmpB(p39,ORF2) [Borrelia garinii]	613	9.20E-82
f542.aa	gnllPIDle23 7209	membrane protein A [Borrelia garinii]	153	1.70E-32
f542.aa	gnllPIDle11 72828	bmpA(p39,ORF1) [Borrelia burgdorferi]	144	3.80E-32
f542.aa	gnllPIDle23 7214	membrane protein A [Borrelia garinii]	153	2.00E-31
f542.aa	gil1753225	BmpA protein [Borrelia burgdorferi]	155	2.80E-31
f542.aa	gnllPIDle11 72833	bmpA(p39,ORF1) [Borrelia burgdorferi]	155	2.80E-31
f542.aa	gil508421	antigen P39 [Borrelia burgdorferi] >gil2688281 (AE001143) basic	155	2.80E-31
f542.aa	gnllPIDle11 72837	membrane protein A [Borrelia garinii]	156	1.00E-30
f542.aa	gnllPIDle11 72829	membrane protein A [Borrelia afzelii]	144	1.90E-30
f542.aa	gnllPIDle11 72830	membrane protein A [Borrelia afzelii]	144	2.70E-30
f544.aa	gil2688284	(AE001143) Mg2+ transport protein (mgtE) [Borrelia burgdorferi]	860	4.20E-119
f544.aa	gil1753228	MgtE [Borrelia burgdorferi]	855	2.20E-118
f544.aa	gil619724	MgtE [Bacillus firmus] >pirlI40201lI40201 mgtE protein - Bacillus	176	3.70E-37
f544.aa	gil780282	extended ORF of mgtE gene; transcription from this start point is	182	1.30E-34
f544.aa	gnllPIDle31 5479	unknown [Mycobacterium tuberculosis]	183	4.50E-31
f544.aa	gnllPIDld10 18132	Mg2+ transporter [Synechocystis sp.] >pirlS77552lS77552 Mg2+	165	4.60E-31
f544.aa	gnllPIDle11 81529	(AJ002571) YkoK [Bacillus subtilis] >gnllPIDle1183350 similar	142	2.30E-30
f544.aa	gil2621701	(AE000843) Mg2+ transporter [Methanobacterium thermoautotrophicum]	142	3.20E-21

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f545.aa	gi|2688284	(AE001143) Mg2+ transport protein (mgtE) [Borrelia burgdorferi]	860	4.20E-119
f545.aa	gi|1753228	MgtE [Borrelia burgdorferi]	855	2.20E-118
f545.aa	gi|619724	MgtE [Bacillus firmus] >pir|I40201|I40201 mgtE protein - Bacillus	176	3.70E-37
f545.aa	gi|780282	extended ORF of mgtE gene; transcription from this start point is	182	1.30E-34
f545.aa	gnl|PID|e31 5479	unknown [Mycobacterium tuberculosis]	183	4.50E-31
f545.aa	gnl|PID|d10 18132	Mg2+ transporter [Synechocystis sp.] >pir|S77552|S77552 Mg2+	165	4.60E-31
f545.aa	gnl|PID|e11 81529	(AJ002571) YkoK [Bacillus subtilis] >gnl|PID|e1183350 similar	142	2.30E-30
f545.aa	gi|2621701	(AE000843) Mg2+ transporter [Methanobacterium thermoautotrophicum]	142	3.20E-21
f561.aa	gi|49245	lipoprotein [Borrelia burgdorferi] >gi|2688271 (AE001142) lipoprotein	1000	1.30E-132
f561.aa	gi|495738	P22 [Borrelia burgdorferi]	982	3.70E-130
f577.aa	gi|2688261	(AE001141) B. burgdorferi predicted coding region BB0352 [Borrelia	1930	4.00E-264
f584.aa	gi|2688246	(AE001140) B. burgdorferi predicted coding region BB0346 [Borrelia	1094	4.10E-147
f596.aa	gi|2688241	(AE001140) P26 [Borrelia burgdorferi] >pir|G70141|G70141 P26	1322	1.20E-180
f596.aa	gi|2281465	(AF000366) P26 [Borrelia burgdorferi] >gi|2281465 (AF000366) P26	1010	5.90E-137
f598.aa	gi|2281462	(AF000366) oligopeptide permease homolog D [Borrelia burgdorferi]	652	1.20E-85
f598.aa	gi|143607	sporulation protein [Bacillus subtilis]	372	1.20E-45
f598.aa	gnl|PID|e11 83166	oligopeptide ABC transporter (ATP-binding protein) [Bacillus	372	1.20E-45
f598.aa	gi|1574676	oligopeptide transport ATP-binding protein (oppD) [Haemophilus	344	6.70E-42
f598.aa	gi|677943	AppD [Bacillus subtilis] >gnl|PID|e1183156 oligopeptide ABC	344	8.00E-42
f598.aa	gi|1787051	(AE000185) o612; 48 pct identical (33 gaps) to 525 residues from	346	2.50E-41
f598.aa	gi|47346	AmiE protein [Streptococcus pneumoniae] >pir|S11152|S11152 amiE	338	1.10E-40
f598.aa	gi|47805	Opp D (AA1-335) [Salmonella typhimurium] >sp|P04285|OPPD_SALTY	332	5.70E-40
f598.aa	pir|A03413| QREBOT	oligopeptide transport protein oppD - Salmonella typhimurium	332	5.70E-40
f598.aa	gi|1787499	(AE000223) oligopeptide transport ATP-binding protein OppD	332	5.90E-40
f598.aa	gnl|PID|d10 15494	Oligopeptide transport ATP-binding protein OppD. [Escherichia	332	5.90E-40
f598.aa	gi|495177	ATP binding protein [Lactococcus lactis] >sp|P50980|OPPD_LACLC	331	8.40E-40

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

<table>
<tr><td>f598.aa</td><td>gnl|PID|e18 7587</td><td>oligopeptidepermease [Streptococcus pyogenes]</td><td>331</td><td>1.10E-39</td></tr>
<tr><td>f598.aa</td><td>gi|308850</td><td>ATP binding protein [Lactococcus lactis] >pir|A53290|A53290</td><td>329</td><td>1.60E-39</td></tr>
<tr><td>f598.aa</td><td>gi|2313399</td><td>(AE000548) dipeptide ABC transporter, ATP-binding protein (dppD)</td><td>322</td><td>2.30E-39</td></tr>
<tr><td>f6-21.aa</td><td>gi|2281468</td><td>(AF000948) OppAIV [Borrelia burgdorferi] >gi|2689891 (AE000792)</td><td>565</td><td>4.30E-73</td></tr>
<tr><td>f6-21.aa</td><td>gi|2253286</td><td>(AF005657) plasminogen binding protein [Borrelia burgdorferi]</td><td>315</td><td>1.20E-37</td></tr>
<tr><td>f6-21.aa</td><td>gi|2688228</td><td>(AE001139) oligopeptide ABC transporter, periplasmic</td><td>314</td><td>1.60E-37</td></tr>
<tr><td>f6-21.aa</td><td>gi|2809544</td><td>(AF043071) oligopeptide permease periplasmic binding protein</td><td>314</td><td>1.60E-37</td></tr>
<tr><td>f6-21.aa</td><td>gi|2281457</td><td>(AF000366) oligopeptide permease homolog AI [Borrelia burgdorferi]</td><td>314</td><td>1.60E-37</td></tr>
<tr><td>f6-21.aa</td><td>gi|2688227</td><td>(AE001139) oligopeptide ABC transporter, periplasmic</td><td>290</td><td>3.90E-34</td></tr>
<tr><td>f6-21.aa</td><td>gi|2281458</td><td>(AF000366) oligopeptide permease homolog AII [Borrelia burgdorferi]</td><td>290</td><td>3.90E-34</td></tr>
<tr><td>f6-21.aa</td><td>gi|2281455</td><td>(AF000365) oligopeptide permease homolog AV [Borrelia burgdorferi]</td><td>279</td><td>9.90E-34</td></tr>
<tr><td>f6-21.aa</td><td>gi|2690261</td><td>(AE000790) oligopeptide ABC transporter, periplasmic</td><td>282</td><td>5.30E-33</td></tr>
<tr><td>f6-21.aa</td><td>gi|1616644</td><td>P30 [Borrelia burgdorferi]</td><td>271</td><td>6.70E-32</td></tr>
<tr><td>f6-21.aa</td><td>gi|2688226</td><td>(AE001139) oligopeptide ABC transporter, periplasmic</td><td>268</td><td>5.00E-31</td></tr>
<tr><td>f6-21.aa</td><td>gi|2281459</td><td>(AF000366) oligopeptide permease homolog AIII [Borrelia</td><td>268</td><td>5.00E-31</td></tr>
<tr><td>f6-21.aa</td><td>gi|2809546</td><td>(AF043071) oligopeptide permease periplasmic binding protein</td><td>268</td><td>5.00E-31</td></tr>
<tr><td>f6-21.aa</td><td>bbs|161785</td><td>60 kda antigen [Borrelia coriaceae, C053, ATCC 4338, Peptide, 514</td><td>255</td><td>2.90E-30</td></tr>
<tr><td>f6-21.aa</td><td>gi|2983834</td><td>(AE000740) transporter (extracellular solute binding protein family</td><td>154</td><td>3.50E-14</td></tr>
<tr><td>f6-27.aa</td><td>gi|2689911</td><td>(AE000792) B. burgdorferi predicted coding region BBB09 [Borrelia</td><td>1773</td><td>7.30E-240</td></tr>
<tr><td>f6-5.aa</td><td>gi|2689905</td><td>(AE000792) B. burgdorferi predicted coding region BBB27 [Borrelia</td><td>932</td><td>7.50E-126</td></tr>
<tr><td>f600.aa</td><td>gi|2281461</td><td>(AF000366) oligopeptide permease homolog C [Borrelia burgdorferi]</td><td>731</td><td>1.40E-100</td></tr>
<tr><td>f600.aa</td><td>gi|2688244</td><td>(AE001140) oligopeptide ABC transporter, permease protein (oppC-1)</td><td>731</td><td>1.40E-100</td></tr>
<tr><td>f600.aa</td><td>gi|143606</td><td>sporulation protein [Bacillus subtilis] >pir|C38447|C38447</td><td>372</td><td>5.00E-48</td></tr>
<tr><td>f600.aa</td><td>gi|40007</td><td>OppC gene product [Bacillus subtilis] >gnl|PID|e1183165 oligopeptide</td><td>372</td><td>5.00E-48</td></tr>
<tr><td>f600.aa</td><td>gi|1574677</td><td>oligopeptide transport system permease protein (oppC)C [Haemophilus</td><td>372</td><td>7.30E-48</td></tr>
<tr><td>f600.aa</td><td>gi|47804</td><td>Opp C (AA1-301) [Salmonella typhimurium] >pir|C29333|QREBOC</td><td>366</td><td>4.20E-47</td></tr>
<tr><td>f600.aa</td><td>gnl|PID|d10 15493</td><td>Oligopeptide transport system permease protein OppC.</td><td>366</td><td>4.20E-47</td></tr>
<tr><td>f600.aa</td><td>gnl|PID|e11 81495</td><td>(AJ002571) DppC [Bacillus subtilis] >gnl|PID|e1183314</td><td>267</td><td>1.70E-42</td></tr>
</table>

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f600.aa	gi|1732315	transport system permease homolog [Listeria monocytogenes]	335	5.30E-42
f600.aa	gi|580851	dciAC [Bacillus subtilis] >sp|P26904|DPPC_BACSU DIPEPTIDE TRANSPORT	258	1.50E-40
f600.aa	gnl|PID|d1011164	oligopeptide transport system permease protein [Synechocystis	240	2.50E-39
f600.aa	gi|677947	AppC [Bacillus subtilis] >gnl|PID|e1183160 oligopeptide ABC	236	2.80E-37
f600.aa	gi|1813497	dipeptide transporter protein dppC [Bacillus firmus]	281	1.20E-35
f600.aa	sp|Q10623|Y021_MYCTU	PUTATIVE PEPTIDE TRANSPORT PERMEASE PROTEIN CY373.01C.	290	1.50E-35
f600.aa	gi|1532201	BldKA [Streptomyces coelicolor]	291	1.60E-35
f603.aa	gi|2281460	(AF000366) oligopeptide permease homolog B [Borrelia burgdorferi]	1522	5.80E-214
f603.aa	gi|1574678	dipeptide transport system permease protein (dppB) [Haemophilus	392	1.30E-100
f603.aa	gnl|PID|e1183164	oligopeptide ABC transporter (permease) [Bacillus subtilis]	374	3.40E-96
f603.aa	gi|580897	OppB gene product [Bacillus subtilis] >pir|S15231|B38447	373	6.60E-96
f603.aa	gi|47803	Opp B (AA1-306) [Salmonella typhimurium] >pir|B29333|QREBOB	371	6.70E-96
f603.aa	gi|1787497	(AE000223) oligopeptide transport system permease protein OppB	364	3.50E-95
f603.aa	gnl|PID|d1015492	Oligopeptide transport system permease protein OppB.	357	3.50E-94
f603.aa	gi|580850	dciAB [Bacillus subtilis] >gnl|PID|e1181494 (AJ002571) DppB	350	9.10E-90
f603.aa	gi|551726	sporulation protein [Bacillus subtilis] >gi|143605 sporulation	374	2.40E-87
f603.aa	gi|349226	transmembrane protein [Escherichia coli] >gi|466682 dppB	293	9.60E-79
f603.aa	gi|1787053	(AE000185) o306; This 306 aa ORF is 46 pct identical (32 gaps) to	284	3.80E-77
f603.aa	gi|972895	DppB [Haemophilus influenzae] >gi|1574114 dipeptide transport system	301	2.50E-76
f603.aa	gi|2182646	(AE000098) Y4tP [Rhizobium sp. NGR234] >sp|Q53191|Y4TP_RHISN	294	9.10E-74
f603.aa	gi|2983140	(AE000692) transporter (OppBC family) [Aquifex aeolicus]	169	2.30E-73
f603.aa	gi|677946	AppB [Bacillus subtilis] >gnl|PID|e1183159 oligopeptide ABC	218	8.70E-73
f604.aa	gi|2281459	(AF000366) oligopeptide permease homolog AIII [Borrelia	2818	0
f604.aa	gi|2809546	(AF043071) oligopeptide permease periplasmic binding protein	2818	0
f604.aa	gi|2688226	(AE001139) oligopeptide ABC transporter, periplasmic	2823	0
f604.aa	gi|2688227	(AE001139) oligopeptide ABC transporter, periplasmic	1738	1.40E-234

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f604.aa	gi|2281458	(AF000366) oligopeptide permease homolog AII [Borrelia burgdorferi]	1731	1.30E-233
f604.aa	gi|2281468	(AF000948) OppAIV [Borrelia burgdorferi] >gi|2689891 (AE000792)	1675	3.60E-229
f604.aa	gi|2688228	(AE001139) oligopeptide ABC transporter, periplasmic	718	1.60E-204
f604.aa	gi|2809544	(AF043071) oligopeptide permease periplasmic binding protein	718	3.00E-204
f604.aa	gi|2253286	(AF005657) plasminogen binding protein [Borrelia burgdorferi]	718	4.10E-204
f604.aa	gi|2281457	(AF000366) oligopeptide permease homolog AI [Borrelia burgdorferi]	714	2.00E-203
f604.aa	bbs|161785	60 kda antigen [Borrelia coriaceae, C053, ATCC 4338, Peptide, 514	704	1.20E-190
f604.aa	gi|2281455	(AF000365) oligopeptide permease homolog AV [Borrelia burgdorferi]	1402	1.80E-188
f604.aa	gi|2690261	(AE000790) oligopeptide ABC transporter, periplasmic	1400	3.40E-188
f604.aa	gi|1616644	P30 [Borrelia burgdorferi]	858	4.90E-117
f604.aa	gi|47802	Opp A (AA1-542) [Salmonella typhimurium] >gi|47808 precursor	296	9.00E-114
f606.aa	gi|2281458	(AF000366) oligopeptide permease homolog AII [Borrelia burgdorferi]	2762	0
f606.aa	gi|2688227	(AE001139) oligopeptide ABC transporter, periplasmic	2774	0
f606.aa	gi|2281468	(AF000948) OppAIV [Borrelia burgdorferi] >gi|2689891 (AE000792)	1817	6.50E-245
f606.aa	gi|2809546	(AF043071) oligopeptide permease periplasmic binding protein	1739	3.10E-234
f606.aa	gi|2688226	(AE001139) oligopeptide ABC transporter, periplasmic	1738	4.20E-234
f606.aa	gi|2281459	(AF000366) oligopeptide permease homolog AIII [Borrelia	1733	2.00E-233
f606.aa	bbs|161785	60 kda antigen [Borrelia coriaceae, C053, ATCC 4338, Peptide, 514	762	1.70E-202
f606.aa	gi|2281455	(AF000365) oligopeptide permease homolog AV [Borrelia burgdorferi]	1456	1.80E-195
f606.aa	gi|2690261	(AE000790) oligopeptide ABC transporter, periplasmic	1454	3.30E-195
f606.aa	gi|2253286	(AF005657) plasminogen binding protein [Borrelia burgdorferi]	751	2.00E-192
f606.aa	gi|2688228	(AE001139) oligopeptide ABC transporter, periplasmic	751	2.70E-192
f606.aa	gi|2809544	(AF043071) oligopeptide permease periplasmic binding protein	751	6.90E-192
f606.aa	gi|2281457	(AF000366) oligopeptide permease homolog AI [Borrelia burgdorferi]	748	2.40E-191
f606.aa	gi|1616644	P30 [Borrelia burgdorferi]	1220	7.30E-163
f606.aa	gi|47802	Opp A (AA1-542) [Salmonella typhimurium] >gi|47808 precursor	285	7.80E-106
f607.aa	gi|2281457	(AF000366) oligopeptide permease homolog AI [Borrelia burgdorferi]	2694	0
f607.aa	gi|2253286	(AF005657) plasminogen binding protein [Borrelia burgdorferi]	2706	0
f607.aa	gi|2809544	(AF043071) oligopeptide permease periplasmic binding protein	2708	0
f607.aa	gi|2688228	(AE001139) oligopeptide ABC transporter, periplasmic	2714	0
f607.aa	bbs|161785	60 kda antigen [Borrelia coriaceae, C053, ATCC 4338, Peptide, 514	1272	3.80E-242

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f607.aa	gi|2809546	(AF043071) oligopeptide permease periplasmic binding protein	718	1.40E-204
f607.aa	gi|2688226	(AE001139) oligopeptide ABC transporter, periplasmic	718	3.60E-204
f607.aa	gi|2281459	(AF000366) oligopeptide permease homolog AIII [Borrelia	713	1.70E-203
f607.aa	gi|2688227	(AE001139) oligopeptide ABC transporter, periplasmic	751	2.40E-192
f607.aa	gi|2281458	(AF000366) oligopeptide permease homolog AII [Borrelia burgdorferi]	751	4.50E-192
f607.aa	gi|2281468	(AF000948) OppAIV [Borrelia burgdorferi] >gi|2689891 (AE000792)	806	8.40E-189
f607.aa	gi|2690261	(AE000790) oligopeptide ABC transporter, periplasmic	601	1.20E-144
f607.aa	gi|2281455	(AF000365) oligopeptide permease homolog AV [Borrelia burgdorferi]	600	1.60E-144
f607.aa	gi|1616644	P30 [Borrelia burgdorferi]	709	5.40E-103
f607.aa	gi|47802	Opp A (AA1-542) [Salmonella typhimurium] >gi|47808 precursor	261	8.50E-69
f611.aa	gi|2688231	(AE001139) B. burgdorferi predicted coding region BB0325 [Borrelia	1907	1.10E-261
f617.aa	gi|2688213	(AE001138) conserved hypothetical integral membrane protein	1574	2.70E-226
f617.aa	gi|2649711	(AE001042) ribose ABC transporter, permease protein (rbsC-1)	109	7.00E-12
f631.aa	gi|1165286	FtsW [Borrelia burgdorferi] >gi|2688164 (AE001137) cell division	1820	4.00E-259
f631.aa	gnl|PID|e229592	membrane protein [Borrelia burgdorferi] >gnl|PID|e228289 ftsW	1815	2.10E-258
f631.aa	gi|146039	cell division protein [Escherichia coli] >gi|40857 FtsW protein	362	1.30E-60
f631.aa	gi|580938	internal open reading frame (AA 1-290) [Bacillus subtilis]	407	4.90E-55
f631.aa	gnl|PID|e315953	FtsW [Mycobacterium tuberculosis] >sp|O06223|FTWH_MYCTU	412	5.40E-55
f631.aa	gi|580937	spoVE gene product (AA 1-366) [Bacillus subtilis] >gnl|PID|e1185111	410	2.90E-53
f631.aa	gi|143657	endospore forming protein [Bacillus subtilis]	405	1.20E-52
f631.aa	gnl|PID|d1019002	rod-shape-determining protein [Synechocystis sp.]	358	3.10E-51
f631.aa	gnl|PID|e1287793	(AL022602) cell divisin protein FtsW [Mycobacterium leprae]	396	6.70E-51
f631.aa	gi|1016213	strong sequence similarity to FtsW, RodA, and SpoV-E [Cyanophora	349	1.00E-50
f631.aa	gi|1574692	cell division protein (ftsW) [Haemophilus influenzae]	304	4.20E-50
f631.aa	gnl|PID|e1185075	similar to cell-division protein [Bacillus subtilis]	281	1.80E-46
f631.aa	gi|1469784	putative cell division protein ftsW [Enterococcus hirae]	247	1.60E-38

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f631.aa	gil1572976	rod shape-determining protein (mreB) [Haemophilus influenzae]	196	1.20E-37
f631.aa	gil147695	rod-shape-determining protein [Escherichia coli] >gil1778551	194	5.00E-35
f635.aa	gil1165282	orf7; Method: conceptual translation supplied by author [Borrelia	1166	1.00E-156
f635.aa	gil1448949	ORF 224; The predicted gene product showed weak homology with the	621	2.80E-125
f647.aa	gil2688180	(AE001137) flagellar protein (flbB) [Borrelia burgdorferi]	1032	1.00E-140
f647.aa	gil1196323	putative [Borrelia burgdorferi]	1031	1.50E-140
f647.aa	gil1165270	orf19; Method: conceptual translation supplied by author [Borrelia	1019	7.10E-139
f647.aa	gil2108242	22.5K protein [Treponema pallidum]	200	4.70E-24
f65.aa	gil2688737	(AE001178) B. burgdorferi predicted coding region BB0792 [Borrelia	1095	8.10E-148
f653.aa	gil1165265	MotB [Borrelia burgdorferi] >gil1185054 flagellar motor apparatus	1220	1.70E-164
f653.aa	gil1399286	MotB [Treponema phagedenis]	168	5.80E-57
f653.aa	gil2196896	MotB [Treponema pallidum]	179	1.30E-49
f664.aa	gil1185062	flagellar export protein [Borrelia burgdorferi]	1430	1.90E-199
f664.aa	gil1165257	FlhB [Borrelia burgdorferi] >gil2688194 (AE001137) flagellar	1430	1.90E-199
f664.aa	gil1216382	FlhB' [Treponema pallidum] >pirlPC4115lPC4115 flagellar protein	272	5.30E-64
f664.aa	gil395390	flagellar biosynthetic protein [Bacillus subtilis]	433	1.30E-61
f664.aa	gnllPIDle11 85229	flagella-associated protein [Bacillus subtilis]	433	1.30E-61
f664.aa	gil1147737	third gene in fliQ operon; membrane protein homolog [Caulobacter	353	1.70E-46
f664.aa	gil2313898	(AE000589) flagellar biosynthetic protein (flhB) [Helicobacter	203	1.20E-44
f664.aa	gil2984250	(AE000768) flagellar biosynthetic protein FlhB [Aquifex aeolicus]	319	3.00E-44
f664.aa	gil2459702	FlhB [Agrobacterium tumefaciens]	347	6.20E-44
f664.aa	gil793892	flhB [Yersinia enterocolitica] >pirlS54213lS54213 flhB protein -	330	1.30E-39
f664.aa	gnllPIDld10 16420	Flagellar biosynthetic protein FlhB. [Escherichia coli]	325	2.20E-39
f664.aa	gil475126	yscU [Yersinia pseudotuberculosis] >gil2996233 (AF053946) Yop	309	9.80E-38
f664.aa	gil497216	YscU [Yersinia enterocolitica]	308	1.40E-37
f664.aa	gnllPIDld10 07477	flagellar protein FlhB [Salmonella typhimurium]	312	2.10E-37
f664.aa	gnllPIDle28 3684	secretion system apparatus, SsaU [Salmonella typhimurium]	312	8.20E-37

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f679.aa	gi|2688158	(AE001136) B. burgdorferi predicted coding region BB0259 [Borrelia	3714	0
f679.aa	gnl|PID|d1011473	soluble lytic transglycosylase [Synechocystis sp.]	180	1.10E-25
f679.aa	gnl|PID|e1183177	similar to lytic transglycosylase [Bacillus subtilis]	108	2.10E-22
f679.aa	gi|2984090	(AE000756) hypothetical protein [Aquifex aeolicus]	111	9.30E-17
f680.aa	gi|2688153	(AE001136) bacitracin resistance protein (bacA) [Borrelia	769	3.90E-109
f680.aa	gnl|PID|e1185988	similar to bacitracin resistance protein (undecaprenol	174	7.30E-18
f680.aa	gi|2622542	(AE000905) bacitracin resistance protein [Methanobacterium	116	3.30E-16
f680.aa	gi|2984378	(AE000777) undecaprenol kinase [Aquifex aeolicus]	152	3.90E-15
f680.aa	gi|882579	CG Site No. 29739 [Escherichia coli] >gi|1789437 (AE000387)	139	2.60E-12
f688.aa	gi|2688146	(AE001135) conserved hypothetical integral membrane protein	2497	0
f688.aa	gi|2649351	(AE001019) conserved hypothetical protein [Archaeoglobus fulgidus]	110	3.70E-18
f688.aa	gi|1592186	M. jannaschii predicted coding region MJ1562 [Methanococcus	174	1.10E-16
f7-30.aa	gi|2690009	(AE000786) conserved hypothetical protein [Borrelia burgdorferi]	682	1.90E-90
f704.aa	gi|2688137	(AE001134) glycerol uptake facilitator (glpF) [Borrelia	1307	4.70E-181
f704.aa	gi|142997	glycerol uptake facilitator [Bacillus subtilis] >gnl|PID|e1182917	191	1.50E-50
f704.aa	gi|521003	C01G6.1 [Caenorhabditis elegans]	152	1.60E-50
f704.aa	gi|529582	water channel protein [Rattus norvegicus] >pir|I59266|I59266 water	142	5.80E-50
f704.aa	dbj||AB000507_1	(AB000507) aquaporin 7 [Rattus norvegicus]	155	1.30E-49
f704.aa	pir|A57119|A57119	aquaporin 3 - human	149	4.20E-44
f704.aa	gi|1109920	coded for by C. elegans cDNA cm16b11; strong similarity to MIP	168	9.30E-44
f704.aa	gnl|PID|d1019987	(AB001325) aquaporin 3 [Homo sapiens] >sp|Q92482|AQP3_HUMAN	148	5.30E-43
f704.aa	gnl|PID|d1025786	(AB008775) aquaporin 9 [Homo sapiens]	144	1.40E-42
f704.aa	gi|146188	glycerol diffusion facilitator [Escherichia coli] >gi|305030 CG Site	146	1.30E-40
f704.aa	gi|1065485	strong similarity to the MIP family of transmembrane channel	179	1.40E-39
f704.aa	sp|P31140|	GLYCEROL UPTAKE FACILITATOR PROTEIN.	146	3.30E-39

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

	GLPF_SHIFL			
f704.aa	gi|2587035	(AF026270) PduF [Salmonella typhimurium] >sp|P37451|PDUF_SALTY	168	7.30E-39
f704.aa	gi|1399489	glycerol dfiffusion facilitator [Pseudomonas aeruginosa]	154	7.90E-39
f704.aa	gi|2649144	(AE001005) glycerol uptake facilitator, MIP channel (glpF)	150	1.30E-38
f707.aa	gi|2688143	(AE001134) B. burgdorferi predicted coding region BB0238 [Borrelia	1300	3.90E-176
f709.aa	gi|2688131	(AE001133) B. burgdorferi predicted coding region BB0236 [Borrelia	3437	0
f730.aa	gi|2688111	(AE001132) gufA protein [Borrelia burgdorferi] >pir|C70127|C70127	1376	3.00E-192
f730.aa	gi|1707057	coded for by C. elegans cDNA CEESS55F; coded for by C. elegans cDNA	235	2.80E-83
f730.aa	gi|2621542	(AE000831) conserved protein [Methanobacterium thermoautotrophicum]	259	1.10E-74
f730.aa	gnl|PID|e183440	gufA gene product [Myxococcus xanthus] >gi|49253 orfX gene	175	2.30E-35
f730.aa	gi|2984109	(AE000757) hypothetical protein [Aquifex aeolicus]	171	7.00E-28
f736.aa	gi|2688115	(AE001132) phosphate ABC transporter, periplasmic phosphate-binding	1403	2.10E-186
f736.aa	gi|2622858	(AE000929) phosphate-binding protein PstS [Methanobacterium	151	4.40E-30
f736.aa	gi|2622859	(AE000929) phosphate-binding protein PstS homolog [Methanobacterium	145	2.80E-24
f736.aa	gnl|PID|d1010224	ORF108 [Bacillus subtilis] >gnl|PID|e1185766 alternate gene	120	1.20E-11
f739.aa	gi|2688119	(AE001132) B. burgdorferi predicted coding region BB0213 [Borrelia	1139	1.10E-156
f742.aa	gi|2688100	(AE001131) surface-located membrane protein 1 (lmp1) [Borrelia	5654	0
f742.aa	gi|2621120	(AE000799) O-linked GlcNAc transferase [Methanobacterium	200	9.30E-22
f742.aa	gi|2621106	(AE000798) O-linked GlcNAc transferase [Methanobacterium	180	5.80E-17
f742.aa	pir|E69190|E69190	conserved hypothetical protein MTH68 - Methanobacterium	154	1.60E-14
f742.aa	gi|1591608	transformation sensitive protein [Methanococcus jannaschii]	109	9.90E-14
f742.aa	gi|1589778	SPINDLY [Arabidopsis thaliana]	101	1.40E-13
f742.aa	gi|2984175	(AE000762) hypothetical protein [Aquifex aeolicus]	132	7.30E-13
f742.aa	gi|3037137	(AF056198) Hsp70/Hsp90 organizing protein homolog [Drosophila	105	5.40E-11
f743.aa	gi|2688104	(AE001131) B. burgdorferi predicted coding region BB0209 [Borrelia	1299	1.70E-174
f748.aa	gi|2688089	(AE001130) Lambda CII stability-governing protein (hflC) [Borrelia	1615	5.10E-220

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f748.aa	gil436158	putative integral membrane protease required for high frequency	191	4.80E-35
f748.aa	gil1573107	Lambda CII stability-governing protein (hflC) [Haemophilus	193	4.90E-33
f748.aa	gil507735	HflC [Vibrio parahaemolyticus] >splP40606lHFLC_VIBPA HFLC PROTEIN	212	6.10E-26
f752.aa	gil2688092	(AE001130)	2585	0
f752.aa	gil2984050	(AE000754) UDP-MurNac-tripeptide synthetase [Aquifex aeolicus]	202	9.10E-74
f752.aa	gil40162	murE gene product [Bacillus subtilis] >gnllPIDle1185108	157	6.40E-70
f752.aa	gnllPIDld10 11466	UDP-MurNac-tripeptide synthetase [Synechocystis sp.]	166	5.20E-57
f752.aa	gnllPIDle30 7808	UDP-MurNAc-tripeptide synthetase [Rickettsia prowazekii]	108	2.30E-51
f752.aa	gil1574688	UDP-MurNac-tripeptide synthetase (murE) [Haemophilus influenzae]	166	3.20E-50
f752.aa	gnllPIDle12 87797	(AL022602) udp-n-acetylmuramoylalanyl-d-glutamate	183	3.20E-50
f752.aa	gnllPIDle31 6022	MurE [Mycobacterium tuberculosis]	181	4.10E-46
f752.aa	gil581032	UDP-MurNac-tripeptide synthetase (MurE) [Escherichia coli]	175	1.30E-41
f752.aa	gil2177098	UDP-MurNAc-Dipeptide: meso-diaminopimelate ligase [Escherichia	172	3.70E-41
f752.aa	gil2314673	(AE000648) UDP-MurNac-tripeptide synthetase (murE) [Helicobacter	137	9.80E-41
f752.aa	gil840843	UDP-N-acetylmuramoylalanyl-D-glutamate-- 2,6-diaminopimelate ligase	135	1.70E-20
f76-1.aa	gil1209837	lipoprotein [Borrelia burgdorferi]	395	2.80E-49
f76-1.aa	gil1209873	lipoprotein [Borrelia burgdorferi]	250	7.00E-37
f76-1.aa	gil1209843	lipoprotein [Borrelia burgdorferi]	267	7.30E-32
f76-1.aa	gil2121280	(AF000270) lipoprotein [Borrelia burgdorferi] >gil3095109	258	1.20E-30
f76-1.aa	gnllPIDle26 8244	surface-exposed lipoprotein [Borrelia afzelii]	116	2.40E-18
f76-1.aa	gil1209849	lipoprotein [Borrelia burgdorferi]	146	8.30E-17
f76-1.aa	gil3095105	(AF046998) 2.9-8 lipoprotein [Borrelia burgdorferi]	148	5.80E-14
f76-1.aa	gil3095107	(AF046999) 2.9-9 lipoprotein [Borrelia burgdorferi]	127	7.20E-11
f764.aa	gil2688084	(AE001129) B. burgdorferi predicted coding region BB0193 [Borrelia	1218	1.20E-164
f770.aa	gil2688077	(AE001129) conserved hypothetical protein [Borrelia burgdorferi]	646	7.60E-87
f790.aa	gil2688065	(AE001128) outer membrane protein (tpn50) [Borrelia burgdorferi]	2013	2.50E-271

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f790.aa	gi|458015	TpN50 precursor [Treponema pallidum]	134	4.30E-33
f790.aa	sp|P38369|TP50_TREPA	OUTER MEMBRANE PROTEIN TPN50 PRECURSOR.	134	4.30E-33
f790.aa	gi|532658	antigen [Treponema pallidum] >pir|S61867|S61867 antigen tpp57 -	139	4.30E-31
f792.aa	gi|2688052	(AE001127) B. burgdorferi predicted coding region BB0165 [Borrelia	3185	0
f797.aa	gi|2688056	(AE001127) B. burgdorferi predicted coding region BB0159 [Borrelia	1116	5.30E-148
f798.aa	gi|2688051	(AE001127) antigen, S2, putative [Borrelia burgdorferi]	1223	9.70E-164
f798.aa	gi|1063419	S2 gene product [Borrelia burgdorferi]	116	4.70E-23
f798.aa	gi|2690227	(AE000790) antigen, S2 [Borrelia burgdorferi] >pir|D70207|D70207	116	1.50E-22
f798.aa	gi|2690128	(AE000788) protein p23 [Borrelia burgdorferi] >pir|C70257|C70257	110	1.40E-19
f798.aa	gi|2689956	(AE000785) protein p23 [Borrelia burgdorferi] >pir|D70225|D70225	104	2.70E-15
f799.aa	gi|2688043	(AE001126) B. burgdorferi predicted coding region BB0156 [Borrelia	632	1.40E-83
f8-10.aa	gi|2690052	(AE000784) antigen, P35, putative [Borrelia burgdorferi]	1241	1.10E-167
f8-10.aa	gi|2689955	(AE000785) antigen, P35, putative [Borrelia burgdorferi]	298	1.70E-57
f8-10.aa	gi|2690120	(AE000789) B. burgdorferi predicted coding region BBI34 [Borrelia	254	3.80E-54
f8-10.aa	gi|2690100	(AE000789) B. burgdorferi predicted coding region BBI16 [Borrelia	182	2.90E-31
f8-10.aa	gi|2690207	(AE000787) B. burgdorferi predicted coding region BBJ02 [Borrelia	196	1.50E-20
f8-10.aa	gi|2690116	(AE000789) B. burgdorferi predicted coding region BBI29 [Borrelia	192	5.50E-20
f8-10.aa	gi|2690125	(AE000788) antigen, P35, putative [Borrelia burgdorferi]	129	5.80E-14
f8-10.aa	gi|2690206	(AE000787) B. burgdorferi predicted coding region BBJ01 [Borrelia	103	1.10E-13
f8-10.aa	gi|2690099	(AE000789) B. burgdorferi predicted coding region BBI15 [Borrelia	142	8.50E-13
f8-10.aa	gi|2690115	(AE000789) B. burgdorferi predicted coding region BBI28 [Borrelia	130	3.30E-12
f8-14.aa	gi|2690074	(AE000784) B. burgdorferi predicted coding region BBH37 [Borrelia	1560	2.60E-206
f8-14.aa	gi|2690188	(AE000787) B. burgdorferi predicted coding region BBJ08 [Borrelia	599	3.50E-123
f8-14.aa	gi|2690030	(AE000786) B. burgdorferi predicted coding region BBG01 [Borrelia	337	4.40E-106
f8-14.aa	gi|2690139	(AE000788) B. burgdorferi predicted coding region BBK01 [Borrelia	173	8.00E-91
f8.aa	gi|2688783	(AE001182) B. burgdorferi predicted coding region BB0840 [Borrelia	2765	0
f8.aa	gi|2697112	(AF008219) unknown [Borrelia afzelii]	1494	2.80E-205
f800.aa	gi|2688044	(AE001126) B. burgdorferi predicted coding region BB0155 [Borrelia	1936	1.00E-262
f805.aa	gi|2688039	(AE001126) N-acetylglucosamine-6-phosphate deacetylase (nagA)	641	6.30E-85

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f810.aa	gi|2688024	(AE001125) glycine betaine, L-proline ABC transporter,	1527	4.20E-207
f810.aa	gi|984805	glycine betaine-binding protein precursor [Bacillus subtilis]	179	6.80E-21
f810.aa	gi|1850605	ProX [Streptococcus mutans]	181	2.30E-18
f814.aa	pir|D70117|D70117	acriflavine resistance protein (acrB) homolog - Lyme disease	5105	0
f814.aa	gi|2688027	(AE001125) acriflavine resistance protein (acrB) [Borrelia	5111	0
f814.aa	gi|2983346	(AE000707) cation efflux (AcrB/AcrD/AcrF family) [Aquifex aeolicus]	325	4.80E-119
f814.aa	gi|2313726	(AE000574) acriflavine resistance protein (acrB) [Helicobacter	327	4.50E-111
f814.aa	gi|3068786	(AF059041) RND pump protein [Helicobacter pylori]	297	1.70E-110
f814.aa	gnl|PID|e1182651	similar to acriflavin resistance protein [Bacillus subtilis]	257	8.90E-100
f814.aa	gi|1573914	acriflavine resistance protein (acrB) [Haemophilus influenzae]	294	2.10E-97
f814.aa	gnl|PID|e256815	mexF [Pseudomonas aeruginosa]	300	2.00E-88
f814.aa	gnl|PID|d1019295	cation efflux system protein CzcA [Synechocystis sp.]	198	1.30E-87
f814.aa	gnl|PID|e285274	membrane-bound cation-proton-antiporter [Ralstonia eutropha]	283	2.20E-87
f814.aa	gi|438854	envD homologue; ORFB [Pseudomonas aeruginosa] >pir|S39630|S39630	290	6.50E-87
f814.aa	gnl|PID|d1011721	CzcA [Alcaligenes sp.] >pir|JC4700|JC4700 cadmium, zinc,	275	8.20E-87
f814.aa	gi|2314107	(AE000605) cation efflux system protein (czcA) [Helicobacter	266	2.30E-86
f814.aa	pir|A33830|A33830	cation efflux system membrane protein czcA - Alcaligenes	275	3.10E-86
f814.aa	gnl|PID|d1017073	envD gene product homolog [Escherichia coli] >gi|1788814	283	8.30E-86
f818.aa	gi|2688032	(AE001125) B. burgdorferi predicted coding region BB0139 [Borrelia	664	3.00E-87
f82.aa	gi|2688729	(AE001177) B. burgdorferi predicted coding region BB0776 [Borrelia	991	2.20E-132
f820.aa	gi|2688029	(AE001125) penicillin-binding protein (pbp-1) [Borrelia	3171	0
f820.aa	gi|580936	SpoVD [Bacillus subtilis] >gnl|PID|e1185107 penicillin-binding	149	3.00E-49
f820.aa	gi|150283	penicillin-binding protein 2 [Neisseria meningitidis]	154	6.90E-43
f820.aa	gnl|PID|e12	(AL022602) penicillin binding protein 2 [Mycobacterium	182	4.20E-42

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

	87798			
f820.aa	gil509190	penicillin-binding protein 2 [Neisseria meningitidis]	158	1.70E-41
f820.aa	gil509118	penicillin-binding protein 2 [Neisseria meningitidis]	151	7.10E-41
f820.aa	gil840842	penicillin-binding protein 3 [Pseudomonas aeruginosa]	177	1.20E-40
f820.aa	gil509065	penicillin-binding protein 2 [Neisseria meningitidis]	152	1.40E-40
f820.aa	gil509043	penicillin-binding protein 2 [Neisseria meningitidis]	150	2.70E-40
f820.aa	gil509159	penicillin-binding protein 2 [Neisseria meningitidis]	147	2.80E-40
f820.aa	gil509120	penicillin-binding protein 2 [Neisseria meningitidis]	155	1.60E-39
f820.aa	gil509157	penicillin-binding protein 2 [Neisseria meningitidis]	155	1.60E-39
f820.aa	gil509126	penicillin-binding protein 2 [Neisseria meningitidis]	158	1.70E-39
f820.aa	gil45178	penicillin-binding protein 2 (AA 1 - 581) [Neisseria meningitidis]	155	2.30E-38
f820.aa	gil150279	penicillin binding protein 2 [Neisseria gonorrhoeae]	154	8.70E-38
f831.aa	gil2688018	(AE001124) B. burgdorferi predicted coding region BB0126 [Borrelia	994	1.20E-133
f843.aa	gil2688014	(AE001124) PTS system, maltose and glucose-specific IIABC component	2590	0
f843.aa	gil2688579	(AE001166) PTS system, glucose-specific IIBC component (ptsG)	594	1.80E-129
f843.aa	gil1072418	glcA [Staphylococcus carnosus] >pirlS46952lS46952	283	1.00E-72
f843.aa	gil1072419	glcB [Staphylococcus carnosus] >pirlS63606lS46953	248	1.00E-66
f843.aa	dbjllD86417_11	YflF [Bacillus subtilis] >gnllPIDle1182760 similar to	215	7.90E-65
f843.aa	gil2197104	(AF003742) MalX homolog [Escherichia coli]	182	8.90E-64
f843.aa	gil43819	nagE gene product [Klebsiella pneumoniae] >pirlS18607lS18607	264	8.50E-63
f843.aa	gil146913	N-acetylglucosamine transport protein [Escherichia coli]	256	1.10E-62
f843.aa	gil39956	IIGlc [Bacillus subtilis] >gnllPIDle1184979 phosphotransferase system	315	5.20E-62
f843.aa	dbjllD87820_1	NagE [Vibrio cholerae non-O1] >pirlJC5651lJC5651	263	3.80E-61
f843.aa	gil2689888	(AE000792) PTS system, maltose and glucose-specific IIABC component	198	1.10E-60
f843.aa	gil397363	enzyme II-glc [Salmonella typhimurium] >pirlS36620lS36620	227	1.20E-58
f843.aa	gil147393	glucose-specific enzyme II of phosphotransferase system [Escherichia	226	3.90E-57
f843.aa	gnllPIDle1182187	alternate gene name: yzfA; similar to phosphotransferase	180	9.00E-56
f843.aa	gil1732194	PTS permease for glucose [Vibrio furnissii]	349	4.30E-50

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f850.aa	gi|2687999	(AE001123) B. burgdorferi predicted coding region BB0110 [Borrelia	2374	0
f853.aa	gi|2687994	(AE001123) basic membrane protein [Borrelia burgdorferi]	1672	2.20E-224
f853.aa	gi|155055	basic membrane protein precursor [Treponema pallidum]	130	3.60E-24
f859.aa	gi|2688002	(AE001123) B. burgdorferi predicted coding region BB0102 [Borrelia	888	1.80E-115
f86.aa	gi|2688725	(AE001177) flagellar P-ring protein (flgI) [Borrelia burgdorferi]	1647	1.50E-217
f86.aa	gi|2920802	(AF019213) FlgI [Vibrio cholerae]	143	3.50E-14
f86.aa	gi|405550	flagellar P-ring protein [Pseudomonas putida] >sp|Q52082|FLGI_PSEPU	102	3.70E-13
f86.aa	gi|144241	flagellin [Caulobacter crescentus] >pir|A41891|A41891 basal body	110	6.70E-13
f860.aa	gi|2687998	(AE001123) asparaginyl-tRNA synthetase (asnS) [Borrelia	1110	2.40E-149
f860.aa	gi|1574761	asparaginyl-tRNA synthetase (asnS) [Haemophilus influenzae]	634	1.30E-83
f860.aa	gi|147935	asparaginyl-tRNA synthetase (asnS) [Escherichia coli] >gi|41000	622	6.10E-82
f860.aa	gnl|PID|e12 02698	(AJ222644) asparaginyl-tRNA synthetase [Arabidopsis thaliana]	404	2.40E-80
f860.aa	gnl|PID|d10 11495	asparaginyl-tRNA synthetase [Synechocystis sp.]	618	4.50E-80
f860.aa	gi|530408	Asn-tRNA synthetase [Mycoplasma capricolum] >pir|S77842|S77842	439	1.60E-65
f860.aa	gi|1045792	asparaginyl-tRNA synthetase [Mycoplasma genitalium]	365	2.20E-62
f860.aa	gi|1674281	(AE000057) Mycoplasma pneumoniae, asparaginyl-tRNA synthetase;	338	3.10E-61
f860.aa	gnl|PID|e12 02700	(AJ222645) asparaginyl-tRNA synthetase [Arabidopsis thaliana]	364	3.90E-59
f860.aa	gnl|PID|e26 4488	YCR024c, len:492 [Saccharomyces cerevisiae] >pir|S19435|S19435	150	3.90E-47
f860.aa	gnl|PID|e25 4305	asparaginyl-tRNA synthetase [Salmonella typhi]	370	1.70E-46
f860.aa	gnl|PID|e18 8505	asparagine--tRNA ligase [Lactobacillus delbrueckii]	224	1.30E-44
f860.aa	pir|S71072| S71072	asparagine--tRNA ligase (EC 6.1.1.22) asnS1 - Lactobacillus	224	1.30E-44
f860.aa	gnl|PID|e18 8572	asparagine--tRNA ligase [Lactobacillus delbrueckii]	224	2.40E-44
f860.aa	gi|1146247	asparaginyl-tRNA synthetase [Bacillus subtilis] >gnl|PID|e1183681	234	6.10E-44
f861.aa	gi|2687975	(AE001122) glutamate racemase (murI) [Borrelia burgdorferi]	1354	2.90E-186

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f861.aa	gi|396314	glutamate synthase [Escherichia coli] >gi|290428 glutamate synthase	168	1.20E-16
f861.aa	gnl|PID|e11 65353	glutamate racemase [Bacillus subtilis] >gnl|PID|e1184088	120	1.80E-13
f861.aa	pir|JC5587|J C5587	glutamate racemase (EC 5.1.1.3) - Bacillus pumilus	122	1.80E-13
f861.aa	sp|P52973| MURI_HA EIN	PROBABLE GLUTAMATE RACEMASE (EC 5.1.1.3).	114	8.10E-13
f867.aa	gi|2687979	(AE001122) V-type ATPase, subunit A (atpA) [Borrelia burgdorferi]	2826	0
f867.aa	pir|JC5532|J C5532	vacuolar-type ATPase (EC 3.-.-.-) A chain - Desulfurococcus	594	2.20E-162
f867.aa	gi|2104726	V-ATPase A subunit [Desulfurococcus sp. SY]	594	3.10E-162
f867.aa	gi|2605627	ATPase alpha subunit [Thermococcus sp.]	592	7.10E-161
f867.aa	gnl|PID|d10 03475	Na+ -ATPase alpha subunit [Enterococcus hirae]	601	1.60E-153
f867.aa	gi|1590955	H+-transporting ATP synthase, subunit A (atpA) [Methanococcus	585	6.00E-147
f867.aa	gi|496904	membrane ATPase [Haloferax volcanii] >pir|S55895|S45144	728	6.00E-147
f867.aa	gi|152927	ATPase alpha subunit [Sulfolobus acidocaldarius] >pir|A28652|A28652	548	5.00E-163
f867.aa	gi|2649416	(AE001023) H+-transporting ATP synthase, subunit A (atpA)	748	2.00E-146
f867.aa	gi|2622052	(AE000869) ATP synthase, subunit A [Methanobacterium	607	9.40E-146
f867.aa	gi|168926	vacuolar ATPase vma-1 [Neurospora crassa] >pir|A30799|PXNCV7	302	9.00E-145
f867.aa	gi|149820	ATPase alpha subunit [Methanosarcina barkeri] >pir|A34283|A34283	743	1.40E-143
f867.aa	gi|160736	vacuolar ATPase [Plasmodium falciparum] >pir|A48582|A48582 vacuolar	305	9.40E-140
f867.aa	gnl|PID|d10 09732	adenosine triphosphatase A subunit [Acetabularia acetabulum]	307	9.00E-137
f867.aa	gi|49048	ATPase alpha-subunit [Thermus aquaticus thermophilus]	684	4.80E-136
f868.aa	gi|2687980	(AE001122) V-type ATPase, subunit B (atpB) [Borrelia burgdorferi]	2205	1.80E-298
f868.aa	gi|1590954	H+-transporting ATP synthase, subunit B (atpB) [Methanococcus	156	2.00E-114
f868.aa	gi|2605628	ATPase beta subunit [Thermococcus sp.]	151	3.30E-108
f868.aa	gi|2104727	V-ATPase B subunit [Desulfurococcus sp. SY]	151	1.10E-107
f868.aa	gi|43641	ATP synthase subunit [Halobacterium salinarium] >pir|S14733|S14733	150	1.80E-107
f868.aa	gi|149821	ATPase beta subunit [Methanosarcina barkeri] >pir|B34283|B34283	172	1.00E-105

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f868.aa	gnllPIDld10 03476	Na+ -ATPase beta subunit [Enterococcus hirae]	151	1.40E-105
f868.aa	gil2649415	(AE001023) H+-transporting ATP synthase, subunit B (atpB)	151	1.70E-103
f868.aa	gil496905	membrane ATPase [Haloferax volcanii] >pirlS55896lS45145	153	5.80E-103
f868.aa	gil1199639	A1AO H+ ATPase, subunit B [Methanosarcina mazeii]	173	2.20E-102
f868.aa	gil2622051	(AE000869) ATP synthase, subunit B [Methanobacterium	155	1.00E-101
f868.aa	gnllPIDld10 09734	adenosine triphosphatase B subunit [Acetabularia acetabulum]	159	1.30E-101
f868.aa	gil1086645	Similar to vacuolar ATP synthase (strong). [Caenorhabditis elegans]	163	1.30E-101
f868.aa	gil459198	vacuolar H+-ATPase subunit B [Gossypium hirsutum]	164	4.60E-101
f868.aa	gil167108	vacuolar ATPase B subunit [Hordeum vulgare] >splQ40078lVAT1_HORVU	164	4.60E-101
f872.aa	gil2687986	(AE001122) B. burgdorferi predicted coding region BB0089 [Borrelia	1684	1.60E-230
f874.aa	gil2687965	(AE001121) L-lactate dehydrogenase (ldh) [Borrelia burgdorferi]	1603	2.80E-217
f874.aa	gil39758	L- lactate dehydrogenase [Bacillus psychrosaccharolyticus]	520	3.10E-109
f874.aa	pirlS08183l S08183	L-lactate dehydrogenase (EC 1.1.1.27) X - Bacillus	515	4.30E-109
f874.aa	pirlA25805l A25805	L-lactate dehydrogenase (EC 1.1.1.27) - Bacillus subtilis	520	1.00E-107
f874.aa	gil143136	L-lactate dehydrogenase [Bacillus megaterium] >pirlS00133lDEBSLM	430	5.20E-107
f874.aa	gil143138	lactate dehydrogenase (EC 1.1.1.27) [Bacillus stearothermophilus]	514	6.60E-107
f874.aa	gnllPIDld10 09574	L-lactate dehydrogenase [Bacillus subtilis] >gnllPIDle1182257	512	8.90E-107
f874.aa	gil143134	lactate dehydrogenase (EC 1.1.1.27) [Bacillus caldotenax]	516	1.70E-106
f874.aa	gil143132	lactate dehydrogenase (AC 1.1.1.27) [Bacillus caldolyticus]	506	2.30E-106
f874.aa	gil412392	NAD-dependent dehydrogenase [unidentified]	508	4.40E-106
f874.aa	gil143130	L-lactate dehydrogenase [Bacillus caldotenax] >pirlS00019lS00019	510	1.10E-105
f874.aa	gil642256	L-lactate dehydrogenase [Pediococcus acidilactici]	560	1.70E-91
f874.aa	gil847956	L-lactate dehydrogenase [Lactobacillus sake] >splP50934lLDH_LACSK	381	2.30E-91
f874.aa	gil581305	L-lactate dehydrogenase [Lactobacillus plantarum] >pirlA36957lA36957	547	2.30E-91
f874.aa	gil149575	L(+)-lactate dehydrogenase [Lactobacillus casei]	386	3.20E-91
f886.aa	gil2687958	(AE001120) B. burgdorferi predicted coding region BB0077 [Borrelia	1792	9.50E-237

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f888.aa	gi|2687959	(AE001120) B. burgdorferi predicted coding region BB0075 [Borrelia	2351	3.59999944710933e-318
f893.aa	gi|2687962	(AE001120) B. burgdorferi predicted coding region BB0071 [Borrelia	2514	0
f895.aa	gi|2687954	(AE001120) conserved hypothetical protein [Borrelia burgdorferi]	747	3.60E-100
f895.aa	gnl|PID|e1184285	similar to hypothetical proteins [Bacillus subtilis]	103	2.50E-35
f899.aa	gi|2687946	(AE001119) B. burgdorferi predicted coding region BB0066 [Borrelia	1161	4.30E-158
f924.aa	gi|2687934	(AE001118) B. burgdorferi predicted coding region BB0044 [Borrelia	692	3.90E-93
f925.aa	gi|2687935	(AE001118) B. burgdorferi predicted coding region BB0043 [Borrelia	1771	7.50E-242
f929.aa	gi|2687916	(AE001117) B. burgdorferi predicted coding region BB0038 [Borrelia	2589	0
f93.aa	gi|2688703	(AE001176) pyridoxal kinase (pdxK) [Borrelia burgdorferi]	1334	6.60E-181
f933.aa	gi|2687917	(AE001117) B. burgdorferi predicted coding region BB0034 [Borrelia	902	1.90E-122
f933.aa	gi|2690091	(AE000789) conserved hypothetical protein [Borrelia burgdorferi]	136	3.10E-37
f933.aa	gi|2690225	(AE000790) conserved hypothetical protein [Borrelia burgdorferi]	149	4.50E-37
f933.aa	gi|2690045	(AE000784) conserved hypothetical protein [Borrelia burgdorferi]	126	5.70E-28
f933.aa	gi|2239281	No definition line found [Borrelia burgdorferi]	148	2.40E-14
f939.aa	gi|2687919	(AE001117) B. burgdorferi predicted coding region BB0028 [Borrelia	1796	7.50E-241
f940.aa	gi|2687920	(AE001117) B. burgdorferi predicted coding region BB0027 [Borrelia	1109	1.20E-152
f943.aa	gi|2687905	(AE001116) B. burgdorferi predicted coding region BB0024 [Borrelia	2001	5.00E-273
f943.aa	gi|411592	L-sorbosone dehydrogenase [unidentified]	175	2.30E-15
f943.aa	gnl|PID|d1006418	L-sorbosone dehydrogenase [Acetobacter liquefaciens]	173	4.40E-15
f952.aa	gi|2687880	(AE001115) glpE protein (glpE) [Borrelia burgdorferi]	628	2.90E-84
Query	**GenSeq Access No.**	**GenSeq Gene Description**	**BLAST Score**	**BLAST P-Value**
f07A.aa	R33279	43 kD endoflagellum sheath protein.	120	6.10E-25
f142.aa	R95044	Apoptosis participating protein.	103	4.70E-18
f147.aa	W18209	Staphylococcus aureus Coenzyme A disulphide reductase (CoADR).	194	4.80E-91

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f147.aa	W06425	Water-forming NADH oxidase.	369	8.00E-86
f147.aa	R32089	Benzene dioxygenase polypeptide V.	104	4.70E-11
f147.aa	R66733	Aromatic dihydrodiol/catechol deoxygenase #5.	105	9.00E-11
f152.aa	R81549	High affinity potassium uptake transporter HKT1.	137	3.70E-18
f157.aa	W15192	Staphylococcus aureus cell surface protein.	239	3.40E-37
f17-6.aa	W30763	Mannose-1-phosphate transferase protein MNN4.	178	5.20E-16
f17-6.aa	W03627	Human follicle stimulating hormone GPR N-terminal sequence.	145	1.30E-11
f17-6.aa	W03626	Human thyrotropin GPR N-terminal sequence.	144	1.90E-11
f17-6.aa	W21591	Antibiotic potentiating peptide #3.	141	5.10E-11
f196.aa	W05196	Helicobacter pylori 50 kDa protective antigen G3.8.	183	2.70E-18
f196.aa	W20916	H. pylori inner membrane protein 14gp12015orf12.	180	3.60E-17
f196.aa	W20287	H. pylori inner membrane protein, 24132293.aa.	169	6.50E-15
f196.aa	W20769	H. pylori inner membrane protein, 07ee20513orf28.	169	1.40E-14
f196.aa	W20767	H. pylori cytoplasmic protein, 07ee20513orf1.	140	6.10E-14
f197.aa	W20769	H. pylori inner membrane protein, 07ee20513orf28.	190	2.30E-19
f197.aa	W20287	H. pylori inner membrane protein, 24132293.aa.	190	2.00E-18
f197.aa	W05196	Helicobacter pylori 50 kDa protective antigen G3.8.	179	4.00E-16
f197.aa	W20916	H. pylori inner membrane protein 14gp12015orf12.	182	6.30E-16
f197.aa	W20767	H. pylori cytoplasmic protein, 07ee20513orf1.	150	1.10E-12
f21-4.aa	R69629	B. burgdorferi OspF operon.	321	7.00E-39
f21-4.aa	R89476	B. burgdorferi OspG lipoprotein.	107	6.10E-34
f24-1.aa	W22676	Borrelia variable major protein (VMP)-like protein VlsE.	412	4.60E-72
f291.aa	W20152	H. pylori transporter protein, 1464715.aa.	336	1.70E-41
f291.aa	W24682	Helicobacter pylori transporter protein 4882763.aa.	234	8.20E-27
f291.aa	W20528	H. pylori cell envelope transporter protein 4882763.aa.	234	8.20E-27
f291.aa	W20592	H. pylori transporter protein, 01ce11513orf21.	168	7.60E-17
f301.aa	W20287	H. pylori inner membrane protein, 24132293.aa.	158	1.60E-13
f301.aa	W20916	H. pylori inner membrane protein 14gp12015orf12.	158	1.90E-13
f301.aa	W20769	H. pylori inner membrane protein, 07ee20513orf28.	158	2.40E-13
f301.aa	W05196	Helicobacter pylori 50 kDa protective antigen G3.8.	157	2.80E-13
f301.aa	W20767	H. pylori cytoplasmic protein, 07ee20513orf1.	138	4.30E-11

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f320.aa	R24300	Glycopeptide resistance protein VanY from E.faecium.	142	2.90E-14
f328.aa	R15642	CTP synthetase.	274	3.00E-50
f328.aa	W20778	H. pylori cytoplasmic protein, 07ge20415orf6.	122	1.90E-34
f352.aa	W03626	Human thyrotropin GPR N-terminal sequence.	153	4.70E-12
f352.aa	W21591	Antibiotic potentiating peptide #3.	152	6.60E-12
f352.aa	W03627	Human follicle stimulating hormone GPR N-terminal sequence.	145	5.30E-11
f4-50.aa	W07187	B. garinii IP90 decorin binding protein.	305	1.30E-41
f4-50.aa	W07186	B. afzelii strain pGau decorin binding protein.	161	1.60E-34
f4-50.aa	W07185	B. burgdorferi HB-19 decorin binding protein.	173	2.80E-34
f4-50.aa	W07183	B. burgdorferi B31 decorin binding protein.	176	1.80E-33
f4-50.aa	W07190	B. burgdorferi JD1 decorin binding protein.	177	1.80E-33
f4-50.aa	W07182	B. burgdorferi 297 decorin binding protein.	177	1.10E-32
f4-50.aa	W07189	B. burgdorferi LP7 decorin binding protein.	177	1.10E-32
f4-50.aa	W07188	B. burgdorferi LP4 decorin binding protein.	177	3.90E-32
f4-50.aa	W07184	B. burgdorferi Sh.2.82 decorin binding protein.	177	1.30E-31
f45-2.aa	R89476	B. burgdorferi OspG lipoprotein.	213	1.30E-35
f45-2.aa	R70491	Leucocytozoan protozoa structural protein epitope.	206	2.10E-20
f45-2.aa	W03626	Human thyrotropin GPR N-terminal sequence.	211	6.10E-20
f45-2.aa	W03627	Human follicle stimulating hormone GPR N-terminal sequence.	202	8.90E-19
f45-2.aa	R69629	B. burgdorferi OspF operon.	111	1.10E-14
f45-2.aa	W30763	Mannose-1-phosphate transferase protein MNN4.	166	1.00E-13
f45-2.aa	R97866	Chicken leucocytozoan immunogenic protein for use in vaccines.	154	7.10E-12
f488.aa	W15078	M. leprae gyrA precursor.	390	2.70E-143
f488.aa	R88733	S.aureus mutant grlA protein.	698	6.70E-122
f488.aa	R88731	S.aureus topoisomerase IV grlA subunit.	698	6.70E-122
f49-2.aa	W22676	Borrelia variable major protein (VMP)-like protein VlsE.	497	2.70E-75
f5-14.aa	W03626	Human thyrotropin GPR N-terminal sequence.	234	6.60E-23
f5-14.aa	W03627	Human follicle stimulating hormone GPR N-terminal sequence.	231	1.40E-22
f5-14.aa	R70491	Leucocytozoan protozoa structural protein epitope.	221	1.00E-20
f5-14.aa	W30763	Mannose-1-phosphate transferase protein MNN4.	203	1.60E-18
f5-14.aa	R97866	Chicken leucocytozoan immunogenic protein for use in vaccines.	187	2.10E-15

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f5-14.aa	W21591	Antibiotic potentiating peptide #3.	176	4.60E-15
f5-14.aa	R69629	B. burgdorferi OspF operon.	106	3.50E-13
f5-14.aa	R89476	B. burgdorferi OspG lipoprotein.	157	6.20E-13
f5-14.aa	W26536	Trypanosoma cruzi antigen.	143	5.00E-11
f5-15.aa	R69629	B. burgdorferi OspF operon.	448	1.30E-68
f5-15.aa	R89476	B. burgdorferi OspG lipoprotein.	105	5.80E-24
f502.aa	R69852	Ethylene response (ETR) mutant protein etr1-3.	191	1.90E-35
f502.aa	R69849	Ethylene response (ETR) gene product.	191	2.70E-35
f502.aa	R69853	Ethylene response (ETR) mutant protein etr1-4.	191	2.70E-35
f502.aa	R69850	Ethylene response (ETR) mutant protein etr1-1.	191	3.60E-35
f502.aa	R69851	Ethylene response (ETR) mutant protein etr1-2.	191	3.60E-35
f502.aa	R74632	QETR ethylene response (ETR) protein from Arabidopsis thaliana.	190	5.20E-26
f502.aa	R74629	Tomato ethylene response (TETR) protein.	171	6.50E-23
f502.aa	R74633	Nr (never ripe) tomato ethylene response (ETR) protein.	171	6.50E-23
f502.aa	R74630	Tomato TGETR1 ethylene response protein.	123	1.20E-19
f51-2.aa	W03626	Human thyrotropin GPR N-terminal sequence.	235	2.90E-23
f51-2.aa	R89476	B. burgdorferi OspG lipoprotein.	109	6.90E-23
f51-2.aa	W03627	Human follicle stimulating hormone GPR N-terminal sequence.	228	2.20E-22
f51-2.aa	W30763	Mannose-1-phosphate transferase protein MNN4.	203	1.00E-18
f51-2.aa	R70491	Leucocytozoan protozoa structural protein epitope.	191	7.50E-18
f51-2.aa	R97866	Chicken leucocytozoan immunogenic protein for use in vaccines.	183	4.80E-16
f51-2.aa	W21591	Antibiotic potentiating peptide #3.	159	6.20E-13
f51-2.aa	R68838	Plasmodium falciparum ABRA gene protein.	142	1.10E-12
f51-2.aa	R27530	Plasmodium falciparum bloodand liver stage ABRA antigen.	142	2.80E-12
f51-2.aa	W31186	Human p160 polypeptide 160.2.	148	2.30E-11
f51-2.aa	W31185	Human p160 polypeptide 160.1.	148	2.40E-11
f517.aa	W24296	Staphylococcus aureus Gene #1 polypeptide sequence 2.	237	6.80E-30
f541.aa	R31013	P39-alpha.	1253	3.80E-229
f541.aa	R33280	P39-beta.	504	1.90E-117
f542.aa	R33280	P39-beta.	711	3.20E-96
f542.aa	R31013	P39-alpha.	101	7.90E-16

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f561.aa	R69631	B. burgdorferi T5 protein.	982	6.90E-131
f598.aa	W20289	H. pylori transporter protein, 24218968.aa.	264	9.90E-33
f598.aa	W20640	H. pylori transporter protein, 02ce11022orf8.	264	1.00E-30
f598.aa	W20101	H. pylori transporter protein 11132778.aa.	233	8.50E-27
f598.aa	W20861	H. pylori cell envelope transporter protein, 12ge10305orf16.	233	9.60E-27
f598.aa	W34202	Streptomyces efflux pump protein (frenolicin gene D product).	196	2.80E-21
f598.aa	R71091	C. jejuni PEB1A antigen from ORF3.	168	1.20E-17
f600.aa	W25527	Staphylococcus aureus Gene #20 polypeptide sequence 2.	209	3.40E-26
f600.aa	W34201	Streptomyces efflux pump protein (frenolicin gene C product).	169	6.50E-19
f600.aa	W20639	H. pylori transporter protein, 02ce11022orf7.	127	1.10E-14
f603.aa	W34200	Streptomyces efflux pump protein (frenolicin gene B product).	155	7.40E-32
f604.aa	R48035	Hyaluronic acid synthase of Streptococcus equisimilis.	110	2.30E-20
f606.aa	R48035	Hyaluronic acid synthase of Streptococcus equisimilis.	116	1.20E-25
f607.aa	R48035	Hyaluronic acid synthase of Streptococcus equisimilis.	141	1.50E-26
f631.aa	W15192	Staphylococcus aureus cell surface protein.	160	7.30E-29
f664.aa	W20105	H. pylori flagella-associated protein, 1171928.aa.	202	3.20E-46
f664.aa	W20688	H. pylori flagella-associated protein 04ge11713orf5.	202	2.60E-45
f664.aa	R97245	Virulence gene cluster polypeptide product.	158	3.90E-13
f704.aa	R60153	Nematode-inducible transmembrane pore protein.	104	2.50E-18
f704.aa	R33913	Sequence encoded by TobRB7-5A which encodes a membrane channel	104	2.50E-18
f704.aa	R77082	Tobacco root specific promoter RB7 from clone lambda5A (TobRB7-5A).	104	2.50E-18
f742.aa	W46499	Amino acid sequence of the spindly (SPY) protein of Arabidopsis.	101	2.50E-14
f752.aa	W20733	H. pylori cell envelope protein, 06cp11722orf15.	141	3.00E-37
f752.aa	W20358	H. pylori cell envelope protein 26366312.aa.	110	4.20E-18
f814.aa	W20753	H. pylori transporter protein, 06gp11202orf7.	178	7.90E-35
f814.aa	W20420	H. pylori cell envelope transporter protein 33399142.aa.	160	2.30E-21
f843.aa	R14319	Human T-cell immunosuppressive factor.	167	1.20E-19
f860.aa	W21894	Asparaginyl-tRNA synthetase from Staphylococcus aureus.	245	2.30E-38
f860.aa	W33903	Streptococcus pneumoniae asparaginyl tRNA synthetase.	177	1.10E-22
f867.aa	W34261	An alpha subunit of a thermostable ATPase.	592	1.30E-161
f867.aa	R10098	Alpha subunit of ATP-synthase.	741	4.90E-144

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f867.aa	R31522	Carrot reverse transcriptase.	311	4.60E-130
f867.aa	R10099	Beta subunit of ATP-synthase.	121	7.90E-14
f867.aa	W34262	A beta subunit of a thermostable ATPase.	116	1.00E-12
f868.aa	W34262	A beta subunit of a thermostable ATPase.	151	6.10E-109
f868.aa	R10099	Beta subunit of ATP-synthase.	172	1.90E-106
f868.aa	W34261	An alpha subunit of a thermostable ATPase.	117	3.10E-19
f868.aa	R10098	Alpha subunit of ATP-synthase.	113	2.00E-18
f868.aa	R31522	Carrot reverse transcriptase.	101	7.10E-15
f874.aa	R10591	L-lactic acid dehyrogenase.	538	7.20E-109
f874.aa	R08355	Recombinant thermophilic NAD-dependant dehydrogenase.	455	9.80E-99
f874.aa	R09295	Recombinant thermophilic NAD-dependant dehydrogenase.	455	9.80E-99
f874.aa	R15736	L-lactic acid dehydrogenase.	426	1.60E-85
f874.aa	P91948	Pig H4 isoenzyme.	393	2.00E-82
f874.aa	W33108	Chicken lactic acid dehydrogenase type B subunit.	390	2.20E-80
f874.aa	W33107	Chicken lactic acid dehydrogenase type B subunit.	385	1.10E-79
f874.aa	P80891	Testis-specific lactate dehydrogenase subunit LDH-C4.	339	5.50E-74
f874.aa	R94013	Heat resistant maleate dehydrogenase.	255	1.30E-55
f874.aa	R11119	Recombinant L-2-hydroxyisocaproic acid dehydrogenase.	224	7.90E-49
f874.aa	R62605	P. falciparum lactate dehydrogenase.	255	2.00E-44
f874.aa	W11476	Eimeria lactate dehydrogenase.	203	1.10E-25
f943.aa	P91223	Coenzyme-independent L-sorbosone dehydrogenase from Gluconobacter	175	4.30E-16

TABLE 3. Conservative Amino Acid Substitutions.

Aromatic	Phenylalanine Tryptophan Tyrosine
Hydrophobic	Leucine Isoleucine Valine
Polar	Glutamine Asparagine
Basic	Arginine Lysine Histidine
Acidic	Aspartic Acid Glutamic Acid
Small	Alanine Serine Threonine Methionine Glycine

TABLE 4. Residues Comprising Epito-Bearing Fragments

Query	Residues Comprising Epito-Bearing Fragments
f101.aa	from about Lys-62 to about Gly-64, from about Ser-111 to about Asp-113, from about Arg-136 to about Arg-139, from about Pro-189 to about Asn-193.
f11.aa	from about Pro-38 to about Lys-40, from about Glu-92 to about Lys-96.
f12.aa	from about Pro-288 to about Asp-290, from about Asn-336 to about Gly-338, from about Tyr-410 to about Gly-413, from about Asp-418 to about Arg-420, from about Pro-552 to about Val-555, from
	about Gln-643 to about Asp-645, from about Gln-1061 to about Arg-1063, from about Asn-1130 to about Lys-1132.
f129.aa	from about Glu-76 to about Arg-81, from about Lys-144 to about Asn-146.
f147.aa	from about Gln-94 to about Thr-96.
f152.aa	from about Gly-35 to about Gly-37, from about Gln-321 to about Gly-323.
f154.aa	from about Asn-39 to about Lys-41, from about Ser-74 to about Lys-77, from about Ser-213 to about Gly-215, from about Ser-303 to about Asp-306, from about Asp-422 to about Asn-424.
f157.aa	from about Lys-21 to about Asp-24, from about Ser-45 to about Tyr-47.
f17.aa	from about Arg-17 to about Asn-20, from about Thr-94 to about Gly-96.
f186.aa	from about Lys-305 to about Tyr-308.
f196.aa	from about Lys-121 to about Asn-123, from about Pro-278 to about Lys-282, from about Glu-576 to about Tyr-578.
f899.aa	from about Asn-174 to about Asp-177.
f925.aa	from about Lys-201 to about Asp-204, from about Phe-291 to about Lys-294.
f929.aa	from about Pro-139 to about Asn-141, from about Arg-211 to about Glu-214, from about Thr-370 to about Asn-375.
f933.aa	from about Ser-139 to about Lys-143.
f940.aa	from about Gly-143 to about Asn-148.
f943.aa	from about Asp-58 to about Asp-60, from about Lys-157 to about Asn-159, from about Asp-217 to about Asp-221, from about Lys-250 to about Asn-254, from about Pro-262 to about Asn-264, from about Gly-305 to about Trp-307.
f952.aa	from about Ser-52 to about Ser-54.
f4.aa	from about Arg-64 to about Arg-67.
f43.aa	from about Ser-84 to about Gln-87, from about Asp-231 to about Tyr-233, from about Arg-296 to about Asp-300.
f50.aa	from about Glu-136 to about Gly-138, from about Asp-153 to about Lys-155, from about Asp-289 to about Asp-291, from about Glu-458 to about Asn-461.
f65.aa	from about Glu-120 to about Asp-122, from about Pro-204 to about Tyr-206.
f8.aa	from about Pro-263 to about Arg-265, from about Asp-274 to about Lys-278.
f82.aa	from about Tyr-66 to about Gly-68, from about Ser-116 to about Lys-119, from about Asp-121 to about Gly-123, from about Pro-128 to about Gly-131.

TABLE 4. Residues Comprising Epito-Bearing Fragments

f86.aa	from about Asn-179 to about Asn-181, from about Lys-192 to about Asn-194, from about Lys-270 to about Asn-272, from about Lys-279 to about Lys-282, from about Asp-331 to about Asn-333.
f477.aa	from about Pro-250 to about Lys-253.
f488.aa	from about Lys-76 to about Lys-79, from about Asn-486 to about Asp-489, from about Lys-508 to about Gly-510, from about Asn-559 to about Gly-562.
f494.aa	from about Lys-76 to about Asn-78.
f516.aa	from about Lys-32 to about Asp-34.
f523.aa	from about Pro-202 to about Asn-206, from about Lys-255 to about Tyr-258.
f526.aa	from about Asn-85 to about Lys-88, from about Asp-136 to about Gly-138.
f577.aa	from about Cys-18 to about Lys-22, from about Asn-297 to about Gln-300.
f584.aa	from about Pro-131 to about Lys-133, from about Pro-200 to about Ser-202.
f596.aa	from about Arg-42 to about Asp-44, from about Asp-117 to about Tyr-119, from about Pro-205 to about Asp-207.
f600.aa	from about Pro-143 to about Asp-145.
f603.aa	from about Phe-35 to about Ser-37.
f607.aa	from about Gln-67 to about Lys-70, from about Asp-273 to about Tyr-275, from about Asp-333 to about Gly-338, from about Pro-359 to about Lys-362, from about Arg-409 to about Gly-411.
f611.aa	from about Arg-133 to about Gly-135.
f631.aa	from about Pro-132 to about Asn-136, from about Asn-159 to about Tyr-161, from about Pro-216 to about Asp-218, from about Pro-220 to about Lys-223.
f688.aa	from about Lys-266 to about Asp-268, from about Lys-271 to about Asn-273, from about Lys-315 to about Lys-318.
f704.aa	from about Lys-250 to about Lys-253.
f707.aa	from about Lys-131 to about Asp-134, from about Asp-246 to about Asn-249.
f709.aa	from about Tyr-39 to about Gly-42, from about Lys-148 to about Gly-150, from about Arg-269 to about Gly-272, from about Ser-466 to about Tyr-468, from about Asn-489 to about Asn-491, from
	about Lys-575 to about Asp-578, from about Pro-642 to about Lys-644.
f197.aa	from about Pro-217 to about Asp-219, from about Glu-675 to about Asp-678, from about Pro-687 to about Asn-689, from about Glu-694 to about Gln-696.
f200.aa	from about Arg-174 to about Phe-179.
f208.aa	from about Arg-326 to about Ser-328.
f210.aa	from about Pro-191 to about Ile-194.
f221.aa	from about Asn-133 to about Asn-135.
f253.aa	from about Arg-191 to about Gly-194.
f269.aa	from about Ser-271 to about Thr-273, from about Asp-284 to about Gly-286.
f29.aa	from about Pro-159 to about Ser-161.
f290.aa	from about Pro-240 to about Gly-244.
f291.aa	from about Gln-267 to about Lys-269.

TABLE 4. Residues Comprising Epito-Bearing Fragments

f296.aa	from about Glu-98 to about Lys-101.
f3.aa	from about Asn-241 to about Lys-245.
f30.aa	from about Asn-156 to about Tyr-159, from about Asn-178 to about Lys-180.
f939.aa	from about Ser-245 to about Asn-249.
f739.aa	from about Asn-80 to about Tyr-82, from about Lys-208 to about Ser-210.
f742.aa	from about Ser-141 to about Asp-145, from about Asn-222 to about Gln-225, from about Asp-243 to about Tyr-247, from about Asn-249 to about Asn-251.
f743.aa	from about Arg-111 to about Gly-114, from about Pro-131 to about Asp-134.
f790.aa	from about Thr-40 to about Asn-42, from about Ser-53 to about Ser-55, from about Lys-215 to about Asp-218, from about Asn-274 to about Gly-277.
f792.aa	from about Val-82 to about Ser-84, from about Ser-102 to about Asn-104, from about Gln-127 to about Tyr-130, from about Lys-309 to about Asn-314, from about Lys-375 to about Thr-377, from
	about Pro-511 to about His-513, from about Thr-515 to about Asp-517.
f797.aa	from about Pro-119 to about Gly-122, from about Lys-166 to about Asn-169.
f799.aa	from about Asn-31 to about Asn-34, from about Gln-44 to about Asn-47, from about Pro-123 to about Gly-125.
f814.aa	from about Ser-120 to about Ser-122, from about Arg-636 to about Asn-638, from about Cys-967 to about Ser-969.
f820.aa	from about Thr-563 to about Tyr-565.
f850.aa	from about Tyr-159 to about Tyr-164, from about Gln-375 to about Asp-379.
f853.aa	from about Thr-180 to about Lys-184, from about Arg-231 to about Asp-233, from about Asn-252 to about Gly-254.
f859.aa	from about Lys-46 to about Ser-52, from about Pro-88 to about Asn-91, from about Asn-117 to about Asp-120.
f861.aa	from about Asp-38 to about Lys-40, from about Lys-219 to about Asn-225.
f368.aa	from about Gln-228 to about Asn-231.
f371.aa	from about Tyr-109 to about Asn-111, from about Asn-162 to about Gln-164.
f502.aa	from about Asn-118 to about Lys-122, from about Ser-269 to about Gly-271, from about Lys-370 to about Asp-373, from about Asn-509 to about Lys-511, from about Lys-705 to about Arg-707, from
	about Thr-912 to about Gly-914, from about Pro-1213 to about Asp-1216, from about Asn-1491 to about Arg-1493.
f527.aa	from about Cys-20 to about Gln-22, from about Asn-38 to about Asn-40, from about Phe-112 to about Asp-114, from about Lys-160 to about Asn-162, from about Ser-199 to about Asp-201, from about
	Gln-258 to about Gly-261, from about Arg-282 to about Asn-284, from about Ser-297 to about Asp-299.
f541.aa	from about Ser-68 to about Asn-71.
f604.aa	from about Lys-77 to about Gly-79, from about Lys-201 to about Asn-203, from about Asp-252 to about Asp-254, from about Tyr-

TABLE 4. Residues Comprising Epito-Bearing Fragments

	347 to about Gly-350, from about Asp-514 to about Trp-516.
f736.aa	from about Lys-20 to about Asn-24, from about Arg-147 to about Ser-153, from about Ser-231 to about Lys-233.
f752.aa	from about Thr-119 to about Lys-122, from about Pro-420 to about Gly-422.
f798.aa	from about Asp-33 to about Thr-36, from about Lys-180 to about His-183.
f635.aa	from about Pro-100 to about Asn-102, from about Asp-145 to about Phe-147.
f32.aa	from about Lys-18 to about Asn-20.
f320.aa	from about Asn-193 to about Leu-195, from about Gln-248 to about Lys-250.
f352.aa	from about Ser-46 to about Asn-49.
f301.aa	from about Lys-178 to about Lys-180, from about Ser-401 to about Tyr-404.
f373.aa	from about Gly-88 to about Lys-90, from about Asn-539 to about Lys-542, from about Glu-654 to about Ser-657.
f384.aa	from about Pro-250 to about Asn-252, from about Asp-266 to about Lys-268.
f446.aa	from about Asp-20 to about Ser-26, from about Asn-146 to about Lys-149.
f542.aa	from about Arg-86 to about Gly-88, from about Arg-163 to about Asn-165.
f93.aa	from about Asn-152 to about Asp-155.
f105.aa	from about Asp-48 to about Phe-50.
f150.aa	from about Thr-214 to about Asp-218, from about Asp-256 to about Asp-259.
f219.aa	from about Asn-77 to about Asn-81, from about Asp-111 to about Asn-115.
f229.aa	from about Gln-61 to about Asn-63.
f32.aa	from about Lys-18 to about Asn-20.
f186.aa	from about Lys-305 to about Tyr-308.
f216.aa	from about Ser-105 to about Asn-107.
f328.aa	from about Asn-105 to about Asp-107.
f352.aa	from about Ser-46 to about Asn-49.
f867.aa	from about Thr-3 to about Gly-5, from about Lys-156 to about Ser-159.
f868.aa	from about Arg-94 to about Gly-96, from about Pro-257 to about Gly-261, from about Pro-295 to about Asp-297, from about Arg-340 to about Asp-342.
f872.aa	from about Ser-19 to about Lys-23, from about Thr-139 to about Asp-142, from about Ser-282 to about Tyr-286, from about Ser-311 to about Ser-313.
f886.aa	from about Thr-83 to about Asp-85, from about Asp-106 to about Lys-108, from about Lys-143 to about Gly-147, from about Asp-186 to about Asn-191.
f888.aa	from about Asn-65 to about Asp-67.
f893.aa	from about Asn-203 to about Asn-207, from about Thr-446 to about Asn-450.
f605.aa	from about Arg-31 to about Asp-33.
f606.aa	from about Asn-68 to about Gly-71, from about Asn-136 to about

TABLE 4. Residues Comprising Epito-Bearing Fragments

	Lys-139, from about Asn-223 to about Tyr-226, from about Ser-276 to about Tyr-279, from about Pro-362 to about Asn-365, from
	about Arg-503 to about Trp-507.
f679.aa	from about Lys-154 to about Asp-156, from about Lys-224 to about Arg-226, from about Asn-260 to about Asp-264, from about Glu-363 to about Lys-366, from about Asp-387 to about Gly-389, from
	about Tyr-441 to about Lys-443, from about Arg-501 to about Tyr-504.
f11-12.aa	from about Pro-91 to about Asn-93, from about Pro-181 to about Asp-186, from about Lys-244 to about Ser-248.
f11-4.aa	from about Asn-160 to about Lys-163.
f14-8.aa	from about Pro-92 to about Gln-95, from about Lys-123 to about Thr-125, from about Lys-215 to about Asp-219.
f17-6.aa	from about Pro-36 to about Glu-38.
f19-2.aa	from about Ser-104 to about Ser-106, from about Gln-230 to about Asn-232.
f19-4.aa	from about Val-79 to about Thr-82, from about Pro-195 to about Gly-201.
f19-6.aa	from about Asp-24 to about Lys-30, from about Pro-36 to about Glu-38.
f21-4.aa	from about Cys-24 to about Asn-26.
f28-2.aa	from about Ser-77 to about Lys-80, from about Tyr-274 to about Asn-277.
f28-3.aa	from about Glu-53 to about Arg-57, from about Gln-82 to about Asn-85, from about Gln-157 to about Asn-159.
f31-2.aa	from about Arg-95 to about Arg-97, from about Asn-297 to about Asn-299.
f4-15.aa	from about Pro-182 to about Asp-184, from about Lys-220 to about Asp-222.
f4-50.aa	from about Thr-109 to about Asn-111.
f42-1.aa	from about Asn-55 to about Asn-57, from about Arg-81 to about Ser-84, from about Asp-94 to about Asn-97.
f45-2.aa	from about Asn-83 to about Gly-86.
f47-2.aa	from about Ser-29 to about Asp-33, from about Asn-94 to about Lys-99, from about Pro-152 to about Lys-157.
f49-2.aa	from about Asn-452 to about Gly-454.
f5-14.aa	from about Glu-102 to about Asp-106, from about Thr-272 to about Asn-275, from about Glu-313 to about Asn-315, from about Ser-370 to about Ser-372.
f5-15.aa	from about Lys-170 to about Gly-173, from about Asn-194 to about Gly-196.
f51-2.aa	from about Asp-302 to about Lys-304.
f6-21.aa	from about Glu-38 to about Asn-42, from about Arg-84 to about Gly-87.
f6-27.aa	from about Asp-67 to about Asn-69, from about Arg-85 to about Asn-89, from about Lys-168 to about Gly-171, from about Lys-179 to about Asn-181, from about Ser-380 to about His-382.
f6-5.aa	from about Ser-67 to about Asn-71.
f7-30.aa	from about Pro-94 to about Asp-96, from about Lys-144 to about Arg-147.
f76-1.aa	from about Asn-30 to about Lys-35, from about Lys-113 to about

TABLE 4. Residues Comprising Epito-Bearing Fragments

	Gly-116, from about Glu-119 to about Lys-121.
f8-10.aa	from about Pro-25 to about Lys-32, from about Ser-168 to about Thr-172.
f01a.aa_bb001	from about Pro-123 to about Asp-125, from about Ser-179 to about Asp-181, from about Lys-255 to about Gly-259.
_bb0011	from about Ala8 about Arg 17, from about Tyr31 to about Gly40, from about Ser65 to about Lys78, from about Val93 to about Asp102, from about Ser120 to about Ile129, from about Pro156 to about Glu170, from about Lys187 to about Asn 196, from about His205 to about Lys214, from about Gly226 to about Glu235, fro about Gln253 to about Asn266, from about Glu283 to about Glu293, from about Leu311 to about Ile320, from about Arg326 to about Gly335, from about Pro340 to about Ala349
f02a.aa_bb002	from about Tyr-169 to about Asn-171, from about Tyr-242 to about Asn-245, from about Lys-264 to about Asp-267.
_bb9	from about Met7 to about Lys16, from about Lys47 to about Ser57, from about Asn80 to about Ser89, from about Gly103 to about Glu113, from about Lys125 to about Pro133, from about Lys138 to about Ala147
f03a.aa_bb006	from about Asp-54 to about Thr-57, from about Lys-201 to about His-204.
_bb014	from about Pro23 to about Gln31, from about Ser37 to about Asp45, from about Leu76 to about Asn84, from about Leu76 to about Val84, from about Ser89 to about Asn97, from about Ser105 to about Lys113, from about Asn120 to about Met128, from about Asn159 to about Gly 167, from about Lys173 to about Bal181
_bb023	from about Asp17 to about Gly27, from about Arg40 to about Asp48, from about Val64 to about Asp72, from about Glu105 to about Thr113, from about Ser141 to about Gly150, from about Asp155 to about Ile163, from about Asn184 to about Lys198, from about Ile219 to about Pro227, from about Ser230 to about Phe238, from about Ser241 to about Asn250, from about Asp270 to about Val278, from about Ser285 to about Leu293, from about Glyu307 to about Ser315, from about Lys327 to about Asn335
f08a.aa_bb024	from about Asn-30 to about Asp-33, from about Ser-116 to about Asn-118, from about Asn-154 to about Gly-156.
f09a.aa_bb025	from about Asn-30 to about Ser-35, from about Thr-145 to about Asn-148.

Applicant's or agent's file reference number PB370PCT2	International application No. Unassigned

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 8, line 8.

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☐

Name of depositary institution
American Type Culture Collection

Address of depositary institution (*including postal code and country*)
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit **August 8, 1998**	Accession Number **202012**

C. ADDITIONAL INDICATIONS (*leave blank if not applicable*) This information is continued on an additional sheet ☐

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (*If the indications are not for all designated States*)

E. SEPARATE FURNISHING OF INDICATIONS (*leave blank if not applicable*)

The indications listed below will be submitted to the International Bureau later (*specify the general nature of the indications, e.g., "Accession Number of Deposit"*)

For receiving Office use only	For International Bureau use only
☐ This sheet was received with the international application	☐ This sheet was received by the International Bureau on:
Authorized officer	Authorized officer

What Is Claimed Is:

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence encoding any one of the amino acid sequences of the polypeptides shown in Table 1; or

(b) a nucleotide sequence complementary to any one of the nucleotide sequences in (a).

(c) a nucleotide sequence at least 95% identical to any one of the nucleotide sequences shown in Table 1; or,

(d) a nucleotide sequence at least 95% identical to a nucleotide sequence complementary to any one of the nucleotide sequences shown in Table 1.

2. An isolated nucleic acid molecule of claim 1 comprising a polynucleotide which hybridizes under stringent hybridization conditions to a polynucleotide having a nucleotide sequence identical to a nucleotide sequence in (a) or (b) of claim 1.

3. An isolated nucleic acid molecule of claim 1 comprising a polynucleotide which encodes an epitope-bearing portion of a polypeptide in (a) of claim 1.

4. The isolated nucleic acid molecule of claim 3, wherein said epitope-bearing portion of a polypeptide comprises an amino acid sequence listed in Table 4.

5. A method for making a recombinant vector comprising inserting an isolated nucleic acid molecule of claim 1 into a vector.

6. A recombinant vector produced by the method of claim 5.

7. A host cell comprising the vector of claim 6.

8. A method of producing a polypeptide comprising:

(a) growing the host cell of claim 7 such that the protein is expressed by the cell; and

(b) recovering the expressed polypeptide.

9. An isolated polypeptide comprising a polypeptide selected from the group consisting of:

(a) a polypeptide consisting of one of the complete amino acid sequences of Table 1;
(b) a polypeptide consisting of one the complete amino acid sequences of Table 1 except the N-terminal residue;
(c) a fragment of the polypeptide of (a) having biological activity; and
(d) a fragment of the polypeptide of (a) which binds to an antibody specific for the polypeptide of (a).

10. An isolated antibody specific for the polypeptide of claim 9.

11. A polypeptide produced according to the method of claim 8.

12. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of an amino acid sequence of any one of the polypeptides in Table 1.

13. An isolated polypeptide antigen comprising an amino acid sequence of an *B. burgdorferi* epitope shown in Table 4.

14. An isolated nucleic acid molecule comprising a polynucleotide with a nucleotide sequence encoding a polypeptide of claim 9.

15. A hybridoma which produces an antibody of claim 10.

16. A vaccine, comprising:
(1) one or more *B. burgdorferi* polypeptides selected from the group consisting of a polypeptide of claim 9; and
(2) a pharmaceutically acceptable diluent, carrier, or excipient;
wherein said polypeptide is present, in an amount effective to elicit protective antibodies in an animal to a member of the *Borrelia* genus.

17. A method of preventing or attenuating an infection caused by a member of the *Borrelia* genus in an animal, comprising administering to said animal a polypeptide of claim 9, wherein said polypeptide is administered in an amount effective to prevent or attenuate said infection.

18. A method of detecting *Borrelia* nucleic acids in a biological sample comprising:
(a) contacting the sample with one or more nucleic acids of claim 1, under conditions such that hybridization occurs, and
(b) detecting hybridization of said nucleic acids to the one or more *Borrelia* nucleic acid

sequences present in the biological sample.

19. A method of detecting *Borrelia* nucleic acids in a biological sample obtained from an animal, comprising:

(a) amplifying one or more *Borrelia* nucleic acid sequences in said sample using polymerase chain reaction, and

(b) detecting said amplified *Borrelia* nucleic acid.

20. A kit for detecting *Borrelia* antibodies in a biological sample obtained from an animal, comprising

(a) a polypeptide of claim 9 attached to a solid support; and

(b) detecting means.

21. A method of detecting *Borrelia* antibodies in a biological sample obtained from an animal, comprising

(a) contacting the sample with a polypeptide of claim 9; and

(b) detecting antibody-antigen complexes.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/12718

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :C12Q 1/68
US CL :435/6
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 5,466,577 A (WEISBURG) 14 November 1995, Abstract and claim 7.	19
X	US 5,582,990 A (BERGSTROM ET AL.) 10 December 1996, Abstract and claim 12.	19

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier document published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
02 SEPTEMBER 1998	OCT 13 1998

Name and mailing address of the ISA/US	Authorized officer
Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231	Dorthea Lawrence For JAMES MARTINELL
Facsimile No. (703) 305-3230	Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)★

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/12718

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: 1-18, 20, and 21
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

The claims refer to tables of nucleotide and amino acid sequences. No sequence data were submitted in computer readable form in the instant application. Accordingly, no meaningful search can be performed for claims 1-18, 20, and 21.

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

B. FIELDS SEARCHED
Electronic data bases consulted (Name of data base and where practicable terms used):

APS, STN Online
borrel?, burgdorfii, afzelii, garinii, andersonii, anserina, japonica, coriaceae, lyme(w)disease, sensu, lato, stricto, pcr, polymerase(w)chain(w)reaction#